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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:25:44 ; Search time 5.27586 Seconds
(without alignments)
21.698 Million cell updates/sec

Title: US-10-720-323-2

Perfect score: 88

Sequence: 1 VISFDGSKYVDVSKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubaa/US09 NEW PUB pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US06 NEW PUB pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US07 NEW PUB pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US08 NEW PUB pep.*
- 5: /cgn2_6/ptodata/1/pubaa/PCT NEW PUB pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US10 NEW PUB pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US11 NEW PUB pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US60 NEW PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	96.6	249	7	US-11-054-515-1109
2	81	92.0	98	7	US-11-054-669-23
3	81	92.0	98	7	US-11-054-669-24
4	81	92.0	98	7	US-11-054-669-25
5	81	92.0	98	7	US-11-054-669-34
6	81	92.0	115	6	US-10-952-535A-2
7	81	92.0	117	7	US-11-127-677-9
8	81	92.0	117	7	US-11-127-677-18
9	81	92.0	120	7	US-11-127-677-12
10	81	92.0	124	7	US-11-127-677-48
11	81	92.0	126	7	US-11-127-677-43
12	81	92.0	238	7	US-11-054-515-1931
13	81	92.0	239	6	US-10-952-535A-6
14	81	92.0	241	7	US-11-054-515-2055
15	81	92.0	247	7	US-11-054-515-924
16	81	92.0	247	7	US-11-054-515-1330
17	81	92.0	248	7	US-11-054-515-1421
18	81	92.0	249	7	US-11-054-515-5
19	81	92.0	249	7	US-11-054-515-397
20	81	92.0	249	7	US-11-054-515-892
21	81	92.0	249	7	US-11-054-515-911
22	81	92.0	249	7	US-11-054-515-1102
23	81	92.0	249	7	US-11-054-515-1105
24	81	92.0	249	7	US-11-054-515-1108
25	81	92.0	249	7	US-11-054-515-1110
26	81	92.0	249	7	US-11-054-515-1111
27	81	92.0	249	7	US-11-054-515-1113
28	81	92.0	249	7	US-11-054-515-1115
29	81	92.0	249	7	US-11-054-515-1117
30	81	92.0	249	7	US-11-054-515-1119
31	81	92.0	249	7	US-11-054-515-1121
32	81	92.0	249	7	US-11-054-515-1123
33	81	92.0	252	7	US-11-054-515-1201
34	81	92.0	252	7	US-11-054-515-1201
35	81	92.0	252	7	US-11-054-515-1201
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42	78	88.6	245	7	US-11-054-515-1201
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49	76	86.4	249	7	US-11-054-515-1118
50	75	85.2	248	7	US-11-054-515-914
51	75	85.2	248	7	US-11-054-515-916
52	75	85.2	248	7	US-11-054-515-1323
53	75	85.2	251	7	US-11-054-515-1114
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56	74	84.1	98	7	US-11-054-669-26
57	74	84.1	98	7	US-11-084-554-35
58	74	84.1	98	7	US-11-093-274-31
59	74	84.1	124	7	US-11-040-159-14
60	74	84.1	244	7	US-11-054-515-1910
61	74	84.1	249	7	US-11-054-515-1120
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63	73	83.0	126	7	US-11-155-775-18
64	72	81.8	240	7	US-11-054-515-1898
65	72	81.8	247	7	US-11-054-515-1912
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67	72	81.8	248	7	US-11-054-515-1890
68	72	81.8	249	7	US-11-054-515-1956
69	72	81.8	251	7	US-11-054-515-952
70	72	81.8	251	7	US-11-054-515-982
71	72	81.8	252	7	US-11-054-515-1690
72	71	80.7	17	7	US-11-093-274-4
73	71	80.7	117	7	US-11-093-274-19
74	71	80.7	239	7	US-11-054-515-1882
75	71	80.7	244	7	US-11-054-515-1933
76	70	79.5	17	7	US-11-093-274-5
77	70	79.5	116	7	US-11-093-274-20
78	70	79.5	124	7	US-11-040-159-16
79	70	79.5	243	7	US-11-054-515-1935
80	70	79.5	248	7	US-11-054-515-835
81	70	79.5	249	7	US-11-054-515-1004
82	70	79.5	249	7	US-11-054-515-896
83	70	79.5	253	7	US-11-054-515-1200
84	70	79.5	253	7	US-11-054-515-1337
85	70	79.5	477	7	US-11-000-463-395
86	69	78.4	112	7	US-11-127-677-3
87	69	78.4	234	7	US-11-054-515-1759
88	68	77.3	238	7	US-11-054-515-2053
89	68	77.3	251	7	US-11-054-515-1411
90	67	76.1	125	7	US-11-155-775-22
91	67	76.1	125	7	US-11-155-775-30
92	67	76.1	125	7	US-11-155-775-46
93	67	76.1	125	7	US-11-155-775-50
94	67	76.1	126	7	US-11-155-775-34
95	67	76.1	256	7	US-11-054-515-1189
96	66	75.0	119	7	US-11-127-677-21
97	66	75.0	121	7	US-11-127-677-20
98	66	75.0	254	7	US-11-054-515-1428

Sequence 1111, Ap
Sequence 1113, Ap
Sequence 1115, Ap
Sequence 1117, Ap
Sequence 1119, Ap
Sequence 1121, Ap
Sequence 1123, Ap
Sequence 1201, Ap
Sequence 1201, Ap
Sequence 1394, Ap
Sequence 1519, Ap
Sequence 1627, Ap
Sequence 1731, Ap
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Sequence 977, App
Sequence 981, App
Sequence 983, App
Sequence 839, App
Sequence 3241, App
Sequence 512, App
Sequence 1302, App
Sequence 51, Appl
Sequence 5, Appl
Sequence 1887, Ap
Sequence 1901, Ap
Sequence 1118, Ap
Sequence 914, App
Sequence 916, App
Sequence 1323, Ap
Sequence 1114, Ap
Sequence 881, App
Sequence 1075, Ap
Sequence 26, Appl
Sequence 35, Appl
Sequence 31, Appl
Sequence 14, Appl
Sequence 1910, Ap
Sequence 120, Ap
Sequence 956, App
Sequence 18, Appl
Sequence 1898, Ap
Sequence 1912, Ap
Sequence 1919, Ap
Sequence 1890, Ap
Sequence 1956, App
Sequence 952, App
Sequence 982, App
Sequence 1690, Ap
Sequence 4, Appl
Sequence 19, Appl
Sequence 1882, Ap
Sequence 1933, Ap
Sequence 5, Appl
Sequence 20, Appl
Sequence 16, Appl
Sequence 1335, Ap
Sequence 835, App
Sequence 1004, Ap
Sequence 836, App
Sequence 1200, Ap
Sequence 1337, Ap
Sequence 395, App
Sequence 3, Appl
Sequence 1759, Ap
Sequence 2053, Ap
Sequence 1411, Ap
Sequence 22, Appl
Sequence 30, Appl
Sequence 46, Appl
Sequence 50, Appl
Sequence 34, Appl
Sequence 1189, Ap
Sequence 21, Appl
Sequence 1428, Ap

99 66 75.0 261 7 US-11-054-515-1503 Sequence 1503, Ap
100 65 73.9 97 7 US-11-093-274-35 Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-11-054-515-1109
; Sequence 1109, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; CURRENT APPLICATION NUMBER: US/11/054,515
; FILE REFERENCE: PE523P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1109
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1109

Query Match 96.6%; Score 85; DB 7; Length 249;
Best Local Similarity 94.1%; Pred. No. 1e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
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Db 50 VISYDGSNKYYADSVKG 66

RESULT 2
US-11-054-669-23
; Sequence 23, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-23

; ORGANISM: Homo sapiens
US-11-054-669-23

Query Match 92.0%; Score 81; DB 7; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 3
US-11-054-669-24
; Sequence 24, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-24

Query Match 92.0%; Score 81; DB 7; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 4
US-11-054-669-25
; Sequence 25, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-25

Query Match 92.0%; Score 81; DB 7; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66


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RESULT 5
US-11-084-554-34
; Sequence 34, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084.554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-34

Query Match          92.0%; Score 81; DB 7; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDVSKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 6
US-10-952-535A-2
; Sequence 2, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952.535A
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-2

Query Match          92.0%; Score 81; DB 6; Length 115;
Best Local Similarity 88.2%; Pred. No. 1.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDVSKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 7
US-11-127-677-9
; Sequence 9, Application US/11127677
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; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127.677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-9
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Query Match          92.0%; Score 81; DB 7; Length 117;
Best Local Similarity 88.2%; Pred. No. 1.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDVSKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66
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RESULT 8
US-11-127-677-18
; Sequence 18, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127.677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-18
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Query Match          92.0%; Score 81; DB 7; Length 117;
Best Local Similarity 88.2%; Pred. No. 1.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDVSKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66
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RESULT 9
US-11-127-677-12
; Sequence 12, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
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; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 43
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-12

Query Match          92.0%; Score 81; DB 7; Length 120;
Best Local Similarity 88.2%; Pred. No. 2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVK 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
US-11-127-677-48
; Sequence 48, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-48

Query Match          92.0%; Score 81; DB 7; Length 124;
Best Local Similarity 88.2%; Pred. No. 2.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVK 17
   |||:||||| |||||
Db 52 VISYDGSNKYYADSVKG 68

RESULT 11
US-11-127-677-43
; Sequence 43, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
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; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 43
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-43

Query Match          92.0%; Score 81; DB 7; Length 126;
Best Local Similarity 88.2%; Pred. No. 2.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVK 17
   |||:||||| |||||
Db 52 VISYDGSNKYYADSVKG 68

RESULT 12
US-11-054-515-1931
; Sequence 1931, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23E3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1931
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1931

Query Match          92.0%; Score 81; DB 7; Length 238;
Best Local Similarity 88.2%; Pred. No. 4.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVK 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66
```

RESULT 13
US-10-952-535A-6
; Sequence 6, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecerf, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952.535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-952-535A-6

Query Match 92.0%; Score 81; DB 6; Length 239;
Best Local Similarity 88.2%; Pred. No. 4.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDVK 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 VISYDGSNKYYADSVKG 66

RESULT 14
US-11-054-515-2055
; Sequence 2055, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2001-02-11
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2055

Query Match 92.0%; Score 81; DB 7; Length 241;
Best Local Similarity 88.2%; Pred. No. 4.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 VISFDGSKNYVDVK 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15
US-11-054-515-924
; Sequence 924, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 924
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-924

Query Match 92.0%; Score 81; DB 7; Length 247;
Best Local Similarity 88.2%; Pred. No. 4.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDVK 17
| | | | | | | | | | | | | | | | | | | | |
Db 50 VISYDGSNKYYADSVKG 66

RESULT 16
US-11-054-515-1330
; Sequence 1330, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469

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; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1330
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1330

Query Match          92.0%; Score 81; DB 7; Length 247;
Best Local Similarity 88.2%; Pred. No. 4.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDVK 17
Db      50 VISYDGSNKYADSVKG 66
      |||:||||| |||||

RESULT 17
US-11-054-515-1421
; Sequence 1421, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 5
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-5

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDVK 17
Db      50 VISYDGSNKYADSVKG 66
      |||:||||| |||||

RESULT 19
US-11-054-515-397
; Sequence 397, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1421
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1421

Query Match          92.0%; Score 81; DB 7; Length 248;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

.QY      1 VISFDGSKNYVDVK 17
```

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Db      50 VISYDGSNKYADSVKG 66
      |||:||||| |||||

RESULT 18
US-11-054-515-5
; Sequence 5, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 5
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-5

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDVK 17
Db      50 VISYDGSNKYADSVKG 66
      |||:||||| |||||

RESULT 19
US-11-054-515-397
; Sequence 397, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 5
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-5
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; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 397
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-397.

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVSKG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 20
US-11-054-515-892
; Sequence 892, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 892
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-892

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVSKG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 21
US-11-054-515-911
; Sequence 911, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 911
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-911

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVSKG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 22
US-11-054-515-1102
; Sequence 1102, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 911
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-911

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVSKG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66
```

```
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1102
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1102

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDVSVKG 17
      |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 23
US-11-054-515-1105
/ Sequence 1105, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1108
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1108

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDVSVKG 17
      |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 24
US-11-054-515-1108
/ Sequence 1108, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
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/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1108
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1108

Query Match          92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDVSVKG 17
      |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 25
US-11-054-515-1110
/ Sequence 1110, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
```

; SEQ ID NO 1110
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1110

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
||:|||||
Db 50 VISYDGSNKYYADSVKVG 66

RESULT 26
US-11-054-515-1111
; Sequence 1111, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1111
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1111

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
||:|||||
Db 50 VISYDGSNKYYADSVKVG 66

RESULT 27
US-11-054-515-1113
; Sequence 1113, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1111
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1111

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
||:|||||
Db 50 VISYDGSNKYYADSVKVG 66

RESULT 28
US-11-054-515-1115
; Sequence 1115, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1115
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1115

; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1113
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1113

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
||:|||||
Db 50 VISYDGSNKYYADSVKVG 66

RESULT 29
US-11-054-515-1115
; Sequence 1115, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1115
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1115

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:||||||| |||||
DB 50 VISYDGSNKYYADSVKG 66

RESULT 29

US-11-054-515-1117
; Sequence 1117, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1117
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1117

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:||||||| |||||
DB 50 VISYDGSNKYYADSVKG 66

RESULT 30

US-11-054-515-1119
; Sequence 1119, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1119
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1119

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:||||||| |||||
DB 50 VISYDGSNKYYADSVKG 66

RESULT 31

US-11-054-515-1724
; Sequence 1724, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1724
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1724

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 32
US-11-054-515-1725
; Sequence 1725, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1725
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1725

Query Match 92.0%; Score 81; DB 7; Length 249;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 33
US-11-054-515-1201
; Sequence 1201, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1201
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1201

Query Match 92.0%; Score 81; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 34
US-11-054-515-1394
; Sequence 1394, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1394
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1394

Query Match 92.0%; Score 81; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 35
US-11-054-515-1394
; Sequence 1394, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1394
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1394

Query Match 92.0%; Score 81; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

```
RESULT 35
US-11-054-515-1519
; Sequence 1519, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1519
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1519

Query Match          92.0%; Score 81; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDSVKG 17
      |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 36
US-11-054-515-1627
; Sequence 1627, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1519
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1519

Query Match          92.0%; Score 81; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDSVKG 17
      |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 36
US-11-054-515-1627
; Sequence 1627, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1519
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1519
```

```
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1627
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1627

Query Match          92.0%; Score 81; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDSVKG 17
      |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 37
US-11-054-515-1731
; Sequence 1731, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1731
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1731

Query Match          92.0%; Score 81; DB 7; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDSVKG 17
      |||:||||| |||||
Db      50 VISYDGSNKYYADSVKG 66

RESULT 38
US-11-054-515-977
; Sequence 977, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 977
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-977

Query Match      92.0%; Score 81; DB 7; Length 254;
Best Local Similarity 88.2%; Pred. No. 4.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVKVG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKVG 66

RESULT 39
US-11-054-515-981
; Sequence 981, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 983
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-983

Query Match      92.0%; Score 81; DB 7; Length 254;
Best Local Similarity 88.2%; Pred. No. 4.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVKVG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKVG 66
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Search completed: December 14, 2005, 07:38:15
Job time : 6.27586 secs

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; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 981
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-981

Query Match      92.0%; Score 81; DB 7; Length 254;
Best Local Similarity 88.2%; Pred. No. 4.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVKVG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKVG 66

RESULT 40
US-11-054-515-983
; Sequence 983, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 983
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-983

Query Match      92.0%; Score 81; DB 7; Length 254;
Best Local Similarity 88.2%; Pred. No. 4.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VISFDGSKNYVDVKVG 17
        |||:||||| |||||
Db      50 VISYDGSNKYYADSVKVG 66
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:38 ; Search time 18.4655 Seconds
(without alignments)
88.581 Million cell updates/sec

Title: US-10-720-323-2

Perfect score: 88

Sequence: 1 VISFDGSKYVDSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Pir1:**

2: Pir2:**

3: Pir3:**

4: Pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	92.0	94	2	PL0120
2	81	92.0	97	2	S41115
3	81	92.0	98	2	PL0116
4	81	92.0	98	2	S29546
5	81	92.0	109	2	PH1646
6	81	92.0	109	2	PH1644
7	81	92.0	111	2	PH1643
8	81	92.0	111	2	PH1645
9	81	92.0	113	2	S38490
10	81	92.0	114	2	S46390
11	81	92.0	114	2	S46392
12	81	92.0	117	2	S36270
13	81	92.0	118	2	S31677
14	81	92.0	118	2	S31116
15	81	92.0	119	2	F36005
16	81	92.0	120	2	S31112
17	81	92.0	121	2	S19666
18	81	92.0	121	2	S36005
19	81	92.0	122	2	S36005
20	81	92.0	122	2	S31119
21	81	92.0	123	2	S38493
22	81	92.0	130	2	PL0098
23	81	92.0	132	2	S31603
24	81	92.0	134	2	S31679
25	81	92.0	139	2	S31674
26	79	89.8	137	2	S31701
27	78	88.6	118	2	PH1660
28	75	85.2	121	2	PH1661
29	74	84.1	108	2	PH1642

30	74	84.1	114	2	S46391	Ig heavy chain V r
31	74	84.1	119	2	S31111	Ig heavy chain - h
32	74	84.1	122	2	S31117	Ig heavy chain - h
33	74	84.1	128	2	S48797	Ig heavy chain V-I
34	74	84.1	133	2	A49028	Ig heavy chain V-I
35	74	84.1	151	2	A60943	Ig heavy chain pre
36	73	83.0	118	2	PH1662	Ig heavy chain V r
37	73	83.0	133	2	S31510	Ig heavy chain - h
38	72	81.8	98	2	S29543	Ig heavy chain V r
39	72	81.8	117	2	S36259	Ig heavy chain V r
40	72	81.8	134	2	S31688	Ig heavy chain V r
41	72	81.8	135	2	S31598	Ig heavy chain V r
42	72	81.8	140	2	S70442	Ig heavy chain pre
43	70	79.5	122	1	M3H0AM	Ig heavy chain pre
44	68	77.3	101	2	JT0511	Ig heavy chain V-I
45	67	76.1	76	2	S31592	Ig heavy chain V r
46	67	76.1	119	2	S37453	Ig mu chain - huma
47	65	73.9	97	2	PH0872	Ig heavy chain V r
48	65	73.9	98	2	PL0123	Ig heavy chain V-I
49	65	73.9	110	2	PH1655	Ig heavy chain V r
50	65	73.9	110	2	S69897	Ig heavy chain V r
51	65	73.9	114	2	S36280	Ig heavy chain V r
52	65	73.9	115	2	S36284	Ig heavy chain V r
53	65	73.9	117	2	S17079	Ig heavy chain V-g
54	65	73.9	117	2	S78486	Ig heavy chain V r
55	65	73.9	122	2	S31675	Ig heavy chain V r
56	65	73.9	130	2	S31601	Ig heavy chain V r
57	65	73.9	136	2	S31587	Ig heavy chain V r
58	65	73.9	139	2	I37781	Ig variable region
59	63	71.6	122	2	S69910	Ig V-D-J region (K
60	63	71.6	125	2	S37455	Ig mu chain - huma
61	63	71.6	133	2	S31590	Ig heavy chain V r
62	63	71.6	135	2	I37778	Ig variable region
63	62	70.5	125	2	S20785	Ig heavy chain V r
64	61	69.3	96	2	PH0873	Ig heavy chain V r
65	61	69.3	98	2	S26929	Ig heavy chain V r
66	61	69.3	115	2	S57445	Ig heavy chain V-J
67	61	69.3	120	2	S44111	Ig heavy chain V-D
68	61	69.3	123	2	S31509	Ig heavy chain - h
69	61	69.3	136	2	S16847	Ig heavy chain V r
70	61	69.3	136	2	S60296	Ig heavy-chain var
71	61	69.3	147	2	I37780	Ig variable region
72	60	68.2	122	1	M3HUGA	Ig heavy chain V-I
73	60	68.2	138	2	S03526	Ig heavy chain pre
74	59	67.0	119	1	A1HUBR	Ig heavy chain V-I
75	59	67.0	119	1	G1HUNI	Ig heavy chain V-I
76	59	67.0	138	2	B56701	Ig heavy chain V r
77	59	67.0	249	2	S69340	Ig heavy chain VHI
78	57	64.8	98	2	S54856	Ig heavy chain V r
79	56	63.6	113	2	PH1018	Ig heavy chain V r
80	56	63.6	115	2	S36267	Ig heavy chain V r
81	56	63.6	148	2	PH0118	Ig heavy chain pre
82	55	62.5	98	2	F47624	Ig heavy chain V-I
83	55	62.5	99	2	S20765	Ig heavy chain V r
84	55	62.5	118	2	A49026	Ig heavy chain V r
85	55	62.5	147	2	PH0124	Ig heavy chain pre
86	55	62.5	509	2	S17597	Ig delta chain (WI
87	54	61.4	115	2	S09382	Ig heavy chain - c
88	54	61.4	119	2	PH1555	Ig H chain V regio
89	54	61.4	121	1	G1HURL	Ig heavy chain V-I
90	54	61.4	140	2	I47204	Ig heavy chain var
91	54	61.4	146	2	I47196	Ig heavy chain var
92	54	61.4	147	2	PH0120	Ig heavy chain pre
93	54	61.4	148	2	PH0121	Ig heavy chain pre
94	54	61.4	148	2	PH0116	Ig heavy chain pre
95	54	61.4	148	2	PH0117	Ig heavy chain pre
96	54	61.4	148	2	PH0115	Ig heavy chain pre
97	54	61.4	148	2	PH0119	Ig heavy chain pre
98	53	60.2	111	2	S20199	anti-DNA autoantib
99	53	60.2	118	2	S20641	Ig heavy chain V r
100	53	60.2	119	2	PH1544	Ig H chain V regio

ALIGNMENTS

RESULT 1

PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C:Accession: PL0120
R:Bird, J.; Galli, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin V region (TD-Vo) from a nonproductive DNA rearrangement
A:Reference number: PL0116; MUID:88286083; PMID:2840480
A:Accession: PL0120
A:Molecule type: mRNA
A:Residues: 1-94 <BIR>
A:Cross-references: UNIPROT:QBWUK1; UNIPROT:Q9UL93; UNIPARC:UPI0000176A2C
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A:Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement
C:Superfamily: immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2

Query Match 92.0%; Score 81; DB 2; Length 94;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDSVKG 17

Db 50 VISYDGSNKYADSVKG 66
||||:|||||

RESULT 2

S44115
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C:Accession: S44115
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable region
A:Reference number: S44105
A:Accession: S44115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <HAW>
A:Cross-references: UNIPARC:UPI000011662B; EMBL:Z31384; NID:G472969; PIDN:CAA83259.1; PIDN:CAA83259.1; PIDN:CAA83259.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 92.0%; Score 81; DB 2; Length 97;
Best Local Similarity 88.2%; Pred. No. 7.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDSVKG 17

Db 50 VISYDGSNKYADSVKG 66
||||:|||||

RESULT 3

PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0116; S26892
R:Bird, J.; Galli, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin V region (AW-Vx) from a nonproductive DNA rearrangement
A:Reference number: PL0116; MUID:88286083; PMID:2840480
A:Accession: PL0116
A:Molecule type: mRNA
A:Residues: 1-98 <BIR>

A:Cross-references: UNIPARC:UPI0000031F3A

A:Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A:Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) sequences

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26892

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TOM>

A:Cross-references: UNIPARC:UPI0000031F3A; EMBL:Z12349; NID:G32918; PIDN:CAA78219.1; PIDN:CAA78219.1; PIDN:CAA78219.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMW>

F:31-35/Region: complementarity-determining 1

F:49-65/Region: complementarity-determining 2

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDSVKG 17

Db 50 VISYDGSNKYADSVKG 66
||||:|||||

RESULT 4

S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29546; S26888
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29546
A:Molecule type: DNA
A:Residues: 1-98 <TOM>

A:Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PIDN:CAA78997.1; PIDN:CAA78997.1

A:Note: designated COS-8

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V(H) sequences

A:Reference number: S26885; MUID:93021117; PMID:1404388

A:Accession: S26888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-98 <TO2>

A:Cross-references: UNIPARC:UPI000002DD16; EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PIDN:CAA78216.1; PIDN:CAA78216.1

A:Note: designated DP-46

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMW>

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDSVKG 17

Db 50 VISYDGSNKYADSVKG 66
||||:|||||

RESULT 5

PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C:Accession: PH1646
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal

```
Qy 1 VISFDGSKYKYYVDSVKG 17
Db 69 VISYDGSNKYYADSVK 85

RESULT 26
S31701
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31701
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <HIL>
A:Cross-references: UNIPARC:UPI000011645D; EMBL:Z14177; NID:G31020; PIDN:CNA78546.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 79; DB 2; Length 137;
Best Local Similarity 88.2%; Pred. No. 2.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
Db 69 VISYDGSNKYYADSVK 85

RESULT 27
PH1660
Ig heavy chain V region (clone RIV) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1660
R:Hillson, J.L.; Kart, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1660
A:Molecule type: mRNA
A:Residues: 1-118 <HIL>
A:Cross-references: UNIPARC:UPI0000176BE1
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 78; DB 2; Length 118;
Best Local Similarity 82.4%; Pred. No. 2.8e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
Db 42 VMSYDGSNKYYADSVK 58

RESULT 28
PH1661
Ig heavy chain V region (clone SJI) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1661
R:Hillson, J.L.; Kart, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1661
A:Molecule type: mRNA
```

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A:Residues: 1-121 <HIL>
A:Cross-references: UNIPARC:UPI0000176BE2
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 121;
Best Local Similarity 88.2%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
Db 42 VISDGSNKYYADSVK 58

RESULT 29
PH1642
Ig heavy chain V region (clone 5A10) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C:Accession: PH1642
R:Hillson, J.L.; Kart, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1642
A:Molecule type: mRNA
A:Residues: 1-108 <HIL>
A:Cross-references: UNIPROT:Q9WUK1; UNIPARC:UPI0000176B78
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 108;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
Db 42 VIWYDGSNKYYADSVK 58

RESULT 30
S46391
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46391
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: UNIPARC:UPI00001137D5; EMBL:Z31687; NID:G509784; PIDN:CAA83492.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 114;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
Db 50 VIWYDGSNKYYADSVK 66

RESULT 31
S31111
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Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31111
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31111
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: UNIPARC:UPI0000176DC2; EMBL:X62959
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|| :||||| |||||
DB 50 VIWYDGSNKYYADSVKG 66

RESULT 32
S31117
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 122;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|| :||||| |||||
DB 50 VIWYDGSNKYYADSVKG 66

RESULT 33
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C:Accession: S48797; S26893
R:Nahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <NAH>
A:Cross-references: UNIPARC:UPI0000116700; EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PI
R:Tomlinson, I.M.; Walker, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V

A:Reference number: S26885; MUID:930211117; PMID:1404388
A:Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI0000038183; EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 128;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|| :||||| |||||
DB 50 VIWYDGSNKYYADSVKG 66

RESULT 34
A49028
Ig heavy chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49028
R:Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuurman
Eur. J. Immunol. 21, 2355-2363, 1991
A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphoblast
A:Reference number: A49028; MUID:92008140; PMID:1915549
A:Accession: A49028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-133 <TIM>
A:Cross-references: UNIPARC:UPI0000113F2C; GB:S64471; NID:G236904; PIDN:AAB20011.1; PID:
A:Experimental source: X-linked agammaglobulinemia patient, B lymphoblastoid cell lines
A:Note: sequence extracted from NCBI backbone (NCBIN:64471, NCBI:P:64470)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 133;
Best Local Similarity 82.4%; Pred. No. 0.00014;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|| :||||| |||||
DB 50 VIWYDGSNKYYADSVKG 66

RESULT 35
A60943
Ig heavy chain precursor V region (clone HN.14) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: A60943; A48165
R:Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.; I
J. Neuroimmunol. 30, 245, 1990
A:Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region w
A:Reference number: A60943; MUID:91036050; PMID:1699976
A:Accession: A60943
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-151 <DES>
A:Cross-references: UNIPARC:UPI00000176C11
R:Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.; I
J. Neuroimmunol. 26, 35-41, 1990
A:Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region w
A:Reference number: A48165; MUID:90094677; PMID:1688442
A:Accession: A48165
A:Molecule type: mRNA
A:Residues: 1-36, 'M', 38-62, 'AR', 67-151 <DE2>
A:Cross-references: UNIPARC:UPI00000176C12
A:Note: this sequence has been corrected in reference A60943
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Db | : ||||| |||||
67 IRYGSNKYADSVKG 82

Search completed: December 14, 2005, 07:31:49
Job time : 18.4655 secs


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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
OR [1]
RN NUCLEOTIDE SEQUENCE.
RA Tange Y., Kayano H.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiootype.";
RJ J. Exp. Med. 174:1639-1652(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=7679990;
RA Griffiths A.D., Malmqvist M., Marks J.D., Bye J.M., Embleton M.J.,
RA McCafferty J., Baier M., Holliger K.P., Gorick B.D.,
RA Hughes-Jones N.C.;
RT "Human anti-self antibodies with high specificity from phage display
RT libraries.";
RL ENBO J. 12:725-734(1993).
DR EMBL; AB035268; BAA87067.1; -; Genomic_DNA.
DR PIR; PH0872; PH0872.
DR PIR; S36280; S36280.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 73.9%; Score 65; DB 2; Length 95;
Best Local Similarity 81.2%; Pred. No. 0.0062;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISFDGSKNKKYYVDSVKG 17
| ||| |||||
DB 50 IKQDGEKYYVDSVKG 65

RESULT 9
Q6N093 HUMAN
ID G6N093_HUMAN PRELIMINARY; PRT; 417 AA.
AC G6N093;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686I04196 (Fragment).
GN Name=DKFZp686I04196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
OR [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Human esophagus tumor;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640623; CAB45777.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.

Query Match 73.9%; Score 65; DB 2; Length 417;
Best Local Similarity 64.7%; Pred. No. 0.033;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VISFDGSKNKKYYVDSVKG 17
|::|||::|||::|
DB 22 VIAYDGTQYYADSVRG 38

RESULT 10
Q6PJA4 HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
OR [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.243603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB893C CRC64;

Query Match 73.9%; Score 65; DB 2; Length 417;
Best Local Similarity 64.7%; Pred. No. 0.033;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VISFDGSKNKKYYVDSVKG 17
|::|||::|||::|
DB 22 VIAYDGTQYYADSVRG 38

RESULT 10
Q6PJA4 HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
OR [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.243603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6PJA4; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.  
SQ SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;  
  
Query Match 73.9%; Score 65; DB 2; Length 470;  
Best Local Similarity 81.2%; Pred. No. 0.037;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 ISFDGSKYVDSVKG 17  
DB 70 IKQDSEKYYVDSVKG 85  
  
RESULT 11  
Q6P181 HUMAN  
ID Q6P181_HUMAN PRELIMINARY; PRT; 478 AA.  
AC Q6P181;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE IGHM protein.  
GN Name=IGHM;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan B., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Primary B-Cells;  
RG NIH MGC Project;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC041037; AAH41037.1; -; mRNA.  
DR HSSP; P01861; 1ADQ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig_c1.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.  
SQ SEQUENCE 478 AA; 52852 MW; 52852 MW; EDA75F1901D1A034 CRC64;  
  
Query Match 71.6%; Score 63; DB 2; Length 482;  
Best Local Similarity 70.6%; Pred. No. 0.084;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 VISFDGSKYVDSVKG 17  
DB 69 VISYDGNHKLVSYSVKG 85  
  
RESULT 13  
Q9Y509 HUMAN  
ID Q9Y509_HUMAN PRELIMINARY; PRT; 147 AA.  
AC Q9Y509;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE V3 protein (fragment).  
GN Name=V3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI_TaxID=9606;  
RN [1]_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96071149; PubMed=7475288;  
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
```

RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RL myeloma using PCR with patient-specific immunoglobulin gene primers.";
DR Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -; mRNA.
DR HSSP; P01842; IAQK.
DR DR Ensembl; ENSG00000130076; Homo sapiens.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016866; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 69.3%; Score 61; DB 2; Length 147;
Best Local Similarity 64.7%; Pred. No. 0.048;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VISFDGSKYVDSVKG 17
:|||||:|||||
DB 50 LISYDGSQTYAGSVKG 66
[1]

RESULT 14
Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.
GN Names=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -; mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 69.3%; Score 61; DB 2; Length 469;
Best Local Similarity 64.7%; Pred. No. 0.18;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VISFDGSKYVDSVKG 17
:|||||:|||||
DB 69 LISWDGGSTYYADSVKG 85
[1]

RESULT 15
Q6DDQ7_XENLA PRELIMINARY; PRT; 614 AA.
AC Q6DDQ7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC69066 protein.
GN Name=MGC69066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Initiative";
Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077477; AAH77477.1; -; mRNA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001680; WD40.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 4.
DR PROSITE; PS00678; WD_REPEATS 1; UNKNOWN 1.
SQ SEQUENCE 614 AA; 58254 MW; 2631B7CF955270C0 CRC64;

Query Match 69.3%; Score 61; DB 2; Length 614;
Best Local Similarity 70.6%; Pred. No. 0.24;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
DB 67 VISDPGGSTYYADSVKG 83

RESULT 16
HV3L_HUMAN STANDARD; PRT; 122 AA.
AC HV3L_HUMAN
ID HV3L_HUMAN
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP PROTEIN SEQUENCE.
RX MEDLINE=77070267; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604 (1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR PIR; A91668; G1HUNI.
DR HSSP; P01772; 2FB4.
DR SMR; P01770; 1-119.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13243 MW; C96935A6E55E165B CRC64;

Query Match 67.0%; Score 59; DB 1; Length 119;
Best Local Similarity 52.9%; Pred. No. 0.083;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
DB 50 VMSYGBGBKHVADSVNG 66

RESULT 18
HV3L_HUMAN STANDARD; PRT; 119 AA.
ID HV3L_HUMAN
AC HV3L_HUMAN
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region BUR.
OS Homo sapiens (Human).
OS
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DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 4.
DR PROSITE; PS00678; WD_REPEATS 1; UNKNOWN 1.
SQ SEQUENCE 614 AA; 58254 MW; 2631B7CF955270C0 CRC64;

Query Match 69.3%; Score 61; DB 2; Length 614;
Best Local Similarity 70.6%; Pred. No. 0.24;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
DB 67 VISDPGGSTYYADSVKG 83

RESULT 16
HV3L_HUMAN STANDARD; PRT; 122 AA.
AC HV3L_HUMAN
ID HV3L_HUMAN
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP PROTEIN SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498 (1974).
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR PIR; A02052; M3HUGA.
DR HSSP; P01772; 2FB4.
DR SMR; P01769; 5-122.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13167 MW; 74E5B6959E84100A CRC64;

Query Match 68.2%; Score 60; DB 1; Length 122;
Best Local Similarity 58.8%; Pred. No. 0.058;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
DB 50 VISYGBGBZYAAVSKG 66

RESULT 17
HV3L_HUMAN STANDARD; PRT; 119 AA.
ID HV3L_HUMAN
AC HV3L_HUMAN
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DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS08395; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein_KW
SQ SEQUENCE 470 AA; 51536 MW; 7CB061DFC03D0B2B CRC64;

Query Match 65.9%; Score 58; DB 2; Length 470;
Best Local Similarity 58.8%; Pred.No. 0.57;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VISFDGSKYYVDSVKG 17
Db 69 VISYEGGKHVADSVKG 85
|||||
::|||

RESULT 20
Q9UL71 HUMAN
ID Q9UL71_HUMAN PRELIMINARY; PRT; 121 AA.
AC Q9UL71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DS (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL CBLN. Immunol. Immunopathol. 87:184-192(1998).
DR ENBL; AF035043; AAD56279.1; -; mRNA.
DR HSSP; P01852; INFD.
DR SNR; Q9UL71; 1-121.
DR Ensemble; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS08395; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFASD50736 CRC64;

Query Match 64.8%; Score 57; DB 2; Length 121;
Best Local Similarity 64.7%; Pred.No. 0.18;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VISFDGSKYYVDSVKG 17
Db 50 LISGDGGSTYYADSVKG 66
|||||
::|||

RESULT 21
Q5M7V3 RAT
ID Q5M7V3_RAT PRELIMINARY; PRT; 461 AA.
AC Q5M7V3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE LOC367586 protein.
GN Name=LOC367586.

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OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG NIH MGC Project;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
 CC histocompatibility complex class I molecules (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 DR EMBL; BC088423; AAH8423.1; -; mRNA.
 DR InterPro; IPR003159; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 KW Immunoglobulin domain; Repeat.
 SQ SEQUENCE 461 AA; 50949 MW; 25EA4ECE6FE0F5A9 CRC64;
 Query Match 63.6%; Score 56; DB 2; Length 461;
 Best Local Similarity 68.8%; Pred. No. 1.2;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ISFDGSKNYVDVSVKG 17
 |:::| | | | |
 Db 70 IIVDGSRTYRDSVKG 85
 RESULT 22
 QSEFES HUMAN
 ID QSEFES5 HUMAN PRELIMINARY; PRT; 475 AA.
 AC QSEFES7
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 GAucher C., Klein P., Beliard R.;
 RT "Sequence determination of the recombinant human anti-Rhd monoclonal
 RT antibody T125.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY894992; AAH82028.1; -; mRNA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 3.
 DR Pfam; PF07654; V-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy
 chain.
 SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;
 Query Match 63.6%; Score 56; DB 2; Length 475;
 Best Local Similarity 68.8%; Pred. No. 1.3;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ISFDGSKNYVDVSVKG 17
 |:::| | | | |
 Db 70 ISYDGRNTQYADSVKG 85
 RESULT 23
 QSEK12 RAT
 ID QSEK12 RAT PRELIMINARY; PRT; 479 AA.
 AC QSEK12;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DE Igha protein.
 DE Name-Igha;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.


```
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP PROTEIN SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
RL cytoimmunoglobulin Igg HIL."
RL Biochemistry 18:553-560(1979).
CC -1- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02054; GIHULH.
DR HSP; P01772; 2FB4.
DR SMR; P01771; 2-121.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyroglutamate carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 121 121 Ig-like.
FT NON_TER 121 121 Pyroglutamate carboxylic acid.
SQ SEQUENCE 121 AA; 13566 MW; 480FC536108F5DAB CRC64;

Query Match 61.4%; Score 54; DB 1; Length 121;
Best Local Similarity 64.7%; Pred. No. 0.59;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDVSKG 17
Db 50 VIWNGSRTYGDSVKG 66

RESULT 27
Q5W8X4 XENTR
ID Q5W8X4_XENTR PRELIMINARY; PRT; 367 AA.
AC Q5W8X4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_TaxID=8364;
RN [1]_TaxID=8364;
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins L., Wagner C.M., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,


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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schestz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC087793; RAH87793.1; -; mRNA.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 367 AA; 40058 MW; 66DE2E25CDF0CB34 CRC64;

Query Match 61.4%; Score 54; DB 2; Length 367;
Best Local Similarity 62.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ISFDGSKNYVDVSKG 17
Db 70 ISSDGSSTYYADSVRG 85

RESULT 28
Q6MZQ6 HUMAN
ID Q6MZQ6_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686G11190.
GN Name=DKF2p686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German CDNA Consortium;
RA Bahr A., Lauber J., Newes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6MZQ6; 20-475.
DR InterPro; IPR003599; Ig.
```

DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 61.4%; Score 54; DB 2; Length 475;
 Best Local Similarity 68.8%; Pred. No. 2.7;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISFDGSKNYVDSVKG 17
 |||||
 Db 70 ISSGVNTYYADSVKG 85

RESULT 29

Q8NCL6_HUMAN PRELIMINARY; PRT; 493 AA.
 AC Q8NCL6;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CDNA FLJ90170 fis, clone MAMMAL000370, highly similar to Ig alpha-1 chain C region.
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RA Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J., Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S., Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Negai K., Sugano S., Isogai T.;
 RT "Signal Sequence and Keyword Trap in silico for Selection of Full-Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-Capped cDNA Libraries."
 RL DNA Res. 12:117-126(2005).
 DR EMBL; AK074651; BAC11114.1; -; mRNA.
 DR HSSP; P01876; 10W0.
 DR SMR; Q8NCL6; 263-471.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig v.
 DR Pfam; PF07654; C1-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 493 AA; 53224 MW; 13ECD7E094777101 CRC64;

Query Match 61.4%; Score 54; DB 2; Length 493;
 Best Local Similarity 58.8%; Pred. No. 2.9;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDSVKG 17
 :||:|
 Db 69 LIWYDGTYYSDSVKG 85

RESULT 30

Q9UL72_HUMAN PRELIMINARY; PRT; 118 AA.
 AC Q9UL72;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN [2]
 RP PROTEIN SEQUENCE.
 RC PubMed=1555592;
 RA Makiya R., Strigbrand T.;
 RT "Placental alkaline phosphatase has a binding site for the human immunoglobulin-G Fc portion."
 RL Eur. J. Biochem. 205:341-345(1992).
 DR EMBL; AF035042; AAD56278.1; -; mRNA.
 DR PIR; S21205; S21205.
 DR HSSP; P01783; 1IGC.
 DR SMR; Q9UL72; 1-118.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; IG v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR NON_TER 1
 FT NON_TER 118
 FT NON_TER 118
 SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 60.2%; Score 53; DB 2; Length 118;
 Best Local Similarity 50.0%; Pred. No. 0.84;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ISFDGSKNYVDSVKG 17
 ::|||
 Db 50 VTYSGSSYVADSVKG 65

RESULT 31

HV3K_HUMAN STANDARD; PRT; 126 AA.
 AC P01772;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-III region KOL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
 RC MEDLINE=83289131; PubMed=6884994;
 RA Schmidt W.E., Jung H.-D., Palm W., Hilechmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RC MEDLINE=81072295; PubMed=7441755;
 RA Marquart M., Deisenhofer J., Huber R., Palm W.;
 RT "Crystallographic refinement and atomic models of the intact

```

RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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CC removed.
CC -----
DR PIR; A02055; GIHKUL.
DR PDB; 2FB4; X-ray; H=2-126.
DR PDB; 2IG2; X-ray; H=2-126.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:000323; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Direct_protein_sequencing; Immunoglobulin domain;
KW immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1
FT DISULFID 22 96
FT DISULFID 105 110
FT NON_TER 126 126
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT HELIX 29 31
FT STRAND 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT HELIX 62 64
FT STRAND 65 65
FT TURN 66 67
FT STRAND 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 60.2%; Score 53; DB 1; Length 126;
Best Local Similarity 58.8%; Pred. No. 0.91;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDSVKG 17
Db 50 IIWDDGSDQHYDSVKG 66

RESULT 32
Q62VX0_HUMAN
ID Q62VX0_HUMAN PRELIMINARY; PRT; 487 AA.
AC Q62VX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ41981.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

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OC Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Mateuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK123975; BAC85740.1; -; mRNA.
DR HSSP; P01842; 1AOK.
DR SMR; Q62VX0; 257-465.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 487 AA; 52874 MW; B354EDB82398BF1A CRC64;

Query Match 60.2%; Score 53; DB 2; Length 487;
Best Local Similarity 62.5%; Pred. No. 4.2;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISFDGSKNYVDSVKG 17
Db 70 INKGRDSYVDSVKG 85

RESULT 33
O9GJD3_SIGHI
ID O9GJD3_SIGHI PRELIMINARY; PRT; 71 AA.
AC O9GJD3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=SihI-DOA;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Sigmodontinae; Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pfau R.S., Van Den Bussche R.A., McBees K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF279854; BAG27604.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha_N.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1 1
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8192 MW; ED18CCF1D1A3E143 CRC64;

Query Match 59.1%; Score 52; DB 2; Length 71;
Best Local Similarity 56.2%; Pred. No. 0.7;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDSVK 16
Db 15 IFEDGDEKPYVDSK 30

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RESULT 34
Q9XRR3_SIGHI
ID Q9XRR3_SIGHI PRELIMINARY; PRT; 71 AA.
AC Q9XRR3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Sihi-DQA;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Sigmodontinae; Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99367398; PubMed=10436183; DOI=10.1007/s002510050569;
RA Pfau R.S., Van Den Bussche R.A., McBees K., Lochmiller R.L.;
RT "Allelic diversity at the Mhc-DQA locus in cotton rats (Sigmodon
hispidus) and a comparison of DQA sequences within the family muridae
(Mammalia: Rodentia).";
RL Immunogenetics 49:886-893(1999).
DR EMBL; AF155924; AAD39254.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha_N.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1 71
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8162 MW; F18304D7752180E CRC64;

Query Match 59.1%; Score 52; DB 2; Length 71;
Best Local Similarity 56.2%; Pred. No. 0.7;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVK 16
: ||| | | | | |
Db 15 IFEDGDEKFYVDSK 30

RESULT 35
Q9XRR5_SIGHI
ID Q9XRR5_SIGHI PRELIMINARY; PRT; 71 AA.
AC Q9XRR5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Sihi-DQA;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Sigmodontinae; Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99367398; PubMed=10436183; DOI=10.1007/s002510050569;
RA Pfau R.S., Van Den Bussche R.A., McBees K., Lochmiller R.L.;
RT "Allelic diversity at the Mhc-DQA locus in cotton rats (Sigmodon
hispidus) and a comparison of DQA sequences within the family muridae
(Mammalia: Rodentia).";
RL Immunogenetics 49:886-893(1999).
DR EMBL; AF155922; AAD39252.1; -; Genomic_DNA.
DR SMR; Q9XRR5; 1-71.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha_N.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1 71
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8177 MW; ED18CCB4C4BF8B1D CRC64;
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Query Match 59.1%; Score 52; DB 2; Length 71;
Best Local Similarity 56.2%; Pred. No. 0.7;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVK 16
: ||| | | | | |
Db 15 IFEDGDEKFYVDSK 30

RESULT 36
Q9XRR9_SIGHI
ID Q9XRR9_SIGHI PRELIMINARY; PRT; 71 AA.
AC Q9XRR9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC class II antigen (Fragment).
GN Name=Sihi-DQA;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Sigmodontinae; Sigmodon.
OX NCBI_TaxID=42415;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99367398; PubMed=10436183; DOI=10.1007/s002510050569;
RA Pfau R.S., Van Den Bussche R.A., McBees K., Lochmiller R.L.;
RT "Allelic diversity at the Mhc-DQA locus in cotton rats (Sigmodon
hispidus) and a comparison of DQA sequences within the family muridae
(Mammalia: Rodentia).";
RL Immunogenetics 49:886-893(1999).
DR EMBL; AF155918; AAD39248.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha_N.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1 71
FT NON_TER 71 71
SQ SEQUENCE 71 AA; 8193 MW; ED18CCF1D1AD01AD CRC64;

Query Match 59.1%; Score 52; DB 2; Length 71;
Best Local Similarity 56.2%; Pred. No. 0.7;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVK 16
: ||| | | | | |
Db 15 IFEDGDEKFYVDSK 30

RESULT 37
Q4S056_TETNG
ID Q4S056_TETNG PRELIMINARY; PRT; 111 AA.
AC Q4S056;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 21 SCAF14785, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0026180001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Aihouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
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RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kallia M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacher V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Scallius H.;
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAE01014785; CAG05976.1; -; Genomic DNA.
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12077 MW; 793B852B8B1216B3 CRC64;

Query Match 59.1%; Score 52; DB 2; Length 111;
Best Local Similarity 53.3%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISFDGSKYXVDSVK 16
DB 67 VTIGNSFYDVK 81

RESULT 38
Q4VBH1 RAT
ID Q4VBH1 RAT PRELIMINARY; PRT; 467 AA.
AC Q4VBH1
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE LOC299354 protein.
DE Names=LOC299354;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Beta-2-microglobulin is the beta-chain of major

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CC histocompatibility complex class I molecules (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC095846; AAH95846.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 467 AA; 51651 MW; 1FF0328F50160ED3 CRC64;

Query Match 59.1%; Score 52; DB 2; Length 467;
Best Local Similarity 62.5%; Pred. No. 5.9;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISFDGSKYXVDSVK 17
DB 70 INTDGSYYVDSVK 85

RESULT 39
Q6MZX9 HUMAN
ID Q6MZX9 HUMAN PRELIMINARY; PRT; 483 AA.
AC Q6MZX9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686M08189.
GN Name=DKFZp686M08189;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640822; CAE45898.1; -; mRNA.
DR HSSP; P01842; 1AQR.
DR SMR; Q6MZX9; 253-461.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IGV.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 483 AA; 52235 MW; 4B5F467D5B708DB8 CRC64;

Query Match 59.1%; Score 52; DB 2; Length 483;
Best Local Similarity 62.5%; Pred. No. 6.1;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISFDGSKYXVDSVK 17
DB 70 INEDGSYYVDSVK 85

RESULT 40
Q6INM5_XENLA

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AD Q6INM5_XENLA PRELIMINARY; PRT; 593 AA.
AC Q6INM5_2 ISPDGSKNYVDSVKG 17
DT 05-JUL-2004 (TRENBLrel. 27, Created) | : | : | | | | |
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update) | : | : | | | | |
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update) 68 INPDGSGSTYYADSVKG 83
DE MGC69066 protein.
GN Name=MGC69066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC072253; AAH72253.1; -; mRNA.
DR HSP; P01842; 1AQK.
DR GO; GO:0030106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . . ; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG_v.
DR InterPro; IPR001680; WD40.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_4.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
SQ SEQUENCE 593 AA; 65875 MW; BE314FF9211E12FC CRC64;
Query Match 59.1%; Score 52; DB 2; Length 593;
Best Local Similarity 62.5%; Pred. No. 7.7;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Search completed: December 14, 2005, 07:30:43
Job time : 93.7414 secs

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Query Match          92.0%; Score 81; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 11
IG heavy chain V region (VH-28) - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46392
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46392
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: UNIPARC:UPI0000113706; EMBL:Z11688; NID:g499306; PIDN:CAA83493.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          92.0%; Score 81; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 12
IG heavy chain V region (clone alpha-TNF-E1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36270
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679950
A:Accession: S36270
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-117 <GRI>
A:Cross-references: UNIPARC:UPI0000118DB6; EMBL:Z18839; NID:g33118; PIDN:CAA79291.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          92.0%; Score 81; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 13
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31677
R:Quisnier, A.M.; Gauthier, L.; Boulli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
```

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A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31677
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-118 <CUI>
A:Cross-references: UNIPARC:UPI0000116459; EMBL:Z14172; NID:g31009; PIDN:CAA78541.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          92.0%; Score 81; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 14
IG heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C:Accession: S3116
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S3116
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-118 <RAA>
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          92.0%; Score 81; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
   |||:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15
IG heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C:Accession: F36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: F36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026
C:Genetics:
A:Gene: GDB:IGH@; IGHV1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match          92.0%; Score 81; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
```

A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1646
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B7C
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 6
PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C;Accession: PH1644
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1644
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
A;Cross-references: UNIPROT:Q9UL93; UNIPARC:UPI0000176B7A
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 7
PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C;Accession: PH1643
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1643
A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B79
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 8

PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C;Accession: PH1645
R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1645
A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B7B
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 9
S38490
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38490
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a phage display library
A;Reference number: S38488
A;Accession: S38490
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <MAR>
A;Cross-references: UNIPARC:UPI0000116549; EMBL:Z23030; NID:9414027; PIDN:CAA80565.1; PIR:PI0000116549
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 113;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
S46390
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by a phage display library
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: UNIPARC:UPI000011663P; EMBL:Z31686; NID:9509782; PIDN:CAA83491.1; PIR:PI000011663P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKVG 66

RESULT 16
 S31112
 Ig heavy chain V region (M74) - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
 C:Accession: S31112
 R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
 A:Reference number: S31104; MUID:92111633; PMID:1730252
 A:Accession: S31112
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-120 <RAA>
 A:Cross-references: UNIPARC:UPI0000176C8C; EMBL:X62961
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 120;
 Best Local Similarity 88.2%; Pred. No. 9.3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKVG 66

RESULT 17
 S19666
 Ig heavy chain V region (VH3DJH4) - human
 C:Species: Homo sapiens (man)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
 C:Accession: S19666
 R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
 J. Mol. Biol. 222, 581-597, 1991
 A>Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
 A:Reference number: S19663; MUID:92085276; PMID:1748994
 A:Accession: S19666
 A:Molecule type: mRNA
 A:Residues: 1-121 <VAR>
 A:Cross-references: UNIPARC:UPI0000115FE5; EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 121;
 Best Local Similarity 88.2%; Pred. No. 9.4e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKVG 66

RESULT 18
 G36005
 Ig heavy chain V region (M74) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
 C:Accession: G36005
 R:Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A:Reference number: A36005; MUID:90349571; PMID:21117273

A:Accession: G36005
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-121 <SCH>
 A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C2C; GB:M34031
 C:Genetics:
 A:Gene: GDB:IGH@; IGHDI1
 A:Cross-references: GDB:118731; OMIM:146910
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 121;
 Best Local Similarity 88.2%; Pred. No. 9.4e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKVG 66

RESULT 19
 E36005
 Ig heavy chain V region (M72) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
 C:Accession: E36005
 R:Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
 A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A:Reference number: A36005; MUID:90349571; PMID:21117273
 A:Accession: E36005
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-122 <SCH>
 A:Cross-references: UNIPARC:UPI0000176C30; GB:M34030
 C:Genetics:
 A:Gene: GDB:IGH@; IGHDI1
 A:Cross-references: GDB:118731; OMIM:146910
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 122;
 Best Local Similarity 88.2%; Pred. No. 9.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKVG 66

RESULT 20
 S31119
 Ig heavy chain - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
 C:Accession: S31119
 R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
 A:Reference number: S31104; MUID:92111633; PMID:1730252
 A:Accession: S31119
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-122 <RAA>
 A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C8F; EMBL:X62970
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C:Superfamily: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 122;
Best Local Similarity 88.2%; Pred. No. 9.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSVKG 17
|||:|||||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 21

S31603
IG heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31603
R:Mark, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a B
A:Reference number: S31603
A:Accession: S31603
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <CUI>
A:Cross-references: UNIPARC:UPI000011654F; EMBL:Z23036; NID:G414033; PIDN:CAA80571.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 123;
Best Local Similarity 88.2%; Pred. No. 9.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSVKG 17
|||:|||||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 22

PL0098
IG heavy chain precursor V-III region (FL2-2) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C:Accession: PL0098
R:Nickerson, K.G.; Berman, J.; Glickman, E.; Chess, L.; Alt, F.W.
J. Exp. Med. 169, 1391-1403, 1989
A:Title: Early human IGH gene assembly in Epstein-Barr virus-transformed fetal B cell li
s.

A:Reference number: PL0098; PMID:89176893; PMID:2538551

A:Accession: PL0098

A:Molecule type: DNA

A:Residues: 1-130 <NIC>

A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000116D37

C:Superfamily: immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:17-120/Product: IG heavy chain V-III region FL2-2 #status predicted <MAT>

F:32-115/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 130;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSVKG 17
|||:|||||||
Db 67 VISYDGSNKYYADSVKG 83

RESULT 23

S31603
IG heavy chain V region - human
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31603

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31603
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CUI>

A:Cross-references: UNIPARC:UPI0000116455; EMBL:Z14168; NID:G30999; PIDN:CAA78537.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:30-113/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 132;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSVKG 17
|||:|||||||
Db 65 VISYDGSNKYYADSVKG 81

RESULT 24

S31679
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31679
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31679
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <CUI>

A:Cross-references: UNIPARC:UPI0000116475; EMBL:Z14203; NID:G30965; PIDN:CAA78572.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 134;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSVKG 17
|||:|||||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 25

S31674
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31674
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31674
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CUI>

A:Cross-references: UNIPARC:UPI0000116476; EMBL:Z14204; NID:G30967; PIDN:CAA78573.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 92.0%; Score 81; DB 2; Length 139;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:28 ; Search time 91.7414 Seconds
(without alignments)
130.737 Million cell updates/sec

Title: US-10-720-323-2

Perfect score: 88

Sequence: 1 VISFDGSKYVDSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : 1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	92.0	116	2 Q9UL93_HUMAN	Q9ul93 homo sapien
2	81	92.0	240	2 Q5ZC9_HUMAN	Q5zc9 homo sapien
3	81	92.0	613	2 Q8WUK1_HUMAN	Q8wuk1 homo sapien
4	72	81.8	113	2 Q9UL90_HUMAN	Q9ul90 homo sapien
5	70	79.5	122	1 HV3G_HUMAN	P01768 homo sapien
6	67	76.1	122	2 Q9UL84_HUMAN	Q9ul84 homo sapien
7	67	76.1	519	2 Q6N092_HUMAN	Q6n092 homo sapien
8	65	73.9	95	2 Q9UL86_HUMAN	Q9ul86 homo sapien
9	65	73.9	417	2 Q6N093_HUMAN	Q6n093 homo sapien
10	65	73.9	470	2 Q6PJ44_HUMAN	Q6pja4 homo sapien
11	65	73.9	478	2 Q6PI81_HUMAN	Q6pi81 homo sapien
12	63	71.6	482	2 Q7Z3S1_HUMAN	Q7z3s1 homo sapien
13	61	69.3	147	2 Q9Y509_HUMAN	Q9y509 homo sapien
14	61	69.3	469	2 Q569F4_HUMAN	Q569f4 homo sapien
15	61	69.3	614	2 Q6DDQ7_XENLA	Q6ddq7 xenopus lae
16	60	68.2	122	1 HV3H_HUMAN	P01769 homo sapien
17	59	67.0	119	1 HV3L_HUMAN	P01770 homo sapien
18	59	67.0	119	1 HV3L_HUMAN	P01773 homo sapien
19	58	65.9	470	2 Q8C8N4_HUMAN	Q8c8n4 homo sapien
20	57	64.8	121	2 Q9UL71_HUMAN	Q9ul71 homo sapien
21	56	63.6	461	2 Q5M7V3_RAT	Q5m7v3 rattus norv
22	56	63.6	475	2 Q5EF85_HUMAN	Q5ef85 homo sapien
23	56	63.6	479	2 Q5BK12_RAT	Q5bk12 rattus norv
24	56	63.6	544	2 Q6PJ95_HUMAN	Q6pj95 homo sapien
25	55	62.5	481	2 Q6N097_HUMAN	Q6n097 homo sapien
26	54	61.4	121	1 HV3J_HUMAN	P01771 homo sapien
27	54	61.4	367	2 Q5M8X4_XENTR	Q5m8x4 xenopus tro
28	54	61.4	475	2 Q6MZ06_HUMAN	Q6mz06 homo sapien
29	54	61.4	493	2 Q8NC16_HUMAN	Q8nc16 homo sapien
30	53	60.2	118	2 Q9UL72_HUMAN	Q9ul72 homo sapien
31	53	60.2	126	1 HV3K_HUMAN	P01772 homo sapien

ALIGNMENTS

32	53	60.2	487	2	Q6ZVX0_HUMAN	Q6zvx0 homo sapien
33	52	59.1	71	2	Q9GJD3_SIGHI	Q9gjd3 sigmodon hi
34	52	59.1	71	2	Q9XRR3_SIGHI	Q9xrr3 sigmodon hi
35	52	59.1	71	2	Q9XRR5_SIGHI	Q9xrr5 sigmodon hi
36	52	59.1	71	2	Q9XRR9_SIGHI	Q9xrr9 sigmodon hi
37	52	59.1	111	2	Q4S056_TETNG	Q4s056 tetraodon n
38	52	59.1	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
39	52	59.1	483	2	Q6MZX9_HUMAN	Q6mzx9 homo sapien
40	52	59.1	593	2	Q6INM5_XENLA	Q6inm5 xenopus lae
41	51	58.0	99	2	Q4T5M5_TETNG	Q4t5m5 tetraodon n
42	51	58.0	465	2	Q510J0_RAT	Q5i0j0 rattus norv
43	50	56.8	71	2	Q9XRB6_SIGHI	Q9xrb6 sigmodon hi
44	50	56.8	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien
45	50	56.8	736	2	Q600L2_MYCHY	Q600l2 mycoplasma
46	49	55.7	97	2	Q4SZF9_TETNG	Q4szf9 tetraodon n
47	49	55.7	116	1	HV05_CARAU	P19181 carassius a
48	49	55.7	116	1	HV3T_HUMAN	P01781 homo sapien
49	49	55.7	119	2	Q920E7_MOUSE	Q920e7 mus musculu
50	49	55.7	196	2	Q6SZL8_MOUSE	Q6szl8 mus musculu
51	49	55.7	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
52	49	55.7	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
53	49	55.7	589	2	Q5XHD5_XENLA	Q5xhd5 xenopus lae
54	48.5	55.1	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien
55	48	54.5	98	1	HV57_MOUSE	P18528 mus musculu
56	48	54.5	122	1	HV3A_HUMAN	P01762 homo sapien
57	48	54.5	211	2	Q9D8R6_MOUSE	Q9d8r6 mus musculu
58	48	54.5	556	2	Q69279_MOUSE	Q69279 mus musculu
59	48	54.5	666	2	Q5VLJ8_CEPAC	Q5vlj8 cephalospor
60	48	54.5	960	2	Q8CFV8_MOUSE	Q8cfv8 mus musculu
61	48	54.5	1139	2	Q6NS00_MOUSE	Q6ns00 mus musculu
62	47	53.4	71	2	Q9GJC8_SIGHI	Q9gjc8 sigmodon hi
63	47	53.4	71	2	Q9XRR7_SIGHI	Q9xrr7 sigmodon hi
64	47	53.4	114	1	HV3B_HUMAN	P01763 homo sapien
65	47	53.4	117	1	HV3C_HUMAN	P01764 homo sapien
66	47	53.4	378	2	Q6C5Z4_YARLI	Q6c5z4 yarrowia li
67	47	53.4	1093	2	Q54GV1_DICDI	Q54gv1 dictyosteli
68	46.5	52.8	973	2	Q6SLS5_POXV	Q6s15 calliptamus
69	46.5	52.8	988	2	Q91HP7_POXV	Q91hp7 oedateus as
70	46	52.3	98	2	Q4TJ56_TETNG	Q4tj56 tetraodon n
71	46	52.3	255	2	Q6KB05_MOUSE	Q6kb05 mus musculu
72	46	52.3	266	2	Q8LPR6_ARATH	Q8lpr6 arabidopsis
73	46	52.3	326	2	Q5XK64_ARATH	Q5xk64 arabidopsis
74	46	52.3	326	2	Q8GXP0_ARATH	Q8gxp0 arabidopsis
75	46	52.3	393	2	Q48352_HALSA	Q48352 halobacteri
76	46	52.3	446	2	Q5V7L4_HALMA	Q5v7l4 haloarcula
77	46	52.3	446	2	Q9HHL2_HALSA	Q9hhl2 halobacteri
78	46	52.3	446	2	Q9HQP6_HALSA	Q9hq6 halobacteri
79	46	52.3	479	2	Q91WP5_MOUSE	Q91wp5 mus musculu
80	46	52.3	608	2	Q6FTK0_CANGA	Q6ftk0 candida gla
81	46	52.3	905	2	Q9FXK3_ARATH	Q9fxk3 arabidopsis
82	46	52.3	925	2	Q9FE36_ARATH	Q9fe36 arabidopsis
83	46	52.3	955	2	Q9FE16_ARATH	Q9fe16 arabidopsis
84	45.5	51.7	988	2	Q6S5I4_POXV	Q6s5i4 gomphocerus
85	45.5	51.7	1070	2	Q8GRS8_CITR	Q8grs8 citrobacter
86	45.5	51.7	1100	2	Q9X6J9_XEROX	Q9x6j9 klebsiella
87	45.5	51.7	1126	2	Q6TFV0_ERWAM	Q6tfv0 erwinia amy
88	45	51.1	71	2	Q9GJC7_SIGHI	Q9gjc7 sigmodon hi
89	45	51.1	71	2	Q9GJC9_SIGHI	Q9gjc9 sigmodon hi
90	45	51.1	71	2	Q9GJD4_SIGHI	Q9gjd4 sigmodon hi
91	45	51.1	71	2	Q9GJD6_SIGHI	Q9gjd6 sigmodon hi
92	45	51.1	71	2	Q9XRR4_SIGHI	Q9xrr4 sigmodon hi
93	45	51.1	71	2	Q9XRR8_SIGHI	Q9xrr8 sigmodon hi
94	45	51.1	71	2	Q9XRS0_SIGHI	Q9xrs0 sigmodon hi
95	45	51.1	71	2	Q9XRS1_SIGHI	Q9xrs1 sigmodon hi
96	45	51.1	71	2	Q9XRS2_SIGHI	Q9xrs2 sigmodon hi
97	45	51.1	71	2	Q9XRS3_SIGHI	Q9xrs3 sigmodon hi
98	45	51.1	115	1	HV3F_HUMAN	P01767 homo sapien
99	45	51.1	117	1	HV55_MOUSE	P18526 mus musculu
100	45	51.1	177	2	Q5EQN4_9HYME	Q5eqn4 perga conde

```
RESULT 1
Q9UL93 HUMAN
ID Q9UL93_HUMAN PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
   (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
   fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hilleson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germline-encoded VH3 immunoglobulin binding
   to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2840480;
RA Bird J., Galili N., Link M., Stites D., Sklar J.;
RT "Continuing rearrangement but absence of somatic hypermutation in
   immunoglobulin genes of human B cell precursor leukemia.";
RL J. Exp. Med. 168:229-245(1988).
DR EMBL; AF035021; AAD56257.1; -; mRNA.
DR PIR; PH1644; PH1644.
DR PIR; PLO120; PLO120.
DR HSSP; P01772; 2FB4.
DR SNR; Q9UL93; 1-116.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; Ig_v.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 116 116
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 92.0%; Score 81; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
Db 49 VISYDGSNKYYADSVKG 65
|||||
|||||

RESULT 2
Q65ZC9 HUMAN
ID Q65ZC9_HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1 1
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 92.0%; Score 81; DB 2; Length 240;
Best Local Similarity 88.2%; Pred. No. 3.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
Db 50 VISYDGSNKYYADSVKG 66
|||||
|||||

RESULT 3
Q8WUK1 HUMAN
ID Q8WUK1_HUMAN PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Krausner R.D., Collins F.S., Wagner B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RT TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2117273;
```

RA Schroeder H.W. Jr, Wang J.Y.;
 RT "Preferential utilization of conserved immunoglobulin heavy chain
 RT variable gene segments during human fetal life.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
 RN [4]
 RX PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;
 RA Cuisinier A.M., Fumoux F., Fougereau M., Tonnelie C.;
 RT "TGM kappa/lambda EBV human B cell clone: an early step of
 RT differentiation of fetal B cells or a distinct B lineage?";
 RL Mol. Immunol. 29:1363-1373(1992).
 RN [5]
 RX PubMed=1730252;
 RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
 RA Schuurman R.K.;
 RT "Restricted utilization of germ-line VH3 genes and short diverse third
 RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
 RT immunoglobulin heavy chain rearrangements.";
 RL Eur. J. Immunol. 22:247-251(1992).
 RN [6]
 RX PubMed=1904154;
 RA Neale G.A., Kitchingman G.R.;
 RT "mRNA transcripts initiating within the human immunoglobulin mu heavy
 RT chain enhancer region contain a non-translatable exon and are
 RT extremely heterogeneous at the 5' end.";
 RL Nucleic Acids Res. 19:2427-2433(1991).
 RN [7]
 RX PubMed=2840480; DOI=10.1084/jem.168.1.229;
 RA Bird J., Galili N., Link M., Stiles D., Sklar J.;
 RT "Continuing rearrangement but absence of somatic hypermutation in
 RT immunoglobulin genes of human B cell precursor leukemia.";
 RL J. Exp. Med. 168:229-245(1988).
 RN [8]
 RX PubMed=2338551; DOI=10.1084/jem.169.4.1391;
 RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
 RT "Early human IGH gene assembly in Epstein-Barr virus-transformed fetal
 RT B cell lines. Preferential utilization of the most JH-proximal D
 RT segment (DQ52) and two unusual VH-related rearrangements.";
 RL J. Exp. Med. 169:1391-1403(1989).
 RN [9]
 RX PubMed=3301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
 RA Hilleson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
 RT "The structural basis of germline-encoded VH3 immunoglobulin binding
 RT to staphylococcal protein A";
 RL J. Exp. Med. 178:331-336(1993).
 DR EMBL, BC020240; AAH20240.1; -; mRNA.
 DR PIR; F36005; F36005.
 DR PIR; F36005; F36005.
 DR PIR; PH1642; PH1642.
 DR PIR; PH1643; PH1643.
 DR PIR; PH1645; PH1645.
 DR PIR; PH1646; PH1646.
 DR PIR; PL0098; PL0098.
 DR PIR; PL0120; PL0120.
 DR PIR; S15590; S15590.
 DR PIR; S31116; S31116.
 DR PIR; S31119; S31119.
 DR PIR; S70442; S70442.
 DR HSSP; P01861; IADQ.
 DR SMR; QBWUK1; 20-242.
 DR Ensembl; ENSG00000130076; Homo sapiens.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; Cl-set; 4.
 DR SMART; SM0406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 5.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 KW Immunoglobulin domain.
 SQ SEQUENCE 613 AA; 67296 MW; 60C/F5950671E315 CRC64;
 Query Match 92.0%; Score 81; DB 2; Length 613;
 Best Local Similarity 88.2%; Pred. No. 0.0001;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 VISFDGSKNYVDVSVKG 17
 |||:|||||:|||||
 Db 69 VISYDGSNKYYADSVKG 85
 RESULT 4
 Q9UL90_HUMAN
 ID Q9UL90_HUMAN PRELIMINARY; PRT; 113 AA.
 AC Q9UL90;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1730252;
 RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
 RA Schuurman R.K.;
 RT "Restricted utilization of germ-line VH3 genes and short diverse third
 RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
 RT immunoglobulin heavy chain rearrangements.";
 RL Eur. J. Immunol. 22:247-251(1992).
 DR EMBL; AF035024; AAD56260.1; -; mRNA.
 DR PIR; S78486; S78486.
 DR HSSP; P01772; 2F84.
 DR SMR; Q9UL90; 1-113.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM0406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR NON_TER 1
 DR NON_TER 113
 DR NON_TER 113
 SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086DD07F CRC64;
 Query Match 81.8%; Score 72; DB 2; Length 113;
 Best Local Similarity 81.2%; Pred. No. 0.00049;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 ISFDGSKNYVDVSVKG 17
 |||:|||||:|||||
 Db 51 IRYDGSNKYYADSVKG 66
 RESULT 5
 HV3G_HUMAN
 ID HV3G_HUMAN STANDARD; PRT; 122 AA.
 AC P01768;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-III region CAM.

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:11:28 ; Search time 56.8966 Seconds
(without alignments)
77.224 Million cell updates/sec

Title: US-10-720-323-3
Perfect score: 51
Sequence: 1 EARGSYAFDI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	5	Aau76329 Human ant
2	51	100.0	119	5	Aau76333 Human ant
3	42	82.4	10	5	Aam51160 Anti-tumo
4	38	74.5	309	8	Adn17429 Bacterial
5	38	74.5	349	8	Adm46159 Acinetoba
6	38	74.5	379	6	Ada33932 Acinetoba
7	38	74.5	585	8	Adn95004 Thermoact
8	37	72.5	11	5	Abp47174 Human Bly
9	37	72.5	11	7	Adg98001 scFV VHCD
10	37	72.5	243	5	Abp45924 Human Bly
11	37	72.5	243	7	Adg96751 Single ch
12	36	70.6	76	5	Adp29459 Streptoco
13	36	70.6	76	5	Adp30622 Streptoco
14	36	70.6	76	8	Adv89140 Streptoco
15	36	70.6	76	8	Adv82502 Streptoco
16	36	70.6	76	8	Adv80393 Streptoco
17	36	70.6	170	4	Adg75198 Human col
18	36	70.6	222	4	AAb63659 Human gas
19	36	70.6	433	4	Aau52806 Propionib
20	36	70.6	433	6	Abm49325 Propionib
21	36	70.6	487	7	Abm66397 Klebsiell
22	36	70.6	571	3	Aay78794 Human ant
23	36	70.6	637	4	ABG22566 Novel hum
24	36	70.6	653	3	Aay78796 Human TAC

25	36	70.6	653	4	ABG11232	Abg11232 Novel hum
26	36	70.6	750	4	ABG22567	Abg22567 Novel hum
27	36	70.6	796	7	ADC97438	E. faeciu
28	36	70.6	835	6	ABM65129	Abm65129 Propionib
29	36	70.6	865	4	AAM40464	Aam40464 Human pol
30	36	70.6	865	4	AAM40465	Aam40465 Human pol
31	36	70.6	865	4	AAM40466	Aam40466 Human pol
32	36	70.6	890	6	ABU18303	Abu18303 Protein e
33	36	70.6	966	4	AAM38679	Aam38679 Human pol
34	36	70.6	1013	4	AAM38678	Aam38678 Human pol
35	36	70.6	1025	4	AAM38680	Aam38680 Human pol
36	36	70.6	1026	6	ABO14710	AbO14710 Novel hum
37	36	70.6	1026	9	ADX07286	Adx07286 Cyclin-de
38	36	70.6	1026	9	AEb87755	AbE87755 Human TAC
39	36	70.6	1057	6	ABO14709	AbO14709 Novel hum
40	36	70.6	1219	3	AAy78795	Aay78795 Human ant
41	35	68.6	112	4	ABB11233	Abb11233 Human DNA
42	35	68.6	852	9	AEA00451	Aea00451 Human KRC
43	35	68.6	928	7	ADB67092	AdB67092 Kinesin h
44	35	68.6	929	8	ADL99363	AdL99363 Nanostruc
45	35	68.6	2353	8	ADQ97927	AdQ97927 Mouse can
46	35	68.6	2406	6	ABB82733	Abb82733 Human KRC
47	35	68.6	2406	7	ADJ69698	Adj69698 Human hea
48	35	68.6	2406	8	ADQ97930	Adq97930 Human can
49	35	68.6	2406	9	AEA00446	Aea00446 Human kap
50	34	66.7	13	9	ADW77411	AdW77411 Human pla
51	34	66.7	117	2	AAW76083	Aaw76083 HGV antiig
52	34	66.7	117	2	AAW76083	Aaw76083 HGV antiig
53	34	66.7	117	2	AAW92784	Aaw92784 US5856134
54	34	66.7	117	2	AAW94900	Aaw94900 Hepatitc
55	34	66.7	176	5	AAU97601	Aau97601 Haemophil
56	34	66.7	184	9	ABM91065	Abm91065 M. xanthu
57	34	66.7	192	5	ABP51385	Abp51385 Human MDD
58	34	66.7	232	2	AAW34978	Aaw34978 Hepatitc
59	34	66.7	242	6	ABP60522	Abp60522 APRIL bin
60	34	66.7	283	8	ADP29433	Adp29433 Human sec
61	34	66.7	311	8	ADY09123	Ady09123 Plant ful
62	34	66.7	341	8	ADX71874	Adx71874 Plant ful
63	34	66.7	541	6	ABU49011	Abu49011 Protein e
64	34	66.7	555	7	ADB63857	Adb63857 Human pro
65	34	66.7	570	5	ABB08159	Abb08159 Human cyt
66	34	66.7	785	7	ABM88146	Abm88146 Rice abio
67	34	66.7	853	2	AAW34977	Aaw34977 Hepatitc
68	34	66.7	853	2	AAW34974	Aaw34974 Hepatitc
69	34	66.7	853	2	AAW34975	Aaw34975 Hepatitc
70	34	66.7	857	6	ABU48441	Abu48441 Protein e
71	34	66.7	857	6	ABU48441	Abu48441 Protein e
72	34	66.7	912	5	ABG71106	Abg71106 Human ade
73	34	66.7	2723	2	AAW56448	Aaw56448 Fragment
74	34	66.7	2742	3	AAW23012	Aaw23012 Human APC
75	34	66.7	2841	2	AAW06537	Aaw06537 Hepatitc
76	34	66.7	2842	2	AAR63508	Aar63508 Adenomat
77	34	66.7	2842	5	ABG90968	Abg90968 Human APC
78	34	66.7	2842	7	ADJ92011	Adj92011 Hepatitc
79	34	66.7	2842	8	ADS92839	AdS92839 Hepatitc
80	34	66.7	2843	2	AAW26052	Aaw26052 APC gene
81	34	66.7	2843	2	AAW58634	Aaw58634 Adenomat
82	34	66.7	2843	2	AAW11922	Aaw11922 Adenomat
83	34	66.7	2843	2	AAW35392	Aaw35392 Human ade
84	34	66.7	2843	2	AAW38370	Aaw38370 Human ade
85	34	66.7	2843	2	AAW76140	Aaw76140 Human APC
86	34	66.7	2843	3	AAW76144	Aaw76144 Human APC
87	34	66.7	2843	3	AAW23011	Aaw23011 Human APC
88	34	66.7	2843	5	ABG90964	Abg90964 Human ade
89	34	66.7	2843	5	ABG71105	Abg71105 Human ade
90	34	66.7	2843	7	ADE65846	Ade65846 Human hea
91	34	66.7	2843	7	ADJ70164	Adj70164 Human hea
92	34	66.7	2843	8	ADJ32540	Adj32540 Human ade
93	34	66.7	2843	8	ADU48369	Adu48369 Human aci
94	34	66.7	2843	9	ADV70598	Adv70598 Amino aci
95	34	66.7	2843	9	ADX05614	Adx05614 Cyclin-de
96	34	66.7	2843	9	ADX70429	Adx70429 Human APC
97	34	66.7	2843	9	AEB93528	Aeb93528 Human ade

98 34 66.7 2844 8 ADO08044 Human pol
99 34 66.7 2860 2 AARG3507 Aar63507 Adenonato
100 34 66.7 2860 2 AAW63611 Aaw63611 Hepatitis

ALIGNMENTS

RESULT 1

AAU76329

ID AAU76329 standard; peptide; 10 AA.

AC AAU76329;

DT 21-MAY-2002 (first entry)

DE Human anti-dual integrin antibody heavy chain variable region CDR3.

XX Human; antibody; dual integrin; CDR; heavy chain variable region; HC CDR;
KW medical device; immune related disease; rheumatoid arthritis;
KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
KW neurological disease; multiple sclerosis; Parkinson's disease;
KW Alzheimer's disease; Creutzfeldt-Jakob disease.

XX Homo sapiens.

XX WO200212501-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024784.

XX 07-AUG-2000; 2000US-0223363P.

XX 01-AUG-2001; 2001US-00920267.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Heavner G, Snyder L, Trikha M;

XX WPI; 2002-217193/27.

XX N-PSDB; ABK10116.

XX Novel isolated mammalian anti-dual integrin antibody, useful for
PT diagnosing or treating dual integrin related condition such as rheumatoid
PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

XX Claim 29; Page 133; 144pp; English.

XX The invention relates to an isolated mammalian anti-dual integrin
CC antibody having at least one of the human heavy chain or light chain
CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
CC included are the nucleic acids encoding the CDRs, a vector comprising the
CC nucleic acids, a host cell comprising the vector, an anti-idiotype
CC antibody that binds to the anti-dual integrin, a medical device comprising
CC the antibody suitable for administration by parenteral, subcutaneous,
CC intramuscular, intravenous, intrarticular, intrabronchial,
CC intraabdominal, intracapsular, intracartilaginous, intracavitary,
CC intracelular, or other routes as given in specification. The antibody
CC is useful for diagnosing or treating a dual integrin related condition in
CC an animal for example, immune related disease such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
CC myocardial infarction, infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma, multiple myeloma; neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
CC Creutzfeldt-Jakob disease and many other diseases given in the

CC specification. The present sequence is an anti-dual integrin human heavy
CC chain CDR
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10

Db 1 EARGSYAFDI 10

RESULT 2

AAU76333

ID AAU76333 standard; peptide; 119 AA.

XX AAU76333;

XX 21-MAY-2002 (first entry)

DE Human anti-dual integrin antibody complete variable region #1.

XX Human; antibody; dual integrin; HC CDR; variable region; LC CDR;
KW medical device; immune related disease; rheumatoid arthritis;
KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
KW neurological disease; multiple sclerosis; Parkinson's disease;
KW Alzheimer's disease; Creutzfeldt-Jakob disease.

XX Homo sapiens.

XX WO200212501-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024784.

XX 07-AUG-2000; 2000US-0223363P.

XX 01-AUG-2001; 2001US-00920267.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Heavner G, Snyder L, Trikha M;

XX WPI; 2002-217193/27.

XX Novel isolated mammalian anti-dual integrin antibody, useful for
PT diagnosing or treating dual integrin related condition such as rheumatoid
PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

XX Claim 1; Page 134; 144pp; English.

XX The invention relates to an isolated mammalian anti-dual integrin
CC antibody having at least one of the human heavy chain or light chain
CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
CC included are the nucleic acids encoding the CDRs, a vector comprising the
CC nucleic acids, a host cell comprising the vector, an anti-idiotype
CC antibody that binds to the anti-dual integrin, a medical device comprising
CC the antibody suitable for administration by parenteral, subcutaneous,
CC intramuscular, intravenous, intrarticular, intrabronchial,
CC intraabdominal, intracapsular, intracartilaginous, intracavitary,
CC intracelular, or other routes as given in specification. The antibody
CC is useful for diagnosing or treating a dual integrin related condition in
CC an animal for example, immune related disease such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
CC myocardial infarction, infectious disease in a cell such as bacterial,

CC	given in AAM51165-66, or either all of the CDRs of the heavy chain (see
CC	AAM51158-60) or all of the CDRs of the light chain (see AAM51161-63). The
CC	antibody may inhibit TNF-induced cell adhesion molecules, inhibit TNF
CC	binding to receptor, or provide Arthritic Index improvement in a mouse
CC	model. It is useful for diagnosing or treating a TNF related condition in
CC	a cell, tissue, organ or animal (Claimed) such as rheumatoid arthritis,
CC	gastric ulcer, asthma, allergic rhinitis, Crohn's pathology, sickle cell
CC	anemia, diabetes, a cardiovascular disease such as arteriosclerosis,
CC	atherosclerosis, restenosis, angina pectoris or myocardial infarction, an
CC	infectious disease in a cell such as bacterial, viral, and fungal
CC	infections, pneumonia, leprosy and malaria, a malignant disease such as
CC	leukaemia, chronic myelocytic leukaemia, Burkitt's lymphoma and multiple
CC	myeloma, or a neurological disease such as multiple sclerosis,
CC	Parkinson's disease, spinal ataxia, Alzheimer's disease and Creutzfeldt-
CC	Jakob disease
XX	
SQ	Sequence 10 AA;
Query Match 82.4%; Score 42; DB 5; Length 10;	
Best Local Similarity 90.0%; Pred. No. 0.08;	
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 EARGSYAFDI 10
Dd	1 EARGSTAFDI 10
RESULT 4	
ADN17429	
ID	ADN17429 standard; protein; 309 AA.
XX	
AC	ADN17429;
AC	
DT	02-DEC-2004 (first entry)
XX	
DE	Bacterial polypeptide #82.
XX	
KW	Recombinant DNA construct; transformed plant; improved plant property;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW	pathogen tolerance; pest tolerance; plant disease resistance;
KW	cell cycle pathway modification; plant growth regulator;
KW	homologous recombination; seed oil yield; protein yield; carbohydrate;
KW	nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX	bacterial polypeptide.
OS	
XX	Bacteria.
PN	
PD	US2003233675-A1.
XX	
PD	18-DEC-2003.
XX	
PF	20-FEB-2003; 2003US-00369493.
XX	
PR	21-FEB-2002; 2002US-0360039P.
XX	(CAOY/) CAO Y.
PA	(HINK/) HINKLE G J.
PA	(SLAT/) SLATER S C.
PA	(CHEN/) CHEN X.
PA	(GOLD/) GOLDMAN B S.
XX	
PI	Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX	
DR	WPI; 2004-061375/06.
XX	
PT	New recombinant DNA construct comprising a promoter positioned to provide
PT	for expression of a polynucleotide encoding a polypeptide from a
PT	microbial source, useful for producing plants with improved properties.
XX	
PS	Claim 1; SEQ ID NO 82; 122pp; English.
XX	
CC	The invention relates to a recombinant DNA construct comprising a
CC	promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 309 AA;

Query Match 74.5%; Score 38; DB 8; Length 309;
 Best Local Similarity 70.0%; Pred. No. 26;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSVAFDI 10
 :|:|||||
 Db 98 KAKGVVAFDI 107

RESULT 5
 ADM46159
 ID ADM46159 standard; protein; 349 AA.

XX ADM46159;
 XX 17-JUN-2004 (first entry)

XX Acinetobacter outer membrane protein A (OMP A).

XX Outer membrane protein A; OMP A; IL-8; interleukin-8; peptic ulcer;
 KW cancer; respiratory disease; sepsis; antiulcer; cytostatic;
 KW antibacterial; immunosuppressive.

XX Acinetobacter sp.

XX Key Location/Qualifiers
 FH Region 22..349
 FT /note= "Specifically claimed in Claim 9"
 FT Peptide 36..45
 FT /note= "Antigenic peptide. Specifically claimed in Claim
 2"
 FT Peptide 111..120
 FT /note= "Antigenic peptide. Specifically claimed in Claim
 2"
 FT Peptide 129..147
 FT /note= "Antigenic peptide. Specifically claimed in Claim
 2"
 FT Peptide 337..349
 FT /note= "Antigenic peptide. Specifically claimed in Claim
 2"

XX US6713062-B1.

XX 30-MAR-2004.

XX 17-MAY-2000; 2000US-00573630.

XX 17-MAY-1999; 99US-0134399P.

XX (UNMI) UNIV MICHIGAN.
 PA Merchant JL;
 PI
 XX
 DR WPI; 2004-345078/32.
 DR N-PSDB; ADM46158, ADM46163.

XX New Acinetobacter outer membrane protein and nucleic acids, useful for
 PT diagnosing or treating diseases including peptic ulcers, cancers,
 PT respiratory diseases or sepsis.

XX Claim 9; SEQ ID NO 2; 59pp; English.

XX The present invention relates to the isolation of Acinetobacter sp. outer
 CC membrane protein A (OMP A), and polynucleotide sequences encoding it. The
 CC OMP A polypeptide stimulates IL-8 (interleukin-8) expression and cross-
 CC reacts with an antibody that binds to the Acinetobacter OMP A protein.
 CC Also disclosed are antigenic peptides of the OMP A polypeptide. The OMP A
 CC polypeptide and antigenic peptides are useful for diagnosing or treating
 CC diseases including peptic ulcers, cancers, respiratory diseases, sepsis
 CC and other conditions. The OMP A polypeptide is also useful for preparing
 CC a vaccine in situations where an antibody is not required to cross an
 CC epithelial cell barrier to be effective. The present sequence represents
 CC Acinetobacter OMP A.

XX Sequence 349 AA;

Query Match 74.5%; Score 38; DB 8; Length 349;
 Best Local Similarity 77.8%; Pred. No. 30;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSVAFD 9
 :|:|||||
 Db 169 EARGTHFD 177

RESULT 6
 ADA33932
 ID ADA33932 standard; protein; 379 AA.

XX ADA33932;

XX 20-NOV-2003 (first entry)

XX Acinetobacter baumannii protein #1093.

XX Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
 KW plant biocontrol agent.

XX Acinetobacter baumannii.

XX US6562958-B1.

XX 13-MAY-2003.

XX 04-JUN-1999; 99US-00328352.

XX 09-JUN-1998; 98US-0088701P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton G, Bush D;

XX WPI; 2003-576092/54.

XX N-PSDB; ADA29806.

XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
 PT for diagnosing a bacterial disease, as components of antibacterial
 PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
 PT plants.

XX Example; SEQ ID NO 5219; 328pp; English.

XX The invention relates to isolated Acinetobacter baumannii nucleic acids.
 CC The A. baumannii nucleic acids and polypeptides are useful as reagents
 CC for diagnosing a bacterial disease, as components of antibacterial
 CC vaccines, as targets for antibacterial drugs, to detect the presence of
 CC A. baumannii and other Acinetobacter species in a sample, in screening
 CC compounds for the ability to interfere with the A. baumannii life cycle
 CC or to inhibit A. baumannii infection, and as biocontrol agents for
 CC plants. The present sequence represents the amino acid sequence of an A.
 CC baumannii protein.
 XX
 SQ Sequence 379 AA;

Query Match 74.5%; Score 38; DB 6; Length 379;
 Best Local Similarity 77.8%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFD 9
 |||||
 Db 193 EARGTYNFD 201

RESULT 7
 ADN95004
 ID ADN95004 standard; protein; 585 AA.
 XX
 AC ADN95004;
 DT
 XX
 XX 01-JUL-2004 (first entry)

DE Thermoactinomyces vulgaris alpha-amylase TVAII protein.

XX isomalto oligosaccharide; alpha-1,4-glycoside linkage; pullulan; panose;
 KW glucose; foodstuff; low calorie; health food; alpha-amylase; TVAII;
 KW enzyme; bifidobacterium proliferation factor.
 XX
 OS Thermoactinomyces vulgaris.
 XX

PN JP2004097233-A.

XX 02-APR-2004.

XX 22-DEC-2003; 2003JP-00424104.

XX 12-JUL-1993; 93JP-00193881.

XX (QJIP) OJI CORN STARCH CO LTD.

PA (SAKA/) SAKANO Y.

XX WPI; 2004-394213/37.

DR N-PSDB; ADN95003.

XX Producing isomalto oligosaccharide for use in the food industry,
 PT comprises reacting an enzyme which hydrolyzes an alpha-1, 4-glycoside
 PT linkage on pullulan or panose in the presence of glucose.

XX Disclosure; Fig 1; 12pp; Japanese.

XX The invention relates to a novel method for producing an isomalto
 CC oligosaccharide which comprises reacting an enzyme that hydrolyses an
 CC alpha-1,4-glycoside linkage on pullulan or panose in the presence of
 CC glucose. The method of the invention may be useful for producing an
 CC isomalto oligosaccharide to be used as a foodstuff material. The isomalto
 CC oligosaccharide produced by the method has reduced sweet taste and low
 CC calorie content, is non-fermentable, has a low bifidobacterium
 CC proliferation factor and is useful as a health food material. The current
 CC sequence is that of the thermoactinomyces vulgaris alpha-amylase TVAII
 CC protein of the invention.

XX Sequence 585 AA;

Query Match 74.5%; Score 38; DB 8; Length 585;
 Best Local Similarity 70.0%; Pred. No. 53;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EARGSYAFDI 10
 |||||
 Db 9 EARGSYAYPI 18
 RESULT 8
 ABP47174
 ID ABP47174 standard; peptide; 11 AA.
 XX
 AC ABP47174;
 XX
 XX 19-AUG-2002 (first entry)
 DT
 XX Human BLYS binding scFv VH CDR3 SEQ ID 3185.
 DE
 XX BLYS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antitumour;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.
 DR Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

XX Claim 2; Page 3130; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (BLYS) polypeptides. BLYS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antitumour, and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BLYS. The antibodies bind to BLYS
 CC and so may be used to detect and quantitate the presence of BLYS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BLYS. They may also be
 CC administered to treat diseases associated with aberrant BLYS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX Sequence 11 AA;

Query Match 72.5%; Score 37; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	4	GSYAFDI 10		
DB	5	GSYAFDI 11		
RESULT 9				
ADG98001				
ID	ADG98001	standard; peptide; 11 AA.		
XX	AC	ADG98001;		
XX	DT	11-MAR-2004 (first entry)		
XX	DE	Human BlyS binding scFv SEQ ID 1935.		
XX	KW	BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiasthmatic; antiallergic; cytostatic.		
OS	Unidentified.			
XX	PN	WO2003055979-A2.		
XX	PD	10-JUL-2003.		
XX	PF	14-NOV-2002; 2002WO-US036496.		
XX	PR	16-NOV-2001; 2001US-0331469P.		
XX	PR	19-DEC-2001; 2001US-0340817P.		
XX	PA	(HUMA-) HUMAN GENOME SCI INC.		
XX	PI	Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D; WPI; 2003-505530/47.		
XX	DR	Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BlyS), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.		
XX	PS	Example 1; SEQ ID NO 3185; 394pp; English.		
XX	CC	This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BlyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BlyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory diseases e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antiasthmatic, antiallergic and cytostatic. This peptide sequence is a single chain antibody variable heavy CDR3 peptide that immunospecifically binds BlyS of the invention.		
XX	SQ	Sequence 11 AA;		
Query Match	72.5%;	Score 37;	DB 7;	Length 11;
Best Local Similarity	100.0%;	Pred. No. 1;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	4	GSYAFDI 10		
DB	5	GSYAFDI 11		
RESULT 10				
ADG45924				
ID	ADG45924	standard; protein; 243 AA.		
XX	AC	ADG45924;		
XX	DT	19-AUG-2002 (first entry)		
XX	DE	Human BlyS binding scFv SEQ ID 1935.		
XX	KW	BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.		
OS	Homo sapiens.			
XX	PN	WO200202641-A1.		
XX	PD	10-JAN-2002.		
XX	PF	15-JUN-2001; 2001WO-US019110.		
XX	PR	16-JUN-2000; 2000US-0212210P.		
XX	PR	17-OCT-2000; 2000US-0240816P.		
XX	PR	16-MAR-2001; 2001US-0276248P.		
XX	PR	21-MAR-2001; 2001US-0277379P.		
XX	PR	25-MAY-2001; 2001US-0293499P.		
XX	PA	(HUMA-) HUMAN GENOME SCI INC.		
XX	PI	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.		
XX	PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D; WPI; 2002-114799/15.		
XX	DR	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.		
XX	PS	Claim 1; Page 2709-2710; 3148pp; English.		
XX	CC	This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BlyS. The antibodies bind to BlyS and so may be used to detect and quantitate the presence of BlyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BlyS. They may also be administered to treat diseases associated with aberrant BlyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention		
XX	SQ	Sequence 243 AA;		
Query Match	72.5%;	Score 37;	DB 5;	Length 243;
Best Local Similarity	100.0%;	Pred. No. 32;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	4	GSYAFDI 10		

```

Db      103 GSYAFDI 109

RESULT 11
ADG96751
ID      ADG96751 standard; protein; 243 AA.
XX
AC      ADG96751;
XX
DT      11-MAR-2004 (first entry)
XX
DE      Single chain antibody that immunospecifically binds Blys SeqID 1935.
XX
KW      antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW      B cell proliferation; differentiation; scfv; myasthenia gravis;
KW      multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW      carcinoma; lymphoma; anti-rheumatic; antiarthritic; neuroprotective;
KW      antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS      Unidentified.
XX
PN      WO2003055979-A2.
XX
PD      10-JUL-2003.
XX
PF      14-NOV-2002; 2002WO-US036496.
XX
PR      16-NOV-2001; 2001US-0331469P.
PR      19-DEC-2001; 2001US-0340817P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR      WPI; 2003-505530/47.
XX
PT      Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT      (Blys), useful for detecting and treating diseases or disorders e.g.
PT      rheumatoid arthritis, asthma and leukemia.
XX
PS      Example 1; SEQ ID NO 1935; 394pp; English.
XX
CC      This invention relates to novel antibodies that immunospecifically bind
CC      to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC      chromosome 13q34 and encodes a protein that is a member of the tumour
CC      necrosis factor superfamily and induces both in vivo and in vitro B cell
CC      proliferation and differentiation. Specifically, it refers to single
CC      chain antibody molecules (scFvs) derived, preferably, from the variable
CC      heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC      fragment thereof, of either human, murine, rat or monkey Blys. The
CC      present invention refers to the use of such antibodies in various methods
CC      for the detection, diagnosis and prognosis of diseases related to the
CC      aberrant expression or inappropriate function of Blys or its receptor. As
CC      such, these compositions are useful for identifying immune disorders
CC      including myasthenia gravis and multiple sclerosis, inflammatory
CC      disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC      as AIDS and proliferative disorders including leukaemia, carcinoma and
CC      lymphoma. Accordingly, they can be described as exhibiting various
CC      activities such as antirheumatic, antiallergic, neuroprotective,
CC      antiinflammatory, antiasthmatic, antiarthritic and cytostatic. This
CC      polypeptide sequence is a single chain antibody that binds Blys of the
CC      invention. NOTE: The sequence data for this patent did not form part of
CC      the printed specification, but was obtained in electronic format
CC      directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
XX
SQ      Sequence 243 AA;

Query Match      72.5%; Score 37; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 32;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 GSYAFDI 10
      |||||

Db      103 GSYAFDI 109

RESULT 12
ABP29459
ID      ABP29459 standard; protein; 76 AA.
XX
AC      ABP29459;
XX
DT      02-JUL-2002 (first entry)
XX
DE      Streptococcus polypeptide SEQ ID NO 8094.
XX
KW      Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW      group A streptococcus; Streptococcus pyogenes; antibacterial;
KW      antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX
OS      Streptococcus pyogenes.
XX
PN      WO200234771-A2.
XX
PD      02-MAY-2002.
XX
PF      29-OCT-2001; 2001WO-GB004789.
XX
PR      27-OCT-2000; 2000GB-00026333.
PR      24-NOV-2000; 2000GB-00028727.
PR      07-MAR-2001; 2001GB-00005640.
XX
PA      (CHIR-) CHIRON SPA.
PA      (GENO-) INST GENOMIC RES.
XX
PI      Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;
PI      Tettelin H;
XX
DR      WPI; 2002-352536/38.
DR      N-PSDB; ABN70090.
XX
PT      New Streptococcus protein for the treatment or prevention of infection or
PT      disease caused by Streptococcus bacteria, such as meningitis, and for
PT      detecting a compound that binds to the protein.
XX
PS      Claim 1; Page 3932; 4525pp; English.
XX
CC      The invention relates to a protein (ABP25413-ABP30895) from group B
CC      streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC      (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC      the specification. The proteins have antibacterial and antiinflammatory
CC      activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
CC      antibodies that bind (I) are used in the manufacture of medicaments for
CC      the treatment or prevention of infection or disease caused by
CC      Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC      Nucleic acids encoding (I) are used to detect Streptococcus in a
CC      biological sample. (I) is used to determine whether a compound binds to
CC      (I). A composition comprising (I) or a nucleic acid encoding (I), may be
CC      used as a vaccine or diagnostic composition. The disease caused by
CC      Streptococcus that is prevented or treated may be meningitis. Nucleic
CC      acid encoding (I) may be used to recombinantly produce (I) and may be
CC      used in gene therapy. Antibodies to (I) are used for affinity
CC      chromatography, immunoassays, and distinguishing/identifying
CC      Streptococcus proteins
XX
SQ      Sequence 76 AA;

Query Match      70.6%; Score 36; DB 5; Length 76;
Best Local Similarity 77.8%; Pred. No. 14;
Matches      7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EARGSYAFD 9
      |||||
Db      54 EARESISFD 62

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RESULT 13
 ABP30622
 ID ABP30622 standard; protein; 76 AA.
 XX
 AC ABP30622;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Streptococcus polypeptide SEQ ID NO 10420.
 XX
 DE Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus agalactiae.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB004789.
 XX
 PR 27-OCT-2000; 2000GB-00026333.
 PR 24-NOV-2000; 2000GB-00028727.
 PR 07-MAR-2001; 2001GB-00005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI: 2002-352536/38.
 DR N-PSDB; ABN71253.
 XX
 XX New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for
 PT detecting a compound that binds to the protein.
 XX
 PS Claim 1; Page 4167; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (II), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins
 XX
 SQ Sequence 76 AA;
 Query Match 70.6%; Score 36; DB 5; Length 76;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EARGSYAFD 9
 ||| |||:
 DB 54 EARESYSPD 62
 RESULT 14
 ADV89140
 ID ADV89140 standard; protein; 76 AA.

XX
 AC ADV89140;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE Streptococcus agalactiae protein sequence, SEQ ID 1534.
 XX
 KW Antibacterial; Vaccine; bacterial infection.
 XX
 OS Streptococcus agalactiae.
 XX
 PN FR2824074-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 26-APR-2001; 2001FR-00005642.
 XX
 PR 26-APR-2001; 2001FR-00005642.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalloui L;
 PI Zouane M, Couve E, Buchrieser C, Poyart C, Trieu CP, Kunst F;
 XX
 DR WPI; 2004-101891/11.
 XX
 PT Genomic nucleotide sequences encoding polypeptides of Streptococcus
 PT agalactiae for the development of vaccines, diagnostic tools, DNA chips
 PT and identification of therapeutic targets.
 XX
 PS Claim 6; SEQ ID NO 1534; 2687pp; French.
 XX
 CC The present invention relates to novel Streptococcus agalactiae
 CC nucleotide sequences (I; ADV87607-ADV87745) and novel polypeptides (II;
 CC ADV87746-ADV89950). The nucleotide sequences encode polypeptides of S.
 CC agalactiae involved in the synthesis of amino acids, cell membranes,
 CC intermediate (central) metabolism, energetic metabolism, fatty acid and
 CC phospholipid metabolism, nucleotide metabolism including purines,
 CC pyrimidines and/or nucleosides, regulatory functions, replication,
 CC transcription, translation, protein transport, adaptation to atypical
 CC conditions, sensitivity to medicines and/or analogues, functions related
 CC to transporters, biosynthesis of cofactors, prosthetic groups and
 CC transposons, cell membrane proteins and cellular machinery. (I) are
 CC useful for the detection and/or amplification of nucleic acids.
 CC Pharmaceutical composition comprising (I) or (II) are useful for
 CC treatment of a bacterial S. agalactiae infection. Notes: WO200292818A2 is
 CC equivalent for the present basic patent FR2824074A1. WO200292818A2
 CC contains 6617 sequence whereas the present patent only contains 2344
 CC sequences.
 XX
 SQ Sequence 76 AA;
 Query Match 70.6%; Score 36; DB 8; Length 76;
 Best Local Similarity 77.8%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EARGSYAFD 9
 ||| |||:
 DB 54 EARESYSPD 62
 RESULT 15
 ADV82502
 ID ADV82502 standard; protein; 76 AA.
 XX
 AC ADV82502;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE Streptococcus agalactiae protein, SEQ ID 3643.
 XX
 KW Antibacterial; vaccine; bacterial infection.


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XX Streptococcus agalactiae.
XX WO200292818-A2.
XX 21-NOV-2002.
XX 26-APR-2002; 2002WO-IB003059.
XX 26-APR-2001; 2001FR-00005642.
XX (INSP ) INST PASTEUR.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX Glaser P, Rusniok C, Chevalier F, Frangeul L, Lalioui L;
XX Zouine M, Couve E, Buchrieser C, Poyart C, Trieu-Cuot P, Kunst F;
XX WPI; 2004-101891/11.
XX Genomic nucleotide sequences encoding polypeptides of Streptococcus
XX agalactiae for the development of vaccines, diagnostic tools, DNA chips
XX and identification of therapeutic targets.
XX Claim 6; SEQ ID NO 3643; 439pp; French.
XX The present invention relates to novel Streptococcus agalactiae
XX nucleotide sequences (I; ADV78860-ADV78998 and ADV83341-ADV85476) and
XX novel polypeptides (II; ADV78999-ADV81203 and ADV81205-ADV83340). The
XX nucleotide sequences encode polypeptides of S. agalactiae involved in the
XX synthesis of amino acids, cell membranes, intermediate (central)
XX metabolism, energetic metabolism, fatty acid and phospholipid metabolism,
XX nucleotide metabolism including purines, pyrimidines and/or nucleosides,
XX regulatory functions, replication, transcription, translation, protein
XX transport, adaptation to atypical conditions, sensitivity to medicines
XX and/or analogues, functions related to transposons, biosynthesis of
XX cofactors, prosthetic groups and transporters, cell membrane proteins and
XX cellular machinery. (I) are useful for the detection and/or amplification
XX of nucleic acids. Pharmaceutical composition comprising (I) or (II) are
XX useful for treatment of a bacterial S. agalactiae infection. The complete
XX genome of Streptococcus agalactiae is given in ADV81204. Note: The
XX present patent is an equivalent for the basic patent FR2824074A1, which
XX contains only 2344 sequences.
XX Sequence 76 AA;
XX Query Match 70.6%; Score 36; DB 8; Length 76;
XX Best Local Similarity 77.8%; Pred. No. 14;
XX Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFD 9
DB 54 EARESYSFD 62

RESULT 16
ADV80393
ID ADV80393 standard; protein; 76 AA.
XX AC ADV80393;
XX DT 24-FEB-2005 (first entry)
XX DE Streptococcus agalactiae protein, SEQ ID 1534.
XX KW Antibacterial; vaccine; bacterial infection.
XX OS Streptococcus agalactiae.
XX PN WO200292818-A2.
XX PD 21-NOV-2002.
XX PF 26-APR-2002; 2002WO-IB003059.

QY 1 EARGSYAFD 9
DB 54 EARESYSFD 62

RESULT 17
AAG75198
ID AAG75198 standard; protein; 170 AA.
XX AC AAG75198;
XX DT 03-SEP-2001 (first entry)
XX DE Human colon cancer antigen protein SEQ ID NO:5962.
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KM colorectal carcinoma; chromosome 10.
XX OS Homo sapiens.
XX PN WO200122920-A2.
XX PD 05-APR-2001.
XX PF 28-SEP-2000; 2000WO-US026524.
XX .XX 29-SEP-1999; 99US-0157137P.
XX PR 03-NOV-1999; 99US-0163280P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA Ruben SM, Barash SC, Birse CE, Rosen CA;
XX PI

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XX DR WPI; 2001-235357/24.
XX DR N-PSDB; AAB34603.
XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX PS Claim 11; Page 7467-7468; 9803pp; English.
XX CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX CC proteins are collectively known as colon cancer antigens. The colon
XX CC cancer antigens have cytostatic activity and can be used in gene therapy
XX CC and vaccine production. N and P may be used in the prevention, diagnosis
XX CC and treatment of diseases associated with inappropriate P expression. For
XX CC example, N and P may be used to treat disorders associated with decreased
XX CC expression by rectifying mutations or deletions in a patient's genome
XX CC that affect the activity of P by expressing inactive proteins or to
XX CC supplement the patient's own production of P. Additionally, N may be used
XX CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
XX CC into a host cell and culturing the cell to express the proteins. N and P
XX CC can be used in the prevention, diagnosis and treatment of colorectal
XX CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
XX CC sequences used in the exemplification of the present invention. N.B.
XX CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
XX CC time of publication, meaning no sequences are present for SEQ ID NO:1027
XX CC to 1052, 7921 and 7922
XX SQ Sequence 170 AA;
    Query Match 70.6%; Score 36; DB 4; Length 170;
    Best Local Similarity 66.7%; Pred. No. 35;
    Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ARGSYAFDI 10
Db 69 AKGTYTFDI 77
    |.:|:|

RESULT 18
AAB63659
ID AAB63659 standard; protein; 222 AA.
AC AAB63659;
XX 26-MAR-2001 (first entry)
XX Human gastric cancer associated antigen protein sequence SEQ ID NO:1021.
XX Human, breast cancer; gastric cancer; prostate cancer; diagnosis;
XX cancer associated antigen; cytostatic; cancer vaccine.
XX Homo sapiens.
XX WO2000073801-A2.
XX 07-DEC-2000.
XX 26-MAY-2000; 2000WO-US014749.
XX 28-MAY-1999; 99US-0136526P.
XX 10-SEP-1999; 99US-0153454P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Obata Y;
XX WPI; 2001-025274/03.
XX Nucleic acids encoding breast, gastric and prostate cancer associated
XX PT antigen precursors, useful for diagnosing and treating a condition
XX PT characterized by expression of an abnormal amount of a protein, e.g.
XX PT cancer.

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XX PS Example 1; Page 658; 799pp; English.
XX CC AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
XX CC represent nucleotide sequences encoding human breast, gastric and
XX CC prostate cancer associated antigen precursors (CAAP) respectively.
XX CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
XX CC represent human breast, gastric and prostate CAAP protein sequence
XX CC respectively. CAAPs have cytostatic activity and can be used in the
XX CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
XX CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
XX CC condition characterised by expression of an abnormal amount of a protein,
XX CC e.g. cancer
XX SQ Sequence 222 AA;
    Query Match 70.6%; Score 36; DB 4; Length 222;
    Best Local Similarity 66.7%; Pred. No. 47;
    Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 ARGSYAFDI 10
Db 140 AKGTYTFDI 148
    |.:|:|

RESULT 19
AAU52806
ID AAU52806 standard; protein; 433 AA.
XX AAU52806;
XX 27-FEB-2002 (first entry)
XX Propionibacterium acnes immunogenic protein #13702.
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant.
XX Propionibacterium acnes.
XX WO200181581-A2.
XX 01-NOV-2001.
XX 20-APR-2001; 2001WO-US012865.
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX (CORI-) CORIXA CORP.
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
XX N-PSDB; AAS59557.
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris.
XX Example 1; SEQ ID NO 14001; 1069pp; English.
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory

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CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 433 AA;

Query Match 70.6%; Score 36; DB 4; Length 433;
 Best Local Similarity 60.0%; Pred. No. 99;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
 Db 347 EARTWYAYDV 356
 ||| :|||:
 1 EARGSYAFDI 10
 347 EARTWYAYDV 356

RESULT 20
 ABM49325
 ID ABM49325 standard; protein; 433 AA.
 XX
 AC ABM49325;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #14001.
 XX
 KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieue-Dougllass J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64486.
 XX
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide; useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 XX Example 1; SEQ ID NO 14001; 1481pp; English.
 PS
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM5624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC polynucleotide; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising P. acnes polypeptides,
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,

CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 433 AA;

Query Match 70.6%; Score 36; DB 6; Length 433;
 Best Local Similarity 60.0%; Pred. No. 99;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
 Db 347 EARTWYAYDV 356
 ||| :|||:
 1 EARGSYAFDI 10
 347 EARTWYAYDV 356

RESULT 21
 ABO66397
 ID ABO66397 standard; protein; 487 AA.
 XX
 AC ABO66397;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Klebsiella pneumoniae polypeptide seqid 12914.
 XX
 KW Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN US6610836-B1.
 XX
 PD 26-AUG-2003.
 XX
 PF 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton GL, Osborne M;
 XX
 DR WPI; 2003-895346/82.
 DR N-PSDB; ACH99948.
 XX
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 PS
 XX Disclosure; SEQ ID NO 12914; 932pp; English.
 XX
 XX The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 487 AA;

Query Match 70.6%; Score 36; DB 7; Length 487;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
||| :|||:
Db 47 ARGEHAFDV 55

RESULT 22
AAY78794
ID AAY78794 standard; protein; 571 AA.
XX AAY78794;
AC
XX
DT 19-MAY-2000 (first entry)
XX
DE Human antizuai-1 (AZ-1) protein sequence.
XX
DE Antizuai-1; AZ-1; human; breast cancer; malignancy reversion;
KW tumour suppressor; malignancy progression marker.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..107
FT /label= SPAZI
FT /note= " Serine and proline rich domain"
FT 109..248
FT /label= Region_I
FT 250..360
FT /label= Region_II
FT 362..571
FT /label= CCD
FT /note= "Coiled-coil domain"
XX
XX WO20000503-A1.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US014482.
XX
XX 26-JUN-1998; 98US-0090747P.
XX
XX (CHEN/) CHEN H.
PA (BISS/) BISSELL M.
XX
XX Chen H, Bissell M;
PI
XX WPI; 2000-170903/15.
DR N-PSDB; AAZ90111.
XX
XX New nucleic acid encoding a tumor suppressor or marker, used for
PT diagnosis, monitoring progress or treatment, and gene therapy of breast
PT cancer.
XX
XX Claim 5; Fig 6; 120pp; English.
XX
XX This sequence represents the human antizuai-1 (AZ-1) protein sequence.
CC The AZ-1 gene is located on chromosome 10q26, and encodes a protein that
CC acts as a tumour suppressor or marker of malignancy progression or
CC reversion. The AZ-1 protein is a tumour suppressor, it interacts with E-
CC cadherin and beta-catenin. The protein has four domains, a serine and
CC proline rich domain (SPAZI), two regions which have immunoglobuline like
CC folds, and a coiled-coil domain which forms amphipathic helices that
CC associate with other like domains. Detecting low levels of AZ-1
CC nucleotide or amino acid sequences are used to diagnose a breast cell
CC malignancy, also for monitoring disease progression, particularly
CC assessment of therapeutic efficacy. The nucleotide sequence is used in
CC vivo or ex vivo gene therapy, and AZ-1 polypeptides are used for treating
CC or preventing breast cancer. AZ-1 polypeptides are also used to raise
CC specific antibodies, for diagnostic detection of AZ-1. Fragments of the

CC AZ-1 nucleotide sequence are useful as probes or primers for detecting
CC expression of the AZ-1 gene
XX
SQ Sequence 571 AA;
Query Match 70.6%; Score 36; DB 3; Length 571;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
|:|:|
Db 35 AKGTYTFDI 43

RESULT 23
ABG22566
ID ABG22566 standard; protein; 637 AA.
XX
AC ABG22566;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22557.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
DR N-PSDB; AAS86753.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 52925; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

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XX SQ Sequence 637 AA;
Query Match 70.6%; Score 36; DB 4; Length 637;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 389 AKGTYTFDI 397
|:|:|

RESULT 24
AAY78796
ID AAY78796 standard; protein; 653 AA.
XX AC AAY78796;
XX DT 19-MAY-2000 (first entry)
XX DE Human TACC2 (AZ-1 variant) amino acid sequence.
XX KW TACC2; AZ-1 variant; human; breast cancer; malignancy progression marker;
XX KM malignancy reversion; tumour suppressor.
XX OS Homo sapiens.
XX PN WO20000503-A1.
XX PD 06-JAN-2000.
XX PF 25-JUN-1999; 99WO-US014482.
XX PR 26-JUN-1998; 98US-0090747P.
XX PA (CHEN/) CHEN H.
XX PA (BISS/) BISSELL M.
XX PI Chen H, Bissell M;
XX WPI; 2000-170903/15.
XX N-PSDB; AAZ90113.
XX New nucleic acid encoding a tumor suppressor or marker, used for
PT diagnosis, monitoring progress or treatment, and gene therapy of breast
PT cancer.
XX Claim 6; Fig 20; 120pp; English.
XX This sequence represents the human TACC2 amino acid sequence. The TACC2
CC gene is a variant of the antizual-1 (AZ-1) gene (see AAZ90111). The AZ-1
CC gene is located on chromosome 10q26, and encodes a protein that acts as a
CC tumour suppressor or marker of malignancy progression or reversion. The
CC AZ-1 protein and its variants are tumour suppressors, AZ-1 interacts with
CC E-cadherin and beta-catenin. Detecting low levels of AZ-1 nucleotide or
CC amino acid sequences are used to diagnose a breast cell malignancy, also
CC for monitoring disease progression, particularly assessment of
CC therapeutic efficacy. The nucleotide sequence is used in vivo or ex
CC vivo gene therapy, and AZ-1 polypeptides are used for treating or
CC preventing breast cancer. AZ-1 polypeptides are also used to raise
CC specific antibodies, for diagnostic detection of AZ-1. Fragments of the
CC AZ-1 nucleotide sequence are useful as probes or primers for detecting
CC expression of the AZ-1 gene
XX SQ Sequence 653 AA;
Query Match 70.6%; Score 36; DB 3; Length 653;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 66 AKGTYTFDI 74
|:|:|

RESULT 25
ABG11232
ID ABG11232 standard; protein; 653 AA.
XX AC ABG11232;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #11223.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KM food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS75419.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 20; SEQ ID NO 41591; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 653 AA;
Query Match 70.6%; Score 36; DB 4; Length 653;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 66 AKGTYTFDI 74
|:|:|

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RESULT 26
ABG22567
ID ABG22567 standard; protein; 750 AA.
XX
AC ABG22567;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22558.
XX
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS86754.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 52926; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activities. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 750 AA;
XX
Query Match 70.6%; Score 36; DB 4; Length 750;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ARGSVAFDI 10
Db 151 AKGTYTFDI 159
|||:|
|:|:|

RESULT 27
,ADC97438
ID ADC97438 standard; protein; 796 AA.
XX
AC ADC97438;
XX
DT 01-JAN-2004 (first entry)
XX
DE E. faecium protein sequence SEQ ID 7065.
XX
DE Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
XX KW abdominal-pelvic infection.
XX
OS Enterococcus faecium.
XX
PN US6583275-B1.
XX
PD 24-JUN-2003.
XX
XX 30-JUN-1998; 98US-00107532.
XX
XX 02-JUL-1997; 97US-0051571P.
XX
XX 14-MAY-1998; 98US-0085598P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Doucette-Stamm LA, Bush D;
XX
XX WPI; 2003-799836/75.
XX
XX N-PSDB; ADC93784.
XX
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
XX Enterococcus faecium polypeptide useful for detection, prevention and
XX treatment of a pathological condition resulting from a bacterial
XX infection.
XX
XX Example 1; SEQ ID NO 7065; 243pp; English.
XX
XX The invention relates to an isolated nucleic acid derived from
XX Enterococcus faecium encoding an Enterococcus faecium polypeptide having
XX one of 10 fully defined sequences given in the (or comprising 40
XX sequential nucleotides chosen from any of the nucleic acids, its
XX complement or sequences hybridising to it). Also included are a
XX recombinant vector comprising the nucleic acid operably linked to a
XX transcription regulatory element, a cell comprising the vector and a
XX single-stranded probe comprising the nucleic acid. The nucleic acids are
XX chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
XX The nucleic acids are useful for diagnosing pathological conditions
XX resulting from E. faecium bacterial infection (e.g. urinary tract
XX infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
XX infection) and for screening drugs such as agonists and antagonists. The
XX nucleic acid is useful for recombinant production of Candida albicans -
XX derived peptides or antisense polypeptides. Pharmaceutical compositions
XX and vaccines containing the nucleic acid are useful for preventing or
XX treating Enterococcus faecium infections. The present sequence represents
XX one if the disclosed E. faecium proteins.
XX
XX Sequence 796 AA;
XX
Query Match 70.6%; Score 36; DB 7; Length 796;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 EARGSVAFDI 10
Db 732 EAKGDFSPDV 741
|||:|
|:|:|

RESULT 28
ABM65129
ID ABM65129 standard; protein; 835 AA.
XX
AC ABM65129;
XX
XX 20-OCT-2003 (first entry)
```

XX DE Propionibacterium acnes immunogenic polypeptide #29805.
 XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KW KW immunostimulant; immune response; vaccine; immunogenic.
 XX OS Propionibacterium acnes.
 XX PN W02003033515-A1.
 XX PD 24-APR-2003.
 XX XX 11-OCT-2002; 2002WO-US032727.
 XX PF 15-OCT-2001; 2001US-00978825.
 XX PR (CORI-) CORIXA CORP.
 XX PA Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallie-Douglass J;
 XX WPI; 2003-381789/36.
 XX XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX PS Claim 7; SEQ ID NO 29805; 1481pp; English.
 XX CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a specifically claimed P. acnes polypeptide which is
 CC thought to contain an immunogenic region. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 835 AA;
 Query Match 70.6%; Score 36; DB 6; Length 835;
 Best Local Similarity 60.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EARGSYAFDI 10
 |||:|:|:
 Db 749 EARTYAYDV 758
 RESULT 29
 AAM40464
 ID AAM40464 standard; protein; 865 AA.
 XX

AAM40464;
 22-OCT-2001 (first entry)
 Human polypeptide SEQ ID NO 5395.
 Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 peripheral nervous system; neuropathy; central nervous system; CNS;
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia.
 Homo sapiens.
 WO200153312-A1.
 26-JUL-2001.
 26-DEC-2000; 2000WO-US034263.
 23-DEC-1999; 99US-00471275.
 21-JAN-2000; 2000US-00488725.
 25-APR-2000; 2000US-00552317.
 20-JUN-2000; 2000US-00598042.
 19-JUL-2000; 2000US-00620312.
 03-AUG-2000; 2000US-00653450.
 14-SEP-2000; 2000US-00662191.
 19-OCT-2000; 2000US-00693036.
 29-NOV-2000; 2000US-00727344.
 (HYSE-) HYSEQ INC.
 Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 Zhou P, Goodrich R, Drmanac RT;
 WPI; 2001-442253/47.
 N-PSDB; AAI59620.
 Novel nucleic acids and polypeptides, useful for treating disorders such
 as central nervous system injuries.
 Example 2; SEQ ID NO 5395; 10078pp; English.
 The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 encoded polypeptides (AAM38642-AAM42213) with nootropic
 immunosuppressant and cytostatic activity. The polynucleotides are useful
 in gene therapy. A composition containing a polypeptide or polynucleotide
 of the invention may be used to treat diseases of the peripheral nervous
 system, such as peripheral nervous injuries, peripheral neuropathy and
 localised neuropathies and central nervous system diseases, such as
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 utilisation of the activities such as: Immune system suppression,
 Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 assays for receptor activity, arthritis and inflammation, leukaemias and
 C.N.S disorders. Note: The sequence data for this patent did not form
 part of the printed specification
 Sequence 865 AA;
 Query Match 70.6%; Score 36; DB 4; Length 865;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ARGSYAFDI 10
 |||:|:|:
 Db 277 AKGTYTFDI 285
 RESULT 30

AAAM40465
ID AAAM40465 standard; protein; 865 AA.

XX AAAM40465;
AC
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5396.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.
OS
XX WO200153312-A1.

XX 26-JUL-2001.
XX
PD
XX
PF 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.
PA
XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR N-PSDB; AAI59621.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

XX Example 2; SEQ ID NO 5396; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAAM38642-AAAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 865 AA;
SQ

Query Match 70.6%; Score 36; DB 4; Length 865;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
Db 277 AKGTYTFDI 285

RESULT 31
AAAM40466

ID AAAM40466 standard; protein; 865 AA.

XX AAAM40466;
AC
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5397.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.
OS
XX WO200153312-A1.

XX 26-JUL-2001.
XX
PD
XX
PF 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-0052317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.
PA
XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
DR N-PSDB; AAI59622.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

XX Example 2; SEQ ID NO 5397; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAAM38642-AAAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 865 AA;
SQ

Query Match 70.6%; Score 36; DB 4; Length 865;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX
 SQ Sequence 966 AA;

Query Match 70.6%; Score 36; DB 4; Length 966;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
 |:|:|:|
 Db 426 AKGTYYFDI 434

RESULT 34
 AAM38678
 ID AAM38678 standard; protein; 1013 AA.

XX AC AAM38678;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 1823.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662191.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa;
 PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI57834.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

XX Example 3; SEQ ID NO 1823; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as; Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX

SQ Sequence 1013 AA;

Query Match 70.6%; Score 36; DB 4; Length 1013;

Best Local Similarity 66.7%; Pred. No. 2.6e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10

:|:|:|

Db 426 AKGTYYFDI 434

RESULT 35

AAM38680

ID AAM38680 standard; protein; 1025 AA.

XX AC AAM38680;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 1825.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662191.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Qa;
 PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI57836.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.

XX Example 3; SEQ ID NO 1825; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful

in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Sequence 1025 AA;
Query Match 70.6%; Score 36; DB 4; Length 1025;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 426 AKGTYTFDI 434
|:|:| |||

RESULT 36
ABO14710
ID ABO14710 standard; protein; 1026 AA.

AC ABO14710;

DT 25-AUG-2003 (first entry)

XX Novel human protein #83.

Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; inflammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis; lung disease; emphysema; obstructive pulmonary disease; haemophilia; stroke; infection.

Homo sapiens.

WO2003023002-A2.

PD 20-MAR-2003.

XX 09-SEP-2002; 2002WO-US028539.

XX 07-SEP-2001; 2001US-0318120P.

PR 07-SEP-2001; 2001US-0318130P.

PR 10-SEP-2001; 2001US-0318430P.

PR 17-SEP-2001; 2001US-0322636P.

PR 17-SEP-2001; 2001US-0322781P.

PR 17-SEP-2001; 2001US-0322816P.

PR 17-SEP-2001; 2001US-0322817P.

PR 19-SEP-2001; 2001US-0323519P.

PR 20-SEP-2001; 2001US-0323631P.

PR 20-SEP-2001; 2001US-0323636P.

PR 25-SEP-2001; 2001US-0324969P.

PR 25-SEP-2001; 2001US-0325091P.

PR 26-SEP-2001; 2001US-0324900P.

PI Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
PI Rieger DK, Taupier RJ, Shency SG, Liu X, Padigaru M, Alsobrook JP;
XX Lepley DM, Edinger SR, Burgess CE;

DR WPI: 2003-313242/30.
DR N-PSDB; ACD19403.

XX New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obesity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.

PS Claim 1; Page 267; 586pp; English.

XX The invention describes a new isolated polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful as therapeutics, particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with NOVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NOVX polypeptide or polynucleotide is useful for treating endocrine/metabolism-related diseases (e.g. obesity or diabetes), central nervous system disorders (e.g. Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus, osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma), liver diseases (e.g. liver cirrhosis), lung diseases (emphysema or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic). These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic applications, and for monitoring the effects of drugs during clinical trials. This is the amino acid sequence of a novel human NOV protein

Sequence 1026 AA;

Query Match 70.6%; Score 36; DB 6; Length 1026;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 409 AKGTYTFDI 417
|:|:| |||

RESULT 37
ADX07286

ID ADX07286 standard; protein; 1026 AA.

XX ADX07286;

DT 21-APR-2005 (first entry)

XX Cyclin-dependent kinase modulation biomarker SEQ ID NO 1851.

XX cytostatic; cyclin-dependent kinase; cdk; biomarker.

OS Homo sapiens.

PN WO2005012875-A2.

XX 10-FEB-2005.

XX 29-JUL-2004; 2004WO-US024424.

XX 29-JUL-2003; 2003US-0490890P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;

XX WPI: 2005-163068/17.

KW psoriasis; allergy; lupus erythematosus; asthma; cancer;
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;
KW stroke; infection.

OS Homo sapiens.

XX WO2003023002-A2.

XX 20-MAR-2003.

XX 09-SEP-2002; 2002WO-US028539.

XX 07-SEP-2001; 2001US-0318120P.

XX 07-SEP-2001; 2001US-0318130P.

XX 10-SEP-2001; 2001US-0318430P.

XX 17-SEP-2001; 2001US-0322636P.

XX 17-SEP-2001; 2001US-0322781P.

XX 17-SEP-2001; 2001US-0322816P.

XX 17-SEP-2001; 2001US-0322817P.

XX 19-SEP-2001; 2001US-0323519P.

XX 20-SEP-2001; 2001US-0323631P.

XX 20-SEP-2001; 2001US-0323636P.

XX 25-SEP-2001; 2001US-0324969P.

XX 25-SEP-2001; 2001US-0325091P.

XX 26-SEP-2001; 2001US-0324990P.

XX 17-APR-2002; 2002US-0373212P.

XX 06-SEP-2002; 2002US-00236177.

XX (CURA-) CURAGEN CORP.

XX Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;
XX Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;
XX Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;
XX Rieser DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
XX Lepley DM, Edinger SR, Burgess CE;

XX WPI; 2003-313242/30.

XX N-PSDB; ACD19402.

XX New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)
XX and polynucleotides, useful in gene therapy, e.g. for treating or
XX preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,
XX stroke or infections.

XX Claim 1; Page 266; 586pp; English.

XX The invention describes a new isolated polypeptide (NOVX). The NOVX
XX polypeptide, nucleic acid and antibody are useful as therapeutics,
XX particularly in the manufacture of a medicament for treating a syndrome
XX associated with a human disease, which includes a pathology associated
XX with NOVX polypeptide. The DNA encoding the protein is useful in gene
XX therapy for treating the disease or condition. In particular, the NOVX
XX polypeptide or polynucleotide is useful for treating endocrine/
XX metabolism-related diseases (e.g. obesity or diabetes), central nervous
XX system disorders (e.g. Alzheimer's disease, Parkinson's disease,
XX epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune
XX and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,
XX asthma, inflammatory bowel disease, rheumatoid arthritis or
XX osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
XX prostate or brain cancers, or melanoma), liver diseases (e.g. liver
XX cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
XX haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
XX These are also useful in developing powerful assay system for functional
XX analysis of various human disorders, as well as in diagnostic
XX applications, and for monitoring the effects of drugs during clinical
XX trials. This is the amino acid sequence of a novel human NOV protein

XX Sequence 1057 AA;

XX Query Match

XX 70.6%; Score 36; DB 6; Length 1057;

Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0;

Qy 2 ARGSYAFDI 10
Db 409 AKGTYTFDI 417
|:|:|

RESULT 40

AAAY78795

ID AAY78795 standard; protein; 1219 AA.

XX AAY78795;

XX 19-MAY-2000 (first entry)

XX Human antizuai-2 (AZ-2) amino acid sequence.

XX Antizuai-2; AZ-2; human; breast cancer; malignancy progression marker;
XX malignancy reversion; tumour suppressor.

XX Homo sapiens.

XX WO200000503-A1.

XX 06-JAN-2000.

XX 25-JUN-1999; 99WO-US014482.

XX 26-JUN-1998; 98US-0090747P.

XX (CHEN/) CHEN H.

XX (BISS/) BISSELL M.

XX Chen H, Bissell M;

XX WPI; 2000-170903/15.

XX N-PSDB; AAZ90112.

XX New nucleic acid encoding a tumor suppressor or marker, used for
XX diagnosis, monitoring progress or treatment, and gene therapy of breast
XX cancer.

XX Claim 6; Page 69-72; 120pp; English.

XX This sequence represents the human antizuai-2 (AZ-2) amino acid sequence.
XX The AZ-2 gene is a variant of the antizuai-1 (AZ-1) gene (see AAZ90111).
XX The AZ-1 gene is located on chromosome 10q26, and encodes a protein that
XX acts as a tumour suppressor or marker of malignancy progression or
XX reversion. The AZ-1 protein and its variants are tumour suppressors, AZ-1
XX interacts with E-cadherin and beta-catenin. Detecting low levels of AZ-1
XX nucleotide or amino acid sequences are used to diagnose a breast cell
XX malignancy, also for monitoring disease progression, particularly
XX assessment of therapeutic efficacy. The nucleotide sequence is used in
XX vivo or ex vivo gene therapy, and AZ-1 polypeptides are used for treating
XX or preventing breast cancer. AZ-1 polypeptides are also used to raise
XX specific antibodies, for diagnostic detection of AZ-1. Fragments of the
XX AZ-1 nucleotide sequence are useful as probes or primers for detecting
XX expression of the AZ-1 gene

XX Sequence 1219 AA;

XX Query Match 70.6%; Score 36; DB 3; Length 1219;

XX Best Local Similarity 66.7%; Pred. No. 3.2e+02;

XX Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 683 AKGTYTFDI 691
|:|:|

Search completed: December 14, 2005, 07:25:25

Job time : 60.8966 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:38 ; Search time 14.6552 Seconds
(without alignments)
56.414 Million cell updates/sec

Title: US-10-720-323-3

Perfect score: 51

Sequence: 1 EARGSVAFDI 10

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/1/iaa/6-COMB.pep:*
 - 3: /cgn2_6/ptodata/1/iaa/H-COMB.pep:*
 - 4: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep:*
 - 5: /cgn2_6/ptodata/1/iaa/RE-COMB.pep:*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	74.5	349	2	US-09-573-630A-2
2	38	74.5	379	2	US-09-328-352-5219
3	36	70.6	107	2	US-09-344-624-7
4	36	70.6	487	2	US-09-489-039A-12914
5	36	70.6	571	2	US-09-344-624-3
6	36	70.6	653	2	US-09-344-624-6
7	36	70.6	796	2	US-09-107-532A-7065
8	36	70.6	1026	2	US-09-949-016-6777
9	36	70.6	1034	2	US-09-949-016-10870
10	36	70.6	1219	2	US-09-344-624-4
11	35	68.6	928	2	US-09-914-259-23
12	34	66.7	117	1	US-08-466-033-164
13	34	66.7	117	1	US-08-444-733-164
14	34	66.7	117	1	US-08-464-134-164
15	34	66.7	117	1	US-08-461-361-164
16	34	66.7	117	1	US-08-485-910-164
17	34	66.7	184	2	US-09-902-540-10264
18	34	66.7	232	1	US-08-638-911A-33
19	34	66.7	555	2	US-10-104-047-2011
20	34	66.7	853	1	US-08-638-911A-25
21	34	66.7	853	1	US-08-638-911A-27
22	34	66.7	853	1	US-08-638-911A-29
23	34	66.7	853	1	US-08-638-911A-31
24	34	66.7	2842	1	US-07-741-940-7
25	34	66.7	2842	1	US-08-289-548A-7
26	34	66.7	2842	1	US-08-452-654-7
27	34	66.7	2842	2	US-08-449-731-7

28	34	66.7	2843	1	US-07-741-940-2	Sequence 2, Appli
29	34	66.7	2843	1	US-08-289-548A-2	Sequence 2, Appli
30	34	66.7	2843	1	US-08-452-654-2	Sequence 2, Appli
31	34	66.7	2843	1	US-08-452-655B-2	Sequence 7, Appli
32	34	66.7	2843	1	US-08-452-655B-7	Sequence 2, Appli
33	34	66.7	2843	2	US-08-370-235A-2	Sequence 2, Appli
34	34	66.7	2843	2	US-08-450-582-2	Sequence 2, Appli
35	34	66.7	2843	2	US-08-450-582-7	Sequence 7, Appli
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37	34	66.7	2843	2	US-10-092-138A-30	Sequence 1007, Ap
38	34	66.7	2843	2	US-09-538-092-1007	Sequence 30, Appl
39	34	66.7	2843	2	US-08-681-219A-30	Sequence 10, Appl
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42	34	66.7	2843	1	US-08-444-733-15	Sequence 15, Appl
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47	34	66.7	2905	2	US-08-469-260A-401	Sequence 401, App
48	34	66.7	2905	2	US-08-488-446-401	Sequence 401, App
49	34	66.7	2905	2	US-08-467-344A-401	Sequence 401, App
50	34	66.7	2905	2	US-08-424-550B-401	Sequence 401, App
51	34	66.7	2910	1	US-08-466-033-183	Sequence 183, App
52	34	66.7	2910	1	US-08-444-733-183	Sequence 183, App
53	34	66.7	2910	1	US-08-464-134-183	Sequence 183, App
54	34	66.7	2910	1	US-08-461-361-183	Sequence 183, App
55	34	66.7	2910	1	US-08-485-910-183	Sequence 183, App
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57	34	66.7	2910	4	PCT-US95-06266-157	Sequence 157, App
58	34	66.7	2973	1	US-08-821-355A-7	Sequence 7, Appli
59	34	66.7	2973	1	US-09-003-687A-7	Sequence 7, Appli
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61	33	64.7	40	1	US-07-998-003A-55	Sequence 55, Appl
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65	33	64.7	40	1	US-08-453-702A-55	Sequence 55, Appl
66	33	64.7	40	1	US-09-099-639-55	Sequence 55, Appl
67	33	64.7	40	4	PCT-US93-12588-55	Sequence 55, Appl
68	33	64.7	40	4	PCT-US95-08071-55	Sequence 55, Appl
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71	33	64.7	488	2	US-09-902-540-15686	Sequence 15686, A
72	33	64.7	547	2	US-09-543-681A-6051	Sequence 6051, Ap
73	33	64.7	557	2	US-09-902-540-14087	Sequence 14087, A
74	33	64.7	640	2	US-09-134-000C-3871	Sequence 3871, Ap
75	33	64.7	711	2	US-09-352-991A-28091	Sequence 28091, A
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77	33	64.7	980	2	US-08-413-118-5	Sequence 5, Appli
78	33	64.7	980	2	US-08-473-446-5	Sequence 5, Appli
79	33	64.7	1620	1	US-08-542-363-2	Sequence 2, Appli
80	33	64.7	1620	2	US-09-100-089-2	Sequence 2, Appli
81	33	64.7	1620	2	US-09-670-827-2	Sequence 2, Appli
82	33	64.7	1620	2	US-09-827-949-2	Sequence 2, Appli
83	32	62.7	173	2	US-09-252-991A-31785	Sequence 31785, A
84	32	62.7	337	2	US-09-489-039A-13994	Sequence 13994, A
85	32	62.7	339	2	US-09-270-767-45916	Sequence 45916, A
86	32	62.7	349	2	US-09-252-991A-26789	Sequence 26789, A
87	32	62.7	350	2	US-09-328-352-6678	Sequence 6678, Ap
88	32	62.7	396	2	US-09-107-532A-6284	Sequence 6284, Ap
89	32	62.7	412	2	US-09-252-991A-24847	Sequence 24847, A
90	32	62.7	450	2	US-09-198-452A-35	Sequence 35, Appl
91	32	62.7	450	2	US-09-438-185A-21	Sequence 21, Appl
92	32	62.7	460	2	US-08-935-263-4	Sequence 4, Appli
93	32	62.7	460	2	US-09-594-185-4	Sequence 4, Appli
94	32	62.7	460	2	US-09-328-352-7352	Sequence 7352, Ap
95	32	62.7	460	2	US-10-033-078-4	Sequence 4, Appli
96	32	62.7	460	2	US-10-763-933-4	Sequence 4, Appli
97	32	62.7	602	2	US-09-583-110-4085	Sequence 4085, Ap
98	32	62.7	635	2	US-09-107-433-5022	Sequence 5022, Ap
99	32	62.7	859	2	US-09-902-540-11347	Sequence 11347, A
100	32	62.7	3218	1	US-08-764-100-27	Sequence 27, Appl

ALIGNMENTS

```
RESULT 1
US-09-573-630A-2
; Sequence 2, Application US/09573630A
; Patent No. 6713062
; GENERAL INFORMATION:
; APPLICANT: MERCHANT, JUNIITA L.
; TITLE OF INVENTION: ACINETOBACTER OUTER MEMBRANE PROTEIN AND GENE SEQUENCE
; FILE REFERENCE: 4100.001700
; CURRENT APPLICATION NUMBER: US/09/573,630A
; CURRENT FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/134,399
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-09-573-630A-2

Query Match      74.5%; Score 38; DB 2; Length 349;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EARGSYAFD 9
      |||||: ||
Db      169 EARGTYHFD 177

RESULT 2
US-09-328-352-5219
; Sequence 5219, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5219
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5219

Query Match      74.5%; Score 38; DB 2; Length 379;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EARGSYAFD 9
      |||||: ||
Db      193 EARGTYNFD 201

RESULT 3
US-09-344-624-7
; Sequence 7, Application US/09344624
; Patent No. 6753154
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; APPLICANT: Bissell, Mina
; TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
; FILE REFERENCE: 2960.44 (HV)
; CURRENT APPLICATION NUMBER: US/09/344,624
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: 60/090,747
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-624-7

Query Match      70.6%; Score 36; DB 2; Length 571;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: 60/090,747
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-624-7

Query Match      70.6%; Score 36; DB 2; Length 107;
Best Local Similarity 66.7%; Pred. No. 8.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 ARGSYAFDI 10
      |:|: |||
Db      35 AKGTYTFDI 43

RESULT 4
US-09-489-039A-12914
; Sequence 12914, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12914
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12914

Query Match      70.6%; Score 36; DB 2; Length 487;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 ARGSYAFDI 10
      ||||: |||
Db      47 ARGHAFDV 55

RESULT 5
US-09-344-624-3
; Sequence 3, Application US/09344624
; Patent No. 6753154
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; APPLICANT: Bissell, Mina
; TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
; FILE REFERENCE: 2960.44 (HV)
; CURRENT APPLICATION NUMBER: US/09/344,624
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: 60/090,747
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-624-3

Query Match      70.6%; Score 36; DB 2; Length 571;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```



```
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 35 AKGTYTFDI 43

RESULT 6
US-09-344-624-6
; Sequence 6, Application US/09344624
; Patent No. 6753154
; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; APPLICANT: Bissell, Mina
; TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
; FILE REFERENCE: 2960.44 (HV)
; CURRENT APPLICATION NUMBER: US/09/344,624
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: 60/090,747
; EARLIER FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-624-6

Query Match 70.6%; Score 36; DB 2; Length 653;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 66 AKGTYTFDI 74

RESULT 7
US-09-107-532A-7065
; Sequence 7065, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER: READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 35 AKGTYTFDI 43

RESULT 6
US-09-344-624-6
; Sequence 6, Application US/09344624
; Patent No. 6753154
; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; APPLICANT: Bissell, Mina
; TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
; FILE REFERENCE: 2960.44 (HV)
; CURRENT APPLICATION NUMBER: US/09/344,624
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: 60/090,747
; EARLIER FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-624-6

Query Match 70.6%; Score 36; DB 2; Length 653;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 66 AKGTYTFDI 74

RESULT 7
US-09-107-532A-7065
; Sequence 7065, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER: READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 35 AKGTYTFDI 43

RESULT 6
US-09-344-624-6
; Sequence 6, Application US/09344624
; Patent No. 6753154
; GENERAL INFORMATION:
; APPLICANT: Chen, Huei-Mei
; APPLICANT: Bissell, Mina
; TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
; FILE REFERENCE: 2960.44 (HV)
; CURRENT APPLICATION NUMBER: US/09/344,624
; CURRENT FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: 60/090,747
; EARLIER FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-624-6

Query Match 70.6%; Score 36; DB 2; Length 796;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
Db 732 EAKGDFSFVDV 741

RESULT 8
US-09-949-016-6777
; Sequence 6777, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6777
; LENGTH: 1026
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6777

Query Match 70.6%; Score 36; DB 2; Length 1026;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 409 AKGTYTFDI 417

RESULT 9
US-09-949-016-10870
; Sequence 10870, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; TELEPHONE: (781)893-8277
; FAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7065:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 796 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...796
; SEQUENCE DESCRIPTION: SEQ ID NO: 7065:
US-09-107-532A-7065
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; PRIOR FILING DATE: 2000-10-03										Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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Best Local Similarity 66.7%; Pred. No. 1e+02;																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
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Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFD 9
|||:|
Db 26 ARGAYLFD 33

RESULT 13

US-08-444-733-164
; Sequence 164, Application US/08444733
; Patent No. 5824507
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungseuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,733
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-444-733-164

Query Match 66.7%; Score 34; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFD 9
|||:|
Db 26 ARGAYLFD 33

RESULT 14

US-08-464-134-164
; Sequence 164, Application US/08464134
; Patent No. 5849532
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungseuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,134
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0960
; TELEFAX: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-134-164

```
Query Match          66.7%; Score 34; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 ARGSYAFD 9
      |||:|||
Db      26 ARGAYLFD 33

US-08-461-361-164
Query Match          66.7%; Score 34; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 ARGSYAFD 9
      |||:|||
Db      26 ARGAYLFD 33

RESULT 15
US-08-461-361-164
; Sequence 164, Application US/08461361
; Patent No. 5856134
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungueh P.
; APPLICANT: Wages, John
; APPLICANT: Young, Lavonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,361
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;

US-08-461-361-164
Query Match          66.7%; Score 34; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 ARGSYAFD 9
      |||:|||
Db      26 ARGAYLFD 33

RESULT 16
US-08-485-910-164
; Sequence 164, Application US/08485910
; Patent No. 5874563
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungueh P.
; APPLICANT: Wages, John
; APPLICANT: Young, Lavonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,910
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
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; MOLECULE TYPE: protein
US-08-485-910-164

Query Match      66.7%; Score 34; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  2 ARGSYAFD 9
Db  26 ARGAYLFD 33

RESULT 17
US-09-902-540-10264
; Sequence 10264, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10264
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10264

Query Match      66.7%; Score 34; DB 2; Length 184;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy  1 EARGSYAFDI 10
Db  141 DATGTAYDL 150

RESULT 18
US-08-638-911A-33
; Sequence 33, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; APPLICANT: Chong, Susan M.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 04/24/96
; APPLICATION NUMBER: US/08/638,911A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-638-911A-33

Query Match      66.7%; Score 34; DB 1; Length 232;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy  2 ARGSYAFD 9
Db  148 ARGAYLFD 155

RESULT 19
US-10-104-047-2011
; Sequence 2011, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2011
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2011

Query Match      66.7%; Score 34; DB 2; Length 555;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy  1 EARGSYAFDI 10
Db  36 DAKGYLFDL 45

RESULT 20
US-08-638-911A-25
; Sequence 25, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; APPLICANT: Chong, Susan M.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 04/24/96
; APPLICATION NUMBER: US/08/638,911A
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-638-911A-25

Query Match 66.7%; Score 34; DB 1; Length 853;
Best Local Similarity 75.0%; Pred. No. 2.le+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFD 9
Db |||:| |
36 ARGAYLFD 43

RESULT 21
US-08-638-911A-27
; Sequence 27, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,911A
; FILING DATE: 04/24/96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-638-911A-29

Query Match 66.7%; Score 34; DB 1; Length 853;
Best Local Similarity 75.0%; Pred. No. 2.le+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFD 9
Db |||:| |
36 ARGAYLFD 43

RESULT 23
US-08-638-911A-31
; Sequence 31, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,911A
; FILING DATE: 04/24/96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-638-911A-27

Query Match 66.7%; Score 34; DB 1; Length 853;
Best Local Similarity 75.0%; Pred. No. 2.le+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFD 9
Db |||:| |
36 ARGAYLFD 43
```

```
RESULT 22
US-08-638-911A-29
; Sequence 29, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,911A
; FILING DATE: 04/24/96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-638-911A-29

Query Match 66.7%; Score 34; DB 1; Length 853;
Best Local Similarity 75.0%; Pred. No. 2.le+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFD 9
Db |||:| |
36 ARGAYLFD 43

RESULT 23
US-08-638-911A-31
; Sequence 31, Application US/08638911A
; Patent No. 5766916
; GENERAL INFORMATION:
; APPLICANT: Belaevy, Alexander S.
; TITLE OF INVENTION: Hepatitis G Virus Protease
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,911A
; FILING DATE: 04/24/96
```

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-638-911A-31

Query Match 66.7%; Score 34; DB 1; Length 853;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFD 9
Db 36 ARGAYLFD 43

RESULT 24
US-07-741-940-7
; Sequence 7, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07741.940
; FILING DATE: 19920109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 66.7%; Score 34; DB 1; Length 2842;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Susan T.
; REGISTRATION NUMBER: 38,443
; REFERENCE/DOCKET NUMBER: 4600-0124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 853 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-638-911A-31

Query Match 66.7%; Score 34; DB 1; Length 853;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFD 9
Db 36 ARGAYLFD 43

RESULT 25
US-08-289-548A-7
; Sequence 7, Application US/08289548A
; Patent No. 5648212
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,548A
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
; US-08-289-548A-7

Query Match 66.7%; Score 34; DB 1; Length 2842;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 RGSYAFD 9
|||:||||
Db 1834 RGSFAFD 1840

RESULT 26

US-08-452-654-7
; Sequence 7, Application US/08452654
; Patent No. 5691454
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/452,654
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE: Homo sapiens
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
US-08-452-654-7
Query Match 66.7%; Score 34; DB 1; Length 2842;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9

Db 1834 RGSFAFD 1840

RESULT 27

US-08-449-731-7

; Sequence 7, Application US/08449731
; Patent No. 6413727
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, LTD
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/449,731
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/289,548
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2842 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE: Homo sapiens
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-449-731-7
Query Match 66.7%; Score 34; DB 2; Length 2842;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
|||:||||
Db 1834 RGSFAFD 1840

RESULT 28
US-07-741-940-2
; Sequence 2, Application US/07741940
; Patent No. 5352775
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY

APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19970109
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.035574
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-940-2

Query Match 66.7%; Score 34; DB 1; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
Db 1835 RGSFAFD 1841
|||:||||

RESULT 29
US-08-289-548A-2
Sequence 2, Application US/08289548A
Patent No. 5648212
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, LTD
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,548A
FILING DATE: 12-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-289-548A-2

Query Match 66.7%; Score 34; DB 1; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
Db 1835 RGSFAFD 1841
|||:||||

RESULT 30
US-08-452-654-2
Sequence 2, Application US/08452654
Patent No. 5691454
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:

; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.035574
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-654-2

Query Match 66.7%; Score 34; DB 1; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
Db 1835 RGSFADF 1841

RESULT 31
US-08-452-655B-2
; Sequence 2, Application US/08452655B
; Patent No. 5783666

; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,655B
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,548
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.49964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-452-655B-7

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-452-655B-2

Query Match 66.7%; Score 34; DB 1; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
Db 1835 RGSFADF 1841

RESULT 32
US-08-452-655B-7
; Sequence 7, Application US/08452655B
; Patent No. 5783666

; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,655B
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,548
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.49964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
US-08-452-655B-7

Query Match 66.7%; Score 34; DB 1; Length 2843;

```
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
Db 1835 RGSFAFD 1841

RESULT 33
US-08-370-235A-2
; Sequence 2, Application US/08370235A
; Patent No. 5910418
; GENERAL INFORMATION:
; APPLICANT: VOGELSTEIN, BERT
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: HILL, DAVID E.
; APPLICANT: JOHNSON, KAREN A.
; TITLE OF INVENTION: ANTIBODIES AND ASSAYS FOR DETERMINING
; TITLE OF INVENTION: MUTATIONS IN THE APC GENE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,235A
; FILING DATE: 01-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.48688
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508 9100
; TELEFAX: 202 508 9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-370-235A-2

Query Match 66.7%; Score 34; DB 1; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
Db 1835 RGSFAFD 1841

RESULT 34
US-08-450-582-2
; Sequence 2, Application US/08450582
; Patent No. 6114124
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.

; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001-4598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,582
; FILING DATE: 12-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/452,655
; FILING DATE: 25-MAY-1995
; APPLICATION NUMBER: US 08/289,548
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 07/741,940
; FILING DATE: 08-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 1107.49964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2843 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-582-2

Query Match 66.7%; Score 34; DB 2; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
Db 1835 RGSFAFD 1841

RESULT 35
US-08-450-582-7
; Sequence 7, Application US/08450582
; Patent No. 6114124
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, HANS
; APPLICANT: ANAND, RAKESH
; APPLICANT: CARLSON, MARY
; APPLICANT: GRODEN, JOANNA
; APPLICANT: HEDGE, PHILIP J.
; APPLICANT: JOSLYN, GEOFF
; APPLICANT: KINZLER, KENNETH
; APPLICANT: MARKHAM, ALEXANDER F.
; APPLICANT: NAKAMURA, YUSUKE
; APPLICANT: THLIVERIS, ANDREW
; TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
; TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
```

STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,582
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-450-582-7

Query Match 66.7%; Score 34; DB 2; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
DB 1835 RGSFAPD 1841

RESULT 36
US-08-449-731-2
Sequence 2, Application US/08449731
Patent No. 6413727
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS

ANAND, RAKESH
CARLSON, MARY
GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
GENE IN COLORECTAL CANCER IN HUMANS

NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, LTD
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,731
FILING DATE: 25-MAY-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/289,548
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-449-731-2

Query Match 66.7%; Score 34; DB 2; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
DB 1835 RGSFAPD 1841

RESULT 37
US-10-092-138A-30
Sequence 30, Application US/10092138A
Patent No. 6743630
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
FILE REFERENCE: 65823/JPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138A
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 2843
TYPE: PRT
ORGANISM: human
US-10-092-138A-30

Query Match 66.7%; Score 34; DB 2; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
DB 1835 RGSFAPD 1841

RESULT 38
US-09-538-092-1007
Sequence 1007, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.

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; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqformatter Version 0.9
; SEQ ID NO 1007
; LENGTH: 2843
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P25054
US-09-538-092-1007

Query Match          66.7%; Score 34; DB 2; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RGSYAFD 9
Db      1835 RGSFAFD 1841

RESULT 39
US-08-681-219A-30
; Sequence 30, Application US/08681219A
; Patent No. 6911526
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; APPLICANT: Yanagisawa, Junn
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
; FILE REFERENCE: 48962
; CURRENT APPLICATION NUMBER: US/08/681,219A
; CURRENT FILING DATE: 1996-07-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 2843
; TYPE: PRT
; ORGANISM: human
US-08-681-219A-30

Query Match          66.7%; Score 34; DB 2; Length 2843;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RGSYAFD 9
Db      1835 RGSFAFD 1841

RESULT 40
US-08-466-033-15
; Sequence 15, Application US/08466033
; Patent No. 5766840
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, Lavonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,033
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2873 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-033-15
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Query Match          66.7%; Score 34; DB 1; Length 2873;
Best Local Similarity 75.0%; Pred. No. 8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:54 ; Search time 45.8621 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-720-323-3

Perfect score: 51

Sequence: 1 EARGSVAFDI 10

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.Main.*

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	10	3	US-09-920-267C-3
2	51	100.0	10	4	US-10-720-323-3
3	51	100.0	10	5	US-10-954-900A-3
4	51	100.0	119	3	US-09-920-267C-7
5	51	100.0	119	4	US-10-720-323-7
6	38	74.5	309	4	US-10-369-493-82
7	38	74.5	466	4	US-10-437-963-121019
8	37	72.5	11	3	US-09-880-748-3185
9	37	72.5	11	4	US-10-293-418-3185
10	37	72.5	173	4	US-10-425-115-355604
11	37	72.5	243	3	US-09-880-748-1935
12	37	72.5	243	4	US-10-293-418-1935
13	37	72.5	1108	5	US-10-732-923-8460
14	37	72.5	1209	4	US-10-437-963-154103
15	36	70.6	133	4	US-10-424-599-248887
16	36	70.6	170	4	US-10-106-698-5972
17	36	70.6	637	5	US-10-450-763-52925
18	36	70.6	653	5	US-10-450-763-41591
19	36	70.6	750	5	US-10-450-763-52926
20	36	70.6	890	4	US-10-282-122A-46227
21	36	70.6	1026	6	US-11-037-713-25
22	35	68.6	112	4	US-10-276-774-1603
23	35	68.6	112	4	US-10-425-115-203294
24	35	68.6	852	5	US-10-701-401-7
25	35	68.6	928	4	US-10-080-608A-23
26	35	68.6	928	4	US-10-370-685-112
27	35	68.6	2406	4	US-10-408-765A-1504

28	35	58.6	2406	5	US-10-701-401-2	Sequence 2, Appli
29	34	66.7	71	4	US-10-425-115-187048	Sequence 187048,
30	34	66.7	192	4	US-10-363-829-407	Sequence 407, App
31	34	66.7	223	4	US-10-425-115-330011	Sequence 330011,
32	34	66.7	242	4	US-10-151-882-16	Sequence 16, Appl
33	34	66.7	254	4	US-10-767-701-43856	Sequence 43856, A
34	34	66.7	308	4	US-10-425-115-330008	Sequence 330008,
35	34	66.7	311	4	US-10-425-114-64938	Sequence 64938, A
36	34	66.7	341	4	US-10-425-114-41240	Sequence 41240, A
37	34	66.7	353	4	US-10-282-122A-76935	Sequence 280829,
38	34	66.7	541	4	US-10-104-047-2011	Sequence 76935, A
39	34	66.7	555	4	US-10-415-187-3	Sequence 2011, Ap
40	34	66.7	570	4	US-10-282-122A-76365	Sequence 3, Appli
41	34	66.7	857	4	US-09-987-482-2	Sequence 76365, A
42	34	66.7	912	3	US-10-437-963-151552	Sequence 151552,
43	34	66.7	1212	4	US-10-324-999A-3479	Sequence 3479, Ap
44	34	66.7	2842	4	US-10-693-258-20	Sequence 20, Appl
45	34	66.7	2842	5	US-08-681-219-32	Sequence 32, Appl
46	34	66.7	2843	3	US-09-987-482-1	Sequence 1, Appli
47	34	66.7	2843	3	US-09-230-111C-30	Sequence 30, Appl
48	34	66.7	2843	4	US-10-092-138-30	Sequence 30, Appl
49	34	66.7	2843	4	US-10-392-113-21	Sequence 21, Appl
50	34	66.7	2843	4	US-10-408-765A-1970	Sequence 1970, Ap
51	34	66.7	2843	5	US-10-862-061A-2	Sequence 30, Appl
52	34	66.7	2843	5	US-10-267-502-370	Sequence 2, Appli
53	34	66.7	2844	4	US-08-424-550B-401	Sequence 401, App
54	34	66.7	2905	2	US-09-828-498-2	Sequence 2, Appli
55	34	66.7	2910	5	US-10-693-258-2	Sequence 2, Appli
56	34	66.7	2910	5	US-10-425-115-223255	Sequence 223255,
57	34	66.7	39	4	US-09-880-573-55	Sequence 55, Appl
58	33	64.7	40	3	US-10-282-122A-60415	Sequence 60415, A
59	33	64.7	319	4	US-10-437-963-151899	Sequence 151899,
60	33	64.7	326	4	US-10-767-701-43573	Sequence 43573, A
61	33	64.7	342	4	US-10-732-923-5820	Sequence 5820, Ap
62	33	64.7	372	5	US-10-437-963-148459	Sequence 148459,
63	33	64.7	374	4	US-10-437-963-121105	Sequence 121105,
64	33	64.7	388	4	US-10-369-493-3356	Sequence 3356, Ap
65	33	64.7	401	4	US-09-815-242-4900	Sequence 4900, Ap
66	33	64.7	513	4	US-09-815-242-10579	Sequence 10579, Ap
67	33	64.7	602	3	US-10-282-122A-42490	Sequence 42490, A
68	33	64.7	602	3	US-10-437-963-106166	Sequence 106166,
69	33	64.7	602	4	US-11-097-143-39093	Sequence 39093, A
70	33	64.7	607	4	US-10-399-411-2	Sequence 2, Appli
71	33	64.7	619	6	US-10-399-411-4	Sequence 4, Appli
72	33	64.7	782	4	US-10-399-411-6	Sequence 6, Appli
73	33	64.7	782	4	US-10-399-411-8	Sequence 8, Appli
74	33	64.7	782	4	US-10-626-832-39	Sequence 39, Appl
75	33	64.7	782	4	US-09-827-949-2	Sequence 2, Appli
76	33	64.7	980	5	US-10-466-162-18	Sequence 18, Appl
77	33	64.7	1620	3	US-10-739-930-6537	Sequence 6537, Ap
78	33	64.7	1620	5	US-10-424-599-155662	Sequence 155662,
79	33	64.7	1620	5	US-10-688-925-39	Sequence 39, Appl
80	33	64.7	3365	5	US-10-424-599-177574	Sequence 177574,
81	32.5	63.7	51	4	US-10-424-599-277085	Sequence 277085,
82	32	62.7	12	4	US-10-425-115-203353	Sequence 203353,
83	32	62.7	54	4	US-10-424-599-246142	Sequence 246142,
84	32	62.7	69	4	US-10-238-075-1474	Sequence 1474, Ap
85	32	62.7	81	4	US-10-424-599-180922	Sequence 180922,
86	32	62.7	87	4	US-10-982-359-64	Sequence 64, Appl
87	32	62.7	103	4	US-10-688-925-10	Sequence 10, Appl
88	32	62.7	108	4	US-10-688-925-22	Sequence 22, Appl
89	32	62.7	116	5	US-10-051-874-170	Sequence 170, App
90	32	62.7	121	4	US-10-767-701-34400	Sequence 34400, A
91	32	62.7	121	4	US-10-282-122A-72435	Sequence 72435, A
92	32	62.7	125	4	US-10-732-923-13367	Sequence 13367, A
93	32	62.7	125	4	US-10-732-923-13381	Sequence 13381, A
94	32	62.7	139	5	US-10-425-115-286658	Sequence 286658,
95	32	62.7	148	5	US-10-424-599-191747	Sequence 191747,
96	32	62.7	162	4	US-10-282-122A-69853	Sequence 69853, A
97	32	62.7	162	4	US-10-425-115-253856	Sequence 253856,
98	32	62.7	205	4		
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ALIGNMENTS

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RESULT 1
US-09-920-267C-3
; Sequence 3, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-3

Query Match      100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EARGSYAFDI 10
Db      1 EARGSYAFDI 10

RESULT 2
US-10-720-323-3
; Sequence 3, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-3

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EARGSYAFDI 10
Db      1 EARGSYAFDI 10

RESULT 3
US-10-954-900A-3
; Sequence 3, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallan
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-3

Query Match      100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EARGSYAFDI 10
Db      1 EARGSYAFDI 10

RESULT 4
US-09-920-267C-7
; Sequence 7, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-7

Query Match      100.0%; Score 51; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EARGSYAFDI 10
Db      99 EARGSYAFDI 108

RESULT 5
US-10-720-323-7
; Sequence 7, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
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; Sequence 3, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallan
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-3
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Query Match      100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EARGSYAFDI 10
Db      1 EARGSYAFDI 10
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RESULT 4
US-09-920-267C-7
; Sequence 7, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
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; ORGANISM: Homo sapiens
US-09-920-267C-7
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Query Match      100.0%; Score 51; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 EARGSYAFDI 10
Db      99 EARGSYAFDI 108
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RESULT 5
US-10-720-323-7
; Sequence 7, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
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; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-7

Query Match      100.0%; Score 51; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EARGSYAFDI 10
Db      99 EARGSYAFDI 108
|||||

RESULT 6
US-10-369-493-82
; Sequence 82, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10 (52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 82
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-10-369-493-82

Query Match      74.5%; Score 38; DB 4; Length 309;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 0;

Qy      1 EARGSYAFDI 10
Db      98 KAGGVYAFDI 107
:|:|||||

RESULT 7
US-10-437-963-121019
; Sequence 121019, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazov, Brad
```

```
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 121019
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_24085C.1.pep
US-10-437-963-121019

Query Match      74.5%; Score 38; DB 4; Length 466;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 EARGSYAFDI 10
Db      418 EASGSYTFDM 427
|||||

RESULT 8
US-09-880-748-3185
; Sequence 3185, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3185
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3185

Query Match      72.5%; Score 37; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GSYAFDI 10
Db      5 GSYAFDI 11
|||||

RESULT 9
US-10-293-418-3185
; Sequence 3185, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
```

```
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3185
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3185
```

```
Query Match          72.5%; Score 37; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GSYAFDI 10
        |||||
Db       5 GSYAFDI 11
```

```
RESULT 10
US-10-425-115-355604
; Sequence 355604, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 355604
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(173)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_87477C.1.pep
US-10-425-115-355604
```

```
Query Match          72.5%; Score 37; DB 4; Length 173;
Best Local Similarity 87.5%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 ARGSYAFD 9
        |||||
Db      144 ARGHYAFD 151
```

```
RESULT 11
US-09-880-748-1935
; Sequence 1935, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1935
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1935
```

```
Query Match          72.5%; Score 37; DB 3; Length 243;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GSYAFDI 10
        |||||
Db      103 GSYAFDI 109
```

```
RESULT 12
US-10-293-418-1935
; Sequence 1935, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1935
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1935
```

```
Query Match          72.5%; Score 37; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GSYAFDI 10
        |||||
Db      103 GSYAFDI 109
```

```
RESULT 13
```

```
US-10-732-923-8460
; Sequence 8460, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8460
; LENGTH: 1108
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1108)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-8460

Query Match          72.5%; Score 37; DB 5; Length 1108;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EARGSYAPD 9
Db 280 KAKGAYAPD 288

RESULT 14
US-10-437-963-154103
; Sequence 154103, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 154103
; LENGTH: 1209
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; OTHER INFORMATION: Clone ID: PAT_MRT4530_53996C.1.pap
US-10-437-963-154103

Query Match          72.5%; Score 37; DB 4; Length 1209;
Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EARGSYAPD 9
Db 2 KAKGAYAPD 10

RESULT 15
US-10-424-599-248887
; Sequence 248887, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
```

```
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 248887
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_66776C.1.pap
US-10-424-599-248887

Query Match          70.6%; Score 36; DB 4; Length 133;
Best Local Similarity 87.5%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
Db 74 RASVAFDI 81

RESULT 16
US-10-106-698-5972
; Sequence 5972, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patent in Ver. 3.0
; SEQ ID NO 5972
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (170)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5972

Query Match          70.6%; Score 36; DB 4; Length 170;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10
Db 69 AKGYTFDI 77

RESULT 17
US-10-450-763-52925
; Sequence 52925, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
```

;/ PRIOR APPLICATION NUMBER: PCT/US01/08631
;/ PRIOR FILING DATE: 2001-03-30
;/ PRIOR APPLICATION NUMBER: 09/540,217
;/ PRIOR FILING DATE: 2000-03-31
;/ PRIOR APPLICATION NUMBER: 09/649,167
;/ PRIOR FILING DATE: 2000-08-23
;/ NUMBER OF SEQ ID NOS: 60736
;/ SOFTWARE: Custom
;/ SEQ ID NO 52925
;/ LENGTH: 637
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: DOMAIN
;/ LOCATION: (110)..(125)
;/ OTHER INFORMATION: WILM'S TUMOUR PROTEIN SIGNATURE domain identified by eMATRIX,
;/ OTHER INFORMATION: accession number PR00049D, p-value=4.661e-09, raw score of 0.00
US-10-450-763-52925

Query Match 70.6%; Score 36; DB 5; Length 637;
Best Local Similarity 66.7%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
Db 389 AKGTYTFDI 397
|:|:|

RESULT 18

US-10-450-763-41591
;/ Sequence 41591, Application US/10450763
;/ Publication No. US20050196754A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Hyseq, Inc
;/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;/ FILE REFERENCE: 790CIP3/US
;/ CURRENT APPLICATION NUMBER: US/10/450,763
;/ CURRENT FILING DATE: 2003-06-11
;/ PRIOR APPLICATION NUMBER: PCT/US01/08631
;/ PRIOR FILING DATE: 2001-03-30
;/ PRIOR APPLICATION NUMBER: 09/540,217
;/ PRIOR FILING DATE: 2000-03-31
;/ PRIOR APPLICATION NUMBER: 09/649,167
;/ PRIOR FILING DATE: 2000-08-23
;/ NUMBER OF SEQ ID NOS: 60736
;/ SOFTWARE: Custom
;/ SEQ ID NO 41591
;/ LENGTH: 653
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
US-10-450-763-41591

Query Match 70.6%; Score 36; DB 5; Length 653;
Best Local Similarity 66.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
Db 66 AKGTYTFDI 74
|:|:|

RESULT 19

US-10-450-763-52926
;/ Sequence 52926, Application US/10450763
;/ Publication No. US20050196754A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Hyseq, Inc
;/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
;/ FILE REFERENCE: 790CIP3/US
;/ CURRENT APPLICATION NUMBER: US/10/450,763
;/ CURRENT FILING DATE: 2003-06-11
;/ PRIOR APPLICATION NUMBER: PCT/US01/08631
;/ PRIOR FILING DATE: 2001-03-30

;/ PRIOR APPLICATION NUMBER: 09/540,217
;/ PRIOR FILING DATE: 2000-03-31
;/ PRIOR APPLICATION NUMBER: 09/649,167
;/ PRIOR FILING DATE: 2000-08-23
;/ NUMBER OF SEQ ID NOS: 60736
;/ SOFTWARE: Custom
;/ SEQ ID NO 52926
;/ LENGTH: 750
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: misc.feature
;/ LOCATION: (1)...(750)
;/ OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52926

Query Match 70.6%; Score 36; DB 5; Length 750;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
Db 151 AKGTYTFDI 159
|:|:|

RESULT 20

US-10-282-122A-46227
;/ Sequence 46227, Application US/10282122A
;/ Publication No. US20040029129A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Wang, Liangeu
;/ APPLICANT: Zamudio, Carlos
;/ APPLICANT: Malone, Cheryl
;/ APPLICANT: Haselbeck, Robert
;/ APPLICANT: Ohlsen, Kari
;/ APPLICANT: Zyskind, Judith
;/ APPLICANT: Wall, Daniel
;/ APPLICANT: Trawick, John
;/ APPLICANT: Carr, Grant
;/ APPLICANT: Yamamoto, Robert
;/ APPLICANT: Foreyth, R.
;/ APPLICANT: Xu, H.
;/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;/ FILE REFERENCE: ELITRA.034A
;/ CURRENT APPLICATION NUMBER: US/10/282,122A
;/ CURRENT FILING DATE: 2003-02-20
;/ PRIOR APPLICATION NUMBER: 60/191,078
;/ PRIOR FILING DATE: 2000-03-21
;/ PRIOR APPLICATION NUMBER: 60/206,848
;/ PRIOR FILING DATE: 2000-05-23
;/ PRIOR APPLICATION NUMBER: 60/207,727
;/ PRIOR FILING DATE: 2000-05-26
;/ PRIOR APPLICATION NUMBER: 60/230,335
;/ PRIOR FILING DATE: 2000-09-06
;/ PRIOR APPLICATION NUMBER: 60/230,347
;/ PRIOR FILING DATE: 2000-09-09
;/ PRIOR APPLICATION NUMBER: 60/242,578
;/ PRIOR FILING DATE: 2000-10-23
;/ PRIOR APPLICATION NUMBER: 60/253,625
;/ PRIOR FILING DATE: 2000-11-27
;/ PRIOR APPLICATION NUMBER: 60/257,931
;/ PRIOR FILING DATE: 2000-12-22
;/ PRIOR APPLICATION NUMBER: 60/267,636
;/ PRIOR FILING DATE: 2001-02-09
;/ PRIOR APPLICATION NUMBER: 60/269,308
;/ PRIOR FILING DATE: 2001-02-16
;/ Remaining Prior Application data removed - See File Wrapper or PALM.
;/ NUMBER OF SEQ ID NOS: 78614
;/ SOFTWARE: PatentIn version 3.1
;/ SEQ ID NO 46227
;/ LENGTH: 890
;/ TYPE: PRT
;/ ORGANISM: Bacillus anthracis

FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (104)..(104)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (291)..(291)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (294)..(294)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (435)..(435)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (454)..(454)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (519)..(519)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (534)..(534)
OTHER INFORMATION: X=any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (657)..(657)
OTHER INFORMATION: X=any amino acid
US-10-282-122A-46227

Query Match 70.6%; Score 36; DB 4; Length 890;
Best Local Similarity 77.8%; Pred. No. 5.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
Db 341 ENRGSYAFN 349

RESULT 21
US-11-037-713-25
Sequence 25, Application US/11037713
Publication No. US20050221398A1
GENERAL INFORMATION:
APPLICANT: JACQUEMIER, JOCELYNE
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: DEBONO, STEPHANE
APPLICANT: TAGETT, REBECCA
TITLE OF INVENTION: PROTEIN EXPRESSION PROFILING AND BREAST CANCER
FILE REFERENCE: 1016-R-04 (B)
CURRENT APPLICATION NUMBER: US/11/037,713
CURRENT FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: 60/537,412
PRIOR FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 25
LENGTH: 1026
TYPE: PRT
ORGANISM: Homo sapiens
US-11-037-713-25

Query Match 70.6%; Score 36; DB 6; Length 1026;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ARGSYAFDI 10

Db 409 AKGTYTFDI 417

RESULT 22
US-10-276-774-1603
Sequence 1603, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 1603
LENGTH: 112
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-774-1603

Query Match 68.6%; Score 35; DB 4; Length 112;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
Db 29 RGSYSFD 35

RESULT 23
US-10-425-115-203294
Sequence 203294, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 203294
LENGTH: 150
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_116992C.1.pep
US-10-425-115-203294

Query Match 68.6%; Score 35; DB 4; Length 150;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSYAFDI 10
Db 131 GSYAFDL 137

RESULT 24
US-10-701-401-7
Sequence 7, Application US/10701401
Publication No. US20050026285A1
GENERAL INFORMATION:

```
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Oukka, Mohamed
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING KRC ACTIVITY
; FILE REFERENCE: HUI-045CP
; CURRENT APPLICATION NUMBER: US/10/701,401
; PRIOR FILING DATE: 2003-11-03
; PRIOR FILING DATE: 2003-11-03
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-701-401-7

Query Match      68.6%; Score 35; DB 5; Length 852;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RGSYAFD 9
      |||:|
Db      355 RGSYSFD 361

RESULT 25
US-10-080-608A-23
; Sequence 23, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-080-608A-23

Query Match      68.6%; Score 35; DB 4; Length 928;
Best Local Similarity 66.7%; Pred. No. 9.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 EARGSYAFD 9
      |||:|
Db      44 EAQGSFTFD 52

RESULT 26
US-10-370-685-112
; Sequence 112, Application US/10370685
; Publication No. US20030215903A1
; GENERAL INFORMATION:
; APPLICANT: Hyman, Paul
; APPLICANT: Goldberg, Edward
; TITLE OF INVENTION: Nanostructures Containing PNA Joining and Functional Elements
; FILE REFERENCE: NANF.P-004
; CURRENT APPLICATION NUMBER: US/10/370,685
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 112
; LENGTH: 928
; TYPE: PRT
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; ORGANISM: Neurospora crassa
US-10-370-685-112

Query Match      68.6%; Score 35; DB 4; Length 928;
Best Local Similarity 66.7%; Pred. No. 9.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 EARGSYAFD 9
      |||:|
Db      44 EAQGSFTFD 52

RESULT 27
US-10-408-765A-1504
; Sequence 1504, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1504
; LENGTH: 2406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1504

Query Match      68.6%; Score 35; DB 4; Length 2406;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RGSYAFD 9
      |||:|
Db      558 RGSYSFD 564

RESULT 28
US-10-701-401-2
; Sequence 2, Application US/10701401
; Publication No. US20050026285A1
; GENERAL INFORMATION:
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Oukka, Mohamed
; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE BY MODULATING KRC ACTIVITY
; FILE REFERENCE: HUI-045CP
; CURRENT APPLICATION NUMBER: US/10/701,401
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: 60/288,369
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-701-401-2

Query Match      68.6%; Score 35; DB 5; Length 2406;
Best Local Similarity 85.7%; Pred. No. 2.4e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 RGSYAFD 9
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Db      558 RGSYSFD 564
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PRIORITY FILING DATE: 2000-09-05
PRIORITY APPLICATION NUMBER: US 60/230,517
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: US 60/230,610
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: US 60/230,597
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: US 60/230,597
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PERL Program
SEQ ID NO 407
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: LG:306284.1.orf2:2000SEP08
US-10-363-829-407

Query Match      66.7%; Score 34; DB 4; Length 192;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 EARGSYAFDI 10
      :|:|:|:|:
Db      70 DAKQYLFDL 79

RESULT 31
US-10-425-115-330011
; Sequence 330011, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 330011
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(223)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_64070C.1.pep
US-10-425-115-330011

Query Match      66.7%; Score 34; DB 4; Length 223;
Best Local Similarity 87.5%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ARGSYAFD 9
      :|:|:|:|:
Db      146 ARGSYAAD 153

RESULT 32
US-10-151-882-16
; Sequence 16, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
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; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A027A11 scFv
US-10-151-882-16

Query Match          66.7%; Score 34; DB 4; Length 242;
Best Local Similarity 77.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
Db 97 ARGSAQFEI 105

RESULT 33
US-10-767-701-43856
; Sequence 43856, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 43856
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C41057_1.pep
US-10-767-701-43856

Query Match          66.7%; Score 34; DB 4; Length 254;
Best Local Similarity 75.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFD 9
Db 1 ARGSGFGD 8

RESULT 34
US-10-425-115-330008
; Sequence 330008, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 330008
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700442752_FLI.pep
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; NAME/KEY: unsure
; LOCATION: (1)..(308)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_64068C.1.pep
US-10-425-115-330008

Query Match          66.7%; Score 34; DB 4; Length 308;
Best Local Similarity 87.5%; Pred. No. 4.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFD 9
Db 98 ARGSYAAD 105

RESULT 35
US-10-425-114-64938
; Sequence 64938, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 64938
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4730-020-G2_FLI.pep
US-10-425-114-64938

Query Match          66.7%; Score 34; DB 4; Length 311;
Best Local Similarity 75.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAF 8
Db 245 EARGGYAY 252

RESULT 36
US-10-425-114-41240
; Sequence 41240, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 41240
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700442752_FLI.pep
;
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US-10-425-114-41240

Query Match 66.7%; Score 34; DB 4; Length 341;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAF 8
|||||
Db 275 EARGGYAY 282

RESULT 37

US-10-425-115-290829
; Sequence 290829, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 290829
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_28325C.1.pap
US-10-425-115-290829

Query Match 66.7%; Score 34; DB 4; Length 353;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAF 8
|||||
Db 287 EARGGYAY 294

RESULT 38

US-10-282-122A-76935
; Sequence 76935, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76935
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-76935

Query Match 66.7%; Score 34; DB 4; Length 541;
Best Local Similarity 75.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
|||||
Db 173 RGSYADV 180

RESULT 39

US-10-104-047-2011
; Sequence 2011, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2011
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2011

Query Match 66.7%; Score 34; DB 4; Length 555;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
:|:|:|
Db 36 DARGQYLDL 45

RESULT 40

US-10-415-187-3
; Sequence 3, Application US/10415187
; Publication No. US20040044184A1
; GENERAL INFORMATION:
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YAO, Monique G.
; APPLICANT: WALLA, Narinder K.
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: LU, Yan
; APPLICANT: DING, Li
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: LAL, Preeti G.

; APPLICANT: BATRA, Sajeev
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: SANJANWALA, Madhu S.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: XU, Yuming
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0828 USN
; CURRENT APPLICATION NUMBER: US/10/415,187
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/50983
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/244,022
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/247,370
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/251,831
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040044184A1 7091536CD1
US-10-415-187-3

Query Match 66.7%; Score 34; DB 4; Length 570;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
Db 36 DAKGQYLFDL 45

Search completed: December 14, 2005, 07:37:53
Job time : 47.8621 secs

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:25:44 ; Search time 3.10345 Seconds
(without alignments)
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Title: US-10-720-323-3

Perfect score: 51

Sequence: 1 EARGSYAFDI 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	72.5	11	7	US-11-054-515-3185
2	37	72.5	243	7	US-11-054-515-1935
3	32	62.7	434	6	US-10-467-657-6894
4	32	62.7	524	6	US-10-467-657-8122
5	31	60.8	9	7	US-11-054-515-3156
6	31	60.8	19	7	US-11-054-515-2183
7	31	60.8	81	6	US-10-467-657-2712
8	31	60.8	244	7	US-11-054-515-2037
9	31	60.8	251	7	US-11-054-515-908
10	31	60.8	251	7	US-11-054-515-1594
11	31	60.8	694	7	US-11-074-176-340
12	31	60.8	697	7	US-11-074-176-150
13	31	60.8	778	6	US-10-467-657-1686
14	31	60.8	1006	6	US-10-467-657-8400
15	30	58.8	12	7	US-11-054-515-3206
16	30	58.8	17	7	US-11-054-515-2201
17	30	58.8	195	7	US-11-074-176-40
18	30	58.8	226	6	US-10-793-626-1932
19	30	58.8	242	7	US-11-054-515-1957
20	30	58.8	252	6	US-10-467-657-3128
21	30	58.8	254	7	US-11-054-515-1893
22	30	58.8	429	6	US-10-793-626-322
23	29.5	57.8	212	6	US-10-467-657-3428
24	29	56.9	154	7	US-11-082-389-424
25	29	56.9	209	6	US-10-467-657-4090

26	29	56.9	253	7	US-11-054-515-1333
27	29	56.9	284	6	US-10-131-826A-242
28	29	56.9	339	6	US-10-467-657-4318
29	29	56.9	437	7	US-11-069-642-92
30	29	56.9	438	7	US-11-069-642-47
31	29	56.9	438	7	US-11-069-642-49
32	29	56.9	438	7	US-11-069-642-51
33	29	56.9	438	7	US-11-069-642-53
34	29	56.9	438	7	US-11-069-642-55
35	29	56.9	438	7	US-11-069-642-57
36	29	56.9	438	7	US-11-069-642-59
37	29	56.9	438	7	US-11-069-642-61
38	29	56.9	438	7	US-11-069-642-63
39	29	56.9	463	6	US-10-793-626-960
40	29	56.9	826	6	US-10-793-626-1066
41	28.5	55.9	249	7	US-11-054-515-1817
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44	28	54.9	124	7	US-11-040-159-12
45	28	54.9	191	6	US-10-821-234-1468
46	28	54.9	250	7	US-11-054-515-1414
47	28	54.9	255	6	US-10-467-657-1144
48	28	54.9	256	6	US-10-793-626-2596
49	28	54.9	267	6	US-10-793-626-334
50	28	54.9	320	6	US-10-793-626-1786
51	28	54.9	483	7	US-11-113-424-24
52	28	54.9	524	7	US-11-113-424-64
53	28	54.9	551	6	US-10-821-234-1580
54	28	54.9	557	6	US-10-467-657-5540
55	28	54.9	581	7	US-11-045-802-30
56	28	54.9	584	7	US-11-045-802-31
57	28	54.9	665	6	US-10-793-626-1232
58	28	54.9	798	6	US-10-770-726-64
59	28	54.9	801	6	US-10-467-657-6470
60	28	54.9	2491	6	US-10-995-561-769
61	27.5	53.9	252	7	US-11-054-515-1329
62	27	52.9	13	7	US-11-054-515-2206
63	27	52.9	14	7	US-11-054-515-3026
64	27	52.9	20	7	US-11-054-515-2808
65	27	52.9	21	7	US-11-054-515-2861
66	27	52.9	90	7	US-11-053-076-17
67	27	52.9	122	7	US-11-127-677-11
68	27	52.9	125	7	US-11-096-074-57
69	27	52.9	189	6	US-10-467-657-4524
70	27	52.9	227	6	US-10-467-657-258
71	27	52.9	227	6	US-10-467-657-3552
72	27	52.9	248	7	US-11-054-515-1890
73	27	52.9	249	7	US-11-054-515-1720
74	27	52.9	251	7	US-11-054-515-1316
75	27	52.9	252	7	US-11-054-515-1612
76	27	52.9	256	7	US-11-054-515-1607
77	27	52.9	258	7	US-11-054-515-1173
78	27	52.9	274	6	US-10-821-234-956
79	27	52.9	344	6	US-10-467-657-4862
80	27	52.9	359	7	US-11-012-762-12
81	27	52.9	374	6	US-10-793-626-3096
82	27	52.9	374	6	US-11-055-822-968
83	27	52.9	425	6	US-10-525-710-22
84	27	52.9	438	7	US-11-067-121-19
85	27	52.9	445	7	US-11-074-176-182
86	27	52.9	448	6	US-10-467-657-4416
87	27	52.9	454	6	US-10-467-657-9009
88	27	52.9	628	6	US-10-467-657-2484
89	27	52.9	668	6	US-10-467-657-5042
90	27	52.9	681	7	US-11-067-121-9
91	27	52.9	826	7	US-11-055-822-214
92	27	52.9	826	7	US-11-055-822-712
93	27	52.9	833	7	US-11-055-822-212
94	27	52.9	833	7	US-11-055-822-710
95	27	52.9	1187	6	US-10-821-234-955
96	27	52.9	1221	6	US-10-858-730-222
97	27	52.9	1704	7	US-11-075-046-40
98	27	52.9	2087	7	US-11-075-046-28

Sequence 1333, Ap
Sequence 242, App
Sequence 4318, Ap
Sequence 92, Appl
Sequence 47, Appl
Sequence 49, Appl
Sequence 51, Appl
Sequence 53, Appl
Sequence 55, Appl
Sequence 57, Appl
Sequence 59, Appl
Sequence 61, Appl
Sequence 63, Appl
Sequence 960, App
Sequence 1066, Ap
Sequence 1817, Ap
Sequence 2898, Ap
Sequence 10, Appl
Sequence 12, Appl
Sequence 1468, Ap
Sequence 1414, Ap
Sequence 1144, Ap
Sequence 2596, Ap
Sequence 334, App
Sequence 1786, Ap
Sequence 24, Appl
Sequence 54, Appl
Sequence 1580, Ap
Sequence 5540, Ap
Sequence 30, Appl
Sequence 31, Appl
Sequence 1232, Ap
Sequence 64, Appl
Sequence 6470, Ap
Sequence 769, App
Sequence 1329, Ap
Sequence 2206, Ap
Sequence 3026, Ap
Sequence 2808, Ap
Sequence 2861, Ap
Sequence 17, Appl
Sequence 11, Appl
Sequence 57, Appl
Sequence 4524, Ap
Sequence 258, App
Sequence 3552, Ap
Sequence 1890, Ap
Sequence 1720, Ap
Sequence 1316, Ap
Sequence 1612, Ap
Sequence 1607, Ap
Sequence 1173, Ap
Sequence 956, App
Sequence 4862, Ap
Sequence 12, Appl
Sequence 3096, Ap
Sequence 968, App
Sequence 22, Appl
Sequence 19, Appl
Sequence 182, App
Sequence 4416, Ap
Sequence 9009, Ap
Sequence 2484, Ap
Sequence 5042, Ap
Sequence 9, Appl
Sequence 214, App
Sequence 712, App
Sequence 212, App
Sequence 710, App
Sequence 955, App
Sequence 222, App
Sequence 40, Appl
Sequence 28, Appl

Sequence 1771, Ap
Sequence 122, App

99 26.5 52.0 248 7 US-11-054-515-1771
100 26.5 52.0 361 6 US-10-763-712A-122

ALIGNMENTS

RESULT 1

US-11-054-515-3185
; Sequence 3185, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3185
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3185

Query Match 72.5%; Score 37; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSYAFDI 10
|||
Db 5 GSYAFDI 11

RESULT 2

US-11-054-515-1935
; Sequence 1935, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1935
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1935

Query Match 72.5%; Score 37; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSYAFDI 10
|||
Db 103 GSYAFDI 109

RESULT 3

US-10-467-657-6894
; Sequence 6894, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6894
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6894

Query Match 62.7%; Score 32; DB 6; Length 434;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSYAFDI 10
|||
Db 132 GSHAFDI 138

RESULT 4

US-10-467-657-8122
; Sequence 8122, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 8122
 ; LENGTH: 524
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-8122

Query Match 62.7%; Score 32; DB 6; Length 524;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RGSVAFD 9
 Db 276 RGLYAFD 282

RESULT 5

US-11-054-515-3156
 ; Sequence 3156, Application US/11054515
 ; Publication No. US2005025532A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3156
 ; SEQ ID NO 3156
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-3156

Query Match 60.8%; Score 31; DB 7; Length 9;
 Best Local Similarity 75.0%; Pred. No. 3.9e+04;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RGSVAFDI 10
 Db 2 RGNQAFDI 9

RESULT 6

US-11-054-515-2183
 ; Sequence 2183, Application US/11054515
 ; Publication No. US2005025532A1
 ; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P3
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 2183
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-2183

Query Match 60.8%; Score 31; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SYAFDI 10
 Db 14 SYAFDI 19

RESULT 7

US-10-467-657-2712
 ; Sequence 2712, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 2712
 ; LENGTH: 81
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-2712

Query Match 60.8%; Score 31; DB 6; Length 81;
 Best Local Similarity 55.6%; Pred. No. 5.1;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
 Db 54 ARGSYFAV 62

```
RESULT 8
US-11-054-515-2037
; Sequence 2037, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2037
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2037

Query Match      60.8%; Score 31; DB 7; Length 244;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 RGSYAEDI 10
        ||: ||||
DB      100 RGNQAEDI 107

RESULT 9
US-11-054-515-908
; Sequence 908, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
```

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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 908
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-908

Query Match      60.8%; Score 31; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 SYAFDI 10
        |||||
DB      112 SYAFDI 117

RESULT 10
US-11-054-515-1594
; Sequence 1594, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1594
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1594

Query Match      60.8%; Score 31; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 SYAFDI 10
        |||||
DB      112 SYAFDI 117

RESULT 11
US-11-074-176-340
; Sequence 340, Application US/11074176
```

; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Russel, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176--340

Query Match 60.8%; Score 31; DB 7; Length 694;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
: : |||||
Db 149 KQGOQYAFD 157

RESULT 12

US-11-074-176-150
; Sequence 150, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-150

Query Match 60.8%; Score 31; DB 7; Length 697;
Best Local Similarity 55.6%; Pred. No. 55;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
: : |||||
Db 152 KQGOQYAFD 160

RESULT 13

US-10-467-657-1686
; Sequence 1686, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1686
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1686

Query Match 60.8%; Score 31; DB 6; Length 778;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
||: |||
Db 645 RGAYALDL 652

RESULT 14

US-10-467-657-8400
; Sequence 8400, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8400
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8400

Query Match 60.8%; Score 31; DB 6; Length 1006;
Best Local Similarity 62.5%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
||: |||
Db 591 RGAYALDL 598

RESULT 15

US-11-054-515-3206
; Sequence 3206, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3206
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3206

Query Match 58.8%; Score 30; DB 7; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARGSAFDI 10
Db 4 ARGREAFDL 12

RESULT 16
US-11-054-515-2201
; Sequence 2201, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYS
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2201
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2201

Query Match 58.8%; Score 30; DB 7; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.4;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSYAFDI 10
Db 11 GSYAMDV 17

RESULT 17
US-11-074-176-40
; Sequence 40, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Perill, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-40

Query Match 58.8%; Score 30; DB 7; Length 195;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARGSAFDI 10
Db 11 ARGERAYDI 19

RESULT 18
US-10-793-626-1932
; Sequence 1932, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1932
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1932

Query Match 58.8%; Score 30; DB 6; Length 226;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GSYAFDI 10
Db 213 GYCFDI 219

RESULT 19

US-11-054-515-1957
; Sequence 1957, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1957
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-054-515-1957

Query Match 58.8%; Score 30; DB 7; Length 249;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Type: PRT
US-11-054-515-1957

Qy 2 ARGSAFADI 10
Db 102 ARGSAFADI 110

RESULT 20
US-10-467-657-3128
; Sequence 3128, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3128
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

Query Match 58.8%; Score 30; DB 6; Length 252;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
Db 134 RGSYAFDI 141

RESULT 21
US-11-054-515-1893
; Sequence 1893, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1893
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 58.8%; Score 30; DB 7; Length 254;
Best Local Similarity 71.4%; Pred. No. 29;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GSYAFDI 10
Db 109 GSYAFDI 115

RESULT 22
US-10-793-626-322
; Sequence 322, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 322
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Artificial Sequence

Query Match 58.8%; Score 30; DB 6; Length 252;
Best Local Similarity 62.5%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1333
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1333

Query Match 56.9%; Score 29; DB 7; Length 253;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
||| :||
Db 96 ARGSLYDI 104

RESULT 27
US-10-131-826A-242
; Sequence 242, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 242
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-131-826A-242

Query Match 56.9%; Score 29; DB 6; Length 284;
Best Local Similarity 44.4%; Pred. No. 52;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
||| :||
Db 231 ARGQHSYDL 239

RESULT 28
US-10-467-657-4318
; Sequence 4318, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4318
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4318

Query Match 56.9%; Score 29; DB 6; Length 339;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
||| :||
Db 223 AVGSRAFDI 231

RESULT 29
US-11-069-642-92
; Sequence 92, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536

; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DnaB intein cyclization scaffold with GFP
US-11-069-642-92

Query Match 56.9%; Score 29; DB 7; Length 437;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
|||:|:
Db 424 RGQYPYDV 431

RESULT 30
US-11-069-642-47
; Sequence 47, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-47

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
|||:|:
Db 424 RGQYPYDV 431

RESULT 31
US-11-069-642-49
; Sequence 49, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR

; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-49

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
|||:|:
Db 424 RGQYPYDV 431

RESULT 32
US-11-069-642-51
; Sequence 51, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-51

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
|||:|:
Db 424 RGQYPYDV 431

RESULT 33
US-11-069-642-53
; Sequence 53, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:

RESULT 34
US-11-069-642-55
; Sequence 55, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-53

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RGSYAFDI 10
Db 424 RGOYPYDV 431

RESULT 35
US-11-069-642-57
; Sequence 57, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-57

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RGSYAFDI 10
Db 424 RGOYPYDV 431

RESULT 36
US-11-069-642-59
; Sequence 59, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-59

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RGSYAFDI 10
Db 424 RGOYPYDV 431

QY 3 RGSYAFDI 10
|||:|:
Db 424 RQQPYDV 431

RESULT 37
US-11-069-642-61
; Sequence 61, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR FILING DATE: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-61

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RGSYAFDI 10
|||:|:
Db 424 RQQPYDV 431

RESULT 38
US-11-069-642-63
; Sequence 63, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR FILING DATE: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Synechocystis PCC6803
US-11-069-642-63

Query Match 56.9%; Score 29; DB 7; Length 438;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 RGSYAFDI 10
|||:|:
Db 424 RQQPYDV 431

RESULT 39
US-10-793-626-960
; Sequence 960, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 960
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (463)
; OTHER INFORMATION: variable amino acid
US-10-793-626-960

Query Match 56.9%; Score 29; DB 6; Length 463;
Best Local Similarity 60.0%; Pred. No. 89;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
|||:|:
Db 142 EANGASAFNI 151

RESULT 40
US-10-793-626-1066
; Sequence 1066, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1066
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (826)
; OTHER INFORMATION: variable amino acid
US-10-793-626-1066

Query Match 56.9%; Score 29; DB 6; Length 826;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
DB 804 EANGASAFNI 813

Search completed: December 14, 2005, 07:38:15
Job time : 3.10345 secs

His Page Mark (1991)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:38 ; Search time 10.8621 Seconds
(without alignments)
88.581 Million cell updates/sec

Title: US-10-720-323-3

Perfect score: 51

Sequence: 1 EARGSVAFDI 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	76.5	201	2 T47113	protocatechuate 3,
2	38	74.5	309	2 F70394	3-oxoacyl-[acyl-ca
3	38	74.5	595	1 JCI486	neopullulanase (EC
4	37	72.5	223	2 B84100	cell-division ATP-
5	36	70.6	558	2 T30418	chitinase (EC 3.2.
6	36	70.6	667	2 T37850	hypothetical prote
7	35	68.6	400	2 AF2609	hypothetical prote
8	35	68.6	410	2 E97391	probable dehydrata
9	35	68.6	928	2 T10164	kinesin heavy chai
10	35	68.6	929	2 T51932	kinesin [imported]
11	35	68.6	2282	2 T42717	DNA-binding protei
12	34	66.7	188	2 G70442	ribosomal protein
13	34	66.7	220	2 T23704	hypothetical prote
14	34	66.7	263	2 D90231	conserved hypothet
15	34	66.7	277	2 A70233	hypothetical prote
16	34	66.7	358	2 S20037	phospholipase C -
17	34	66.7	359	2 D96910	muconate cyclisom
18	34	66.7	463	1 S74845	tlld homolog alr08
19	34	66.7	541	2 E82375	inner membrane pr
20	34	66.7	857	2 E71377	probable ATP-depen
21	34	66.7	2843	1 RBHUAP	adenomatus polypo
22	33	64.7	95	2 B84484	probable replicati
23	33	64.7	103	2 T34790	hypothetical prote
24	33	64.7	128	2 S55436	conserved hypothet
25	33	64.7	135	2 PH1492	Ig heavy chain V r
26	33	64.7	151	2 T00630	hypothetical prote
27	33	64.7	238	2 H86864	hypothetical prote
28	33	64.7	256	2 B57079	hypothetical prote
29	33	64.7	319	2 AH1247	hypothetical prote

30	64.7	319	2	AD1610	hypothetical prote
31	64.7	369	2	F82696	rod shape-determin
32	64.7	385	2	T05049	hypothetical prote
33	64.7	426	1	B71249	hypothetical prote
34	64.7	487	2	C97188	lysine decarboxyla
35	64.7	488	2	T21701	hypothetical prote
36	64.7	709	2	T25874	hypothetical prote
37	64.7	730	2	B83540	hemolytic phosphol
38	64.7	730	2	A26391	phospholipase C (E
39	64.7	782	1	G64157	probable organic s
40	64.7	919	1	VGBOQH	glycoprotein B pre
41	64.7	975	2	T42576	probable envelope
42	64.7	979	2	JH0109	glycoprotein 14 pr
43	64.7	980	1	VGBEZH	glycoprotein B pre
44	64.7	980	1	VGBECH	glycoprotein B pre
45	64.7	1621	2	T30200	protein-tyrosine k
46	64.7	2172	2	T20145	hypothetical prote
47	63.7	553	2	B90153	2-isopropylmalate
48	62.7	118	2	A24754	Ig heavy chain V r
49	62.7	172	2	E83301	hypothetical prote
50	62.7	182	2	S19506	hypothetical prote
51	62.7	256	2	AE2068	hypothetical prote
52	62.7	268	2	S35212	aspartate carbamoy
53	62.7	302	2	H90717	hypothetical prote
54	62.7	323	2	H85567	hypothetical prote
55	62.7	345	2	F83084	rod shape-determin
56	62.7	346	2	E98209	rif17 protein (AFO
57	62.7	346	2	AD3077	alkanal monooxygen
58	62.7	346	2	F95315	conserved hypothet
59	62.7	355	2	S17704	anthranilate phosph
60	62.7	372	2	H69001	App-dependent 26S
61	62.7	404	2	A75192	hypothetical prote
62	62.7	404	2	B71224	hypothetical prote
63	62.7	408	2	D75252	conserved hypothet
64	62.7	418	2	D81992	NADH2 dehydrogenas
65	62.7	418	2	B81222	NADH dehydrogenase
66	62.7	430	2	T34927	probable oxidoredu
67	62.7	444	1	F69904	adenosylmethionine
68	62.7	445	2	E86493	Pmp 5 [imported] -
69	62.7	468	2	H64802	ybfM protein - Esc
70	62.7	472	1	B49340	membrane-bound alc
71	62.7	472	2	S67470	4-aminobutyrate tr
72	62.7	486	2	T39456	zinc finger protei
73	62.7	487	2	E70508	hypothetical prote
74	62.7	500	2	A42481	4-aminobutyrate tr
75	62.7	500	2	JC4022	4-aminobutyrate tr
76	62.7	500	2	I56502	4-aminobutyrate tr
77	62.7	524	2	F81207	phosphate permease
78	62.7	564	2	I61770	keratin 6e, type I
79	62.7	602	2	C95031	hypothetical prote
80	62.7	602	2	E97902	glutamine-fructose
81	62.7	642	2	E87644	sensory box histid
82	62.7	702	2	C69999	DNA translocase st
83	62.7	809	2	F87458	conserved hypothet
84	62.7	1042	2	I50099	H,K-ATPase - giant
85	62.7	1547	1	IJFFTM	cadherin-related t
86	60.8	102	2	A72739	probable DNA-dirc
87	60.8	114	2	PH1667	Ig heavy chain V r
88	60.8	118	2	S38565	Ig heavy chain V r
89	60.8	130	2	D27883	hypothetical prote
90	60.8	133	2	T20418	hypothetical prote
91	60.8	151	2	S68222	M-caveolin - mouse
92	60.8	171	2	G84421	probable auxin-ind
93	60.8	181	2	G75071	phenylacrylic acid
94	60.8	181	2	A71094	probable 3-octapre
95	60.8	196	2	E83153	conserved hypothet
96	60.8	211	2	E75305	hypothetical prote
97	60.8	221	2	AF3195	transcription regu
98	60.8	258	2	T09636	ycsE protein - Lac
99	60.8	260	2	A2840	ABC transporter, m
100	60.8	262	2	B42728	uroporphyrinogen-I

ALIGNMENTS

RESULT 1

T47113
A:Reference number: JCI1486; MUID:93222535; PMID:7763540
A:Accession: JCI1486
A:Molecule type: DNA
A:Residues: 1-585 <TON>
A:Cross-references: UNIPROT:Q08751; UNIPARC:UPI0000000867; GB:D13178; NID:g391625; PIDN:1
C:Function:
A:Description: hydrolysis of alpha-(1->4)-glucosidic linkages of pullulan to produce pan
A:Pathway: pullulan degradation
A>Note: also has alpha-amylose activity
C:Superfamily: neopullulanase; alpha-amylose core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:293-424/Domain: alpha-amylose core homology <AMY>
F:329,354,421/Active site: Glu, Glu, Asp #status predicted
A:Accession: T47113
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-201 <YAN>
A:Cross-references: UNIPROT:Q92FA0; UNIPARC:UPI000009762A; EMBL:AF109386; PIDN:AAD05270.
A:Experimental source: strain 2065
C:Genetics:
A>Note: pcag
C:Superfamily: protocatechuate 3,4-dioxygenase beta chain
C:Keywords: oxidoreductase

Query Match 76.5%; Score 39; DB 2; Length 201;
Best Local Similarity 70.0%; Pred. No. 2.7;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
|||:||||
Db 178 EGRGTYRFDI 187

RESULT 2

F70394
A:Reference number: JCI1486; MUID:93222535; PMID:7763540
A:Accession: JCI1486
A:Molecule type: DNA
A:Residues: 1-309 <AQF>
A:Cross-references: UNIPROT:Q67185; UNIPARC:UPI000005651C; GB:AE000723; NID:g2983569; PI
A:Experimental source: strain VF5
C:Genetics:
A:Gene: fabH
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III

Query Match 74.5%; Score 38; DB 2; Length 309;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
|||:||||
Db 98 KAKGVYAFDI 107

RESULT 3

JCI1486
A:Reference number: JCI1486; MUID:93222535; PMID:7763540
A:Accession: JCI1486
A:Molecule type: DNA
A:Residues: 1-558 <KUJ>
A:Cross-references: UNIPROT:Q9VMQ7; UNIPARC:UPI00000F7DF0; EMBL:AF081810; NID:g3822234; I
N:Alternate names: alpha-amylose II
C:Species: Thermoactinomyces vulgaris
C:Date: 31-Dec-1993 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: JCI1486
R:Onozuka, T.; Ohsuka, M.; Mogi, S.; Sakai, H.; Ohta, T.; Sakano, Y.
Biosci. Biotechnol. Biochem. 57, 395-401, 1993
A:Title: A neopullulanase-type alpha-amylose gene from Thermoactinomyces vulgaris R-47.

A:Reference number: JCI1486; MUID:93222535; PMID:7763540
A:Accession: JCI1486
A:Molecule type: DNA
A:Residues: 1-585 <TON>
A:Cross-references: UNIPROT:Q08751; UNIPARC:UPI0000000867; GB:D13178; NID:g391625; PIDN:1
C:Function:
A:Description: hydrolysis of alpha-(1->4)-glucosidic linkages of pullulan to produce pan
A:Pathway: pullulan degradation
A>Note: also has alpha-amylose activity
C:Superfamily: neopullulanase; alpha-amylose core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:293-424/Domain: alpha-amylose core homology <AMY>
F:329,354,421/Active site: Glu, Glu, Asp #status predicted

Query Match 74.5%; Score 38; DB 1; Length 585;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
|||:||||
Db 9 EAKGSYAYPI 18

RESULT 4

B84100
A:Reference number: JCI1486; MUID:93222535; PMID:7763540
A:Accession: JCI1486
A:Molecule type: DNA
A:Residues: 1-223 <STO>
A:Cross-references: UNIPROT:Q9K6X2; UNIPARC:UPI00000C424E; GB:AP001519; GB:BA000004; NID:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: ftsE
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 72.5%; Score 37; DB 2; Length 223;
Best Local Similarity 60.0%; Pred. No. 7.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
|||:||||
Db 214 EARGNYGVEI 223

RESULT 5

T30418
A:Reference number: JCI1486; MUID:93222535; PMID:7763540
A:Accession: JCI1486
A:Molecule type: DNA
A:Residues: 1-558 <KUJ>
A:Cross-references: UNIPROT:Q9VMQ7; UNIPARC:UPI00000F7DF0; EMBL:AF081810; NID:g3822234; I
N:Alternate names: alpha-amylose II
C:Species: Thermoactinomyces vulgaris
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30418
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohm
Virology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-558 <KUJ>
A:Cross-references: UNIPROT:Q9VMQ7; UNIPARC:UPI00000F7DF0; EMBL:AF081810; NID:g3822234; I
N:Alternate names: alpha-amylose II
C:Species: Thermoactinomyces vulgaris
C:Date: 31-Dec-1993 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: JCI1486
R:Onozuka, T.; Ohsuka, M.; Mogi, S.; Sakai, H.; Ohta, T.; Sakano, Y.
Biosci. Biotechnol. Biochem. 57, 395-401, 1993
A:Title: A neopullulanase-type alpha-amylose gene from Thermoactinomyces vulgaris R-47.

Query Match 74.5%; Score 38; DB 2; Length 309;
Best Local Similarity 70.0%; Pred. No. 6.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
|||:||||
Db 98 KAKGVYAFDI 107

```

Query Match      70.6%; Score 36; DB 2; Length 558;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 ARGSYAFD 9
    |||:||||
Db 492 AKGAYAFD 499

RESULT 6
T37850
hypothetical protein SPAC17G6.18 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37850
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21749
A:Accession: T37850
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-667 <MUR>
A:Cross-references: UNIPROT:O13796; UNIPARC:UPI000013B778; EMBL:Z99162; PIDN:CAB16229.1;
A:Experimental source: strain 972h-; cosmid c17G6
C:Genetics:
A:Gene: SPDB:SPAC17G6.18
A:Map position: 1
A:Introns: 5/2

Query Match      70.6%; Score 36; DB 2; Length 667;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ARGSYAFD 9
    |||:||||
Db 318 ARGLYAFD 325

RESULT 7
AF2609
hypothetical protein Atu0270 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2609
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McGlell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2609
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <KUR>
A:Cross-references: UNIPROT:Q8UIM3; UNIPARC:UPI0000164491; GB:AE008688; PIDN:AAL41292.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu0270
A:Map position: circular chromosome

Query Match      68.6%; Score 35; DB 2; Length 400;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EARGSYAFDI 10
    |||:||||
Db 80 EVRGNSAFDI 89

RESULT 8
E97391
probable dehydratase (AL133423) [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: E97391
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: E97391
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-410 <KUR>
A:Cross-references: UNIPROT:Q8UIM3; UNIPARC:UPI000000D1760; GB:AE007869; PIDN:AAK85086.1
C:Genetics:
A:Gene: AGR_C_463
A:Map position: circular chromosome

Query Match      68.6%; Score 35; DB 2; Length 410;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EARGSYAFDI 10
    |||:||||
Db 90 EVRGNSAFDI 99

RESULT 9
T10164
kinesin heavy chain - Neurospora crassa
C:Species: Neurospora crassa
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10164
R:Kirchner, J.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z16968
A:Accession: T10164
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-928 <KIR>
A:Cross-references: UNIPROT:P48467; UNIPARC:UPI000012D56A; EMBL:L47106; NID:G1947183; PI
C:Genetics:
A:Gene: NKIN
C:Superfamily: kinesin heavy chain; kinesin motor domain homology
C:Keywords: ATP binding; microtubule
F:8-336/Domain: kinesin motor domain homology <KNOT>

Query Match      68.6%; Score 35; DB 2; Length 928;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EARGSYAFD 9
    |||:||||
Db 44 EAQGSFTFD 52

RESULT 10
T51932
kinesin [imported] - Haematonectria haematococca
C:Species: Haematonectria haematococca
C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T51932
R:Wu, Q.; Aist, J.R.; Wirsal, S.G.; Turgeon, B.G.; Yoder, O.C.; Sandrock, T.
submitted to the EMBL Data Library, January 1997
A:Description: Nectria haematococca mating population VI NhrAD6 and NhrK1n1 genes.
A:Reference number: Z25871
A:Accession: T51932
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-929 <WUQ>
A:Cross-references: UNIPROT:P78718; UNIPARC:UPI000006A6CA; EMBL:U86521; PIDN:AAB47851.1
A:Experimental source: strain T213 mating population VI
C:Genetics:

```

A;Gene: NhkINI
A;Introns: 40/3; 848/2
C;Superfamily: kinesin heavy chain; kinesin motor domain homology

Query Match 68.6%; Score 35; DB 2; Length 929;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFD 9
|||:||||
Db 43 EAQGSFTFD 51

RESULT 11
T42717
DNA-binding protein Rc - mouse
N;Alternate names: Ig kappa chain gene enhancer Recognition component
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T42717
R;Wu, L.C.; Liu, Y.; Strandtmann, J.; Mak, C.H.; Lee, B.; Li, Z.; Yu, C.Y.
Genomes 35, 415-424, 1996
A;Title: The mouse DNA binding protein Rc for the kappa B motif of transcription and for
ew family of large transcriptional proteins.
A;Reference number: Z22238; MUID: 97001141; PMID: 8812474
A;Accession: T42717
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2282 <WUL>
A;Cross-references: UNIPARC:UPI00000286E6; EMBL:L46815; NID:gl377885; PID:gl377886; PIDN
A;Experimental source: strain BALB/c; clone T1; thymocyte, brain
C;Genetics:
A;Gene: Rc
C;Function:
A;Description: binds V(D)J recombination signal sequence and kappa B motif
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Keywords: DNA recombination; transcription factor

Query Match 68.6%; Score 35; DB 2; Length 2282;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
|||:||||
Db 551 RGSYSFD 557

RESULT 12
G70442
ribosomal protein L5 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70442
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID: 98196666; PMID: 9537320
A;Accession: G70442
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-188 <AQF>
A;Cross-references: UNIPROT:O67568; UNIPARC:UPI0000056697; GB:AE000749; NID:52983975; PI
A;Experimental source: strain VF5
C;Genetics:
A;Gene: rpl8
C;Superfamily: ribosomal protein L5/L11

Query Match 66.7%; Score 34; DB 2; Length 188;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10

Db 131 DGRGNVAFGI 140
|:|:|:|:|
|:|:|:|:|

RESULT 13
T23704
hypothetical protein M04C7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23704
R;Kershaw, J.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19786
A;Accession: T23704
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-220 <WIL>
A;Cross-references: UNIPROT:P91906; UNIPARC:UPI0000079EA9; EMBL:Z83117; PIDN:CA805569.1;
A;Experimental source: clone M04C7
C;Genetics:
A;Gene: CESP:M04C7.3
A;Map position: 1

Query Match 66.7%; Score 34; DB 2; Length 220;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
|||:|:|:|
Db 39 EGRGTNAFDV 48
|:|:|:|:|

RESULT 14
D90231
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: D90231
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90231
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-263 <KUR>
A;Cross-references: UNIPROT:Q9UXJ3; UNIPARC:UPI0000064A02; GB:AE006641; NID:gl3813991; PJ
C;Genetics:
A;Gene: SSO0808

Query Match 66.7%; Score 34; DB 2; Length 263;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAF 8
|:|:|:|
Db 69 ESRGDYAF 76
|:|:|:|

RESULT 15
A70233
hypothetical protein BG17 - Lyme disease spirochete plasmid G/1p28-2
C;Species: Borrelia burgdorferi (lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C;Accession: A70233
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White,
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: A70233
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-277 <KLE>
A;Cross-references: UNIPROT:O50740; UNIPARC:UPI000005685D; GB:AE000786; NID:G2690008; PIDN:G2690008
A;Experimental source: strain B31
C;Genetics:
A;Genome: plasmid
C;Superfamily: Borrelia burgdorferi hypothetical protein BBG17

Query Match 66.7%; Score 34; DB 2; Length 277;
Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
||| |||
Db 8 EASGSYSADI 17
||| |||

RESULT 16
S20037
phospholipase C - Erwinia chrysanthemi
C;Species: Erwinia chrysanthemi
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S20037
R;Keen, N.T.; Ridgway, D.; Boyd, C.
Mol. Microbiol. 6, 179-187, 1992
A;Title: Cloning and characterization of a phospholipase gene from Erwinia chrysanthemi
A;Reference number: S20037; MUID:92186708; PMID:1545703
A;Accession: S20037
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <KEE>
A;Cross-references: UNIPROT:Q47499; UNIPARC:UPI0000131BD1; EMBL:Z11517; NID:G42421; PIDN:G42421
A;Genetics:
A;Gene: plcA
C;Superfamily: Erwinia chrysanthemi phospholipase C

Query Match 66.7%; Score 34; DB 2; Length 358;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
:||| |||
Db 199 DARGSSAFD 207
:||| |||

RESULT 17
D96910
muonate cycloisomerase related protein, ortholog of YKGB B. subtilis [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: D96910
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D96910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <KUR>
A;Cross-references: UNIPROT:Q97MV5; UNIPARC:UPI00000C9D58; GB:AE001437; PIDN:AAK78071.1; ATCC824
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0086

Query Match 66.7%; Score 34; DB 2; Length 359;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
||| |||

Db 16 ESRGIYSFNI 25
:||| ||| |||

RESULT 18
S74845
tldD homolog slr0863 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 09-Jul-2004
C;Accession: S74845
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74845
A;Molecule type: DNA
A;Residues: 1-463 <KAN>
A;Cross-references: UNIPROT:P73754; UNIPARC:UPI0000139D74; EMBL:D90909; GB:AB001339; NID:AB001339
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Escherichia coli tldD protein

Query Match 66.7%; Score 34; DB 1; Length 463;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
||| |||
Db 289 RGSYGFD 295
||| |||

RESULT 19
E82375
inner membrane protein, 60 kDa VC0004 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82375
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; R. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82375
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-541 <HEI>
A;Cross-references: UNIPROT:Q9KVY4; UNIPARC:UPI00000C2B8B; GB:AE004093; GB:AE003852; NID:AE003852
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0004
A;Map position: 1
C;Superfamily: probable 60K inner membrane protein; stage III sporulation protein homolog

Query Match 66.7%; Score 34; DB 2; Length 541;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
||| |||
Db 173 RGSYAVDV 180
||| |||

RESULT 20
E71377
probable ATP-dependent proteinase LA (lon-1) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: E71377
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A>Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
 A/Reference number: A71250; MUID:98332770; PMID:9685876
 A/Accession: E71377
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-857 <COL>
 A/Cross-references: UNIPROT:O83060; UNIPARC:UPI000000D31E8; GB:AE001186; GB:AE000520; NID:154271
 A/Experimental source: strain Nichols
 C/Genetics:
 A/Gene: TP0016

Query Match 66.7%; Score 34; DB 2; Length 857;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
 |||:|
 Db 188 RGTYSFDL 195

RESULT 21
 RBHUAP
 adenomatous polyposis coli protein - human
 N/Alternate names: polyposis coli locus protein DP2.5; tumor suppressor APC
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C/Accession: A37261; B39658; A44928; A49319; I54271
 R/Kinzler, K.W.; Nilbert, M.C.; Su, L.K.; Vogelstein, B.; Bryan, T.M.; Levy, D.B.; Smith, S.F.; Horii, A.; Ando, H.; Miyoshi, Y.; Miki, Y.; Nishisho, I.; Nakamura, Y.
 Science 253, 661-665, 1991
 A>Title: Identification of APC locus genes from chromosome 5q21.
 A/Reference number: A37261; MUID:91335210; PMID:1651562
 A/Accession: A37261
 A/Molecule type: mRNA
 A/Residues: 1-2843 <KIN>
 A/Cross-references: UNIPROT:P25054; UNIPARC:UPI00000502E5; GB:M74088; NID:g182396; PIDN:R13021
 R/Joslyn, G.; Carlson, M.; Thilveris, A.; Albertsen, H.; Gelbert, L.; Samowitz, W.; Grod, F.; Hershenson, J.; McPherson, J.; Wasmuth, J.; Le Paslier, D.; Abderrahim, J.; Cohen, D.; Le Cell 66, 601-613, 1991
 A>Title: Identification of deletion mutations and three new genes at the familial polyposis locus on chromosome 5.
 A/Reference number: A39658; MUID:91330307; PMID:1678319
 A/Accession: B39658
 A/Molecule type: DNA
 A/Residues: 1-183, 'L', 185-969, 'N', 971-1308, 'G', 1310-1324, 'SS', 1326, 'HSTLE', 1332-1354, 'P'
 A/Cross-references: UNIPARC:UPI000016AEE0; GB:M73548; NID:g190163; PIDN:AAA60354.1; PID:R13021
 R/Miki, Y.; Nishisho, I.; Horii, A.; Miyoshi, Y.; Utsunomiya, J.; Kinzler, K.W.; Vogelstein, P.
 Cancer Res. 52, 643-645, 1992
 A>Title: Disruption of the APC gene by a retrotransposon insertion of L1 sequence in a colorectal cancer cell line.
 A/Reference number: A44928; MUID:92119623; PMID:1310068
 A/Accession: A44928
 A/Molecule type: DNA
 A/Residues: 1506-1525 <MTK>
 A/Cross-references: UNIPARC:UPI00000354E6; GB:S78214; NID:g243541; PIDN:AA821145.1; PID:R13021
 A/Note: Sequence extracted from NCBI backbone (NCBIN:78214, NCBI:78218)
 R/Spirio, L.; Olschwang, S.; Groden, J.; Robertson, M.; Samowitz, W.; Joslyn, G.; Gelbert, C.
 Cell 75, 951-957, 1993
 A>Title: Alleles of the APC gene: an attenuated form of familial polyposis.
 A/Reference number: A49319; MUID:94073973; PMID:8252630
 A/Accession: A49319
 A/Status: preliminary; translated from GB/EMBL/DBDJ
 A/Molecule type: mRNA
 A/Residues: 'G', 143-171, 'P', 173-179 <SPI>
 R/Lambertz, S.; Ballhausen, W.G.
 Hum. Genet. 90, 650-652, 1993
 A>Title: Identification of an alternative 5' untranslated region of the adenomatous polyposis coli gene.
 A/Reference number: I54271; MUID:93186137; PMID:8383094
 A/Accession: I54271
 A/Status: preliminary; translated from GB/EMBL/DBDJ
 A/Molecule type: mRNA
 A/Residues: 1-4 <LAM>

A/Cross-references: UNIPARC:UPI000011EA68; GB:S56365; NID:g266243; PIDN:AAAD14918.1; PID:R13021
 C/Genetics:
 A/Gene: GDB:APC
 A/Cross-references: GDB:119682; OMIM:175100
 A/Map position: 5q21-5q22
 A/Note: mutations of this gene can result in familial adenomatous polyposis or sporadic colorectal cancer
 C/Superfamily: adenomatous polyposis coli protein
 C/Keywords: cancer; familial adenomatous polyposis; tumor suppressor
 F:1-730/Domain: leucine-rich <NTD>
 F:7-72/Region: coil #status predicted
 F:185-227/Region: coil #status predicted
 F:731-2832/Domain: serine-rich <CTD>
 F:1131-1156/Region: acidic
 F:1558-1577/Region: acidic
 F:1866-1893/Region: highly charged

Query Match 66.7%; Score 34; DB 1; Length 2843;
 Best Local Similarity 85.7%; Pred. No. 4.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
 |||:|
 Db 1835 RGSFAFD 1841

RESULT 22
 B84484
 probable replication protein A1 [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C/Accession: B84484
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: B84484
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-95 <STO>
 A/Cross-references: UNIPROT:Q9ZQL2; UNIPARC:UPI000009DC50; GB:AE002093; NID:g4309753; PID:R13021
 C/Genetics:
 A/Gene: At2g07300
 A/Map position: 2

Query Match 64.7%; Score 33; DB 2; Length 95;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
 |||:|
 Db 26 EAHGEYAVDL 35

RESULT 23
 T34790
 hypothetical protein SC2E1.22 SC2E1.22 - Streptomyces coelicolor
 C/Species: Streptomyces coelicolor
 C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C/Accession: T34790
 R/Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 Submitted to the EMBL Data Library, June 1998
 A/Reference number: Z21557
 A/Accession: T34790
 A/Status: preliminary; translated from GB/EMBL/DBDJ
 A/Molecule type: DNA
 A/Residues: 1-103 <MUR>
 A/Cross-references: UNIPROT:O69893; UNIPARC:UPI000000DAC5F; EMBL:AL023797; PIDN:CAAL19397.
 A/Experimental source: strain A3(2)
 C/Genetics:
 A/Gene: SCOEDB:SC2E1.22

Query Match 64.7%; Score 33; DB 2; Length 103;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;

QY 2 ARGSYAFDI 10
| | | | | | | | | |
DB 11 ACGSYAFEV 19

RESULT 24
S55436
conserved hypothetical protein ywkD - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S55436; C70061
R:Glaser, P.; Danchin, A.
submitted to the EMBL Data Library, May 1995
A:Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from 3
A:Reference number: S55414
A:Accession: S55436
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-128 <GLA>
A:Cross-references: UNIPROT:P45971; UNIPARC:UPI0000060BBA; EMBL:Z49782; NID:G853752; PID
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivoita, S.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrane, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C70061
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-128 <KUN>
A:Cross-references: UNIPARC:UPI0000060BBA; GB:Z99122; GB:AL009126; NID:G2636029; PIDN:CA
A:Experimental source: strain 168
C:Genetics:
A:Gene: ywkD

Query Match 64.7%; Score 33; DB 2; Length 129;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
| | | | | | | | | |
DB 38 EERGSYKLDL 47

RESULT 25
PH1492
Ig heavy chain V region (clone PR11-4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: PH1492
R:Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A:Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A:Reference number: PH1482; MUID:93171820; PMID:8436910
A:Accession: PH1492
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <GIU>

A:Cross-references: UNIPARC:UPI0000176C7D
A:Experimental source: hybridoma cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
F:79/Region: ochre stop codon

Query Match 64.7%; Score 33; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSYAFD 9
| | | | | | | | | |
DB 123 GSYAFD 128

RESULT 26
T00630
hypothetical protein T2711.13 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00630
R:Federpspiel, N.A.; Palm, C.J.; Conway, A.B.; Kurtz, D.B.; Conway, A.R.; Au, M.; Araujo,
; Vyotskaia, V.; Yu, G.; Ecker, J.; Theologis, A.; Davis, R.W.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z14193
A:Accession: T00630
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-151 <PED>
A:Cross-references: UNIPROT:O80602; UNIPARC:UPI000009F619; EMBL:AC004122; NID:G3176693;
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: ATSP:T2711.13
A:Map position: 1
A:Introns: 84/2; 111/3; 131/1

Query Match 64.7%; Score 33; DB 2; Length 151;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
| | | | | | | | | |
DB 66 ERPGNYSFDI 75

RESULT 27
H8684
hypothetical protein ytiG [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: H8684
R:Boletini, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissensbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H8684
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <STO>
A:Cross-references: UNIPROT:Q9CEC3; UNIPARC:UPI000000D44C0; GB:AE005176; PID:G12724958; P
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ytiG

Query Match 64.7%; Score 33; DB 2; Length 238;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
| | | | | | | | | |
DB 25 EERGLYFIDL 34

submitted to the Protein Sequence Database, March 1999
A:Reference number: 215396
A:Accession: T05049
A:Molecule type: DNA
A:Residues: 1-385 <BEV>
A:Cross-references: UNIPROT:O65579; UNIPARC:UPI000009FD02; EMBL:AL022223
A:Experimental source: cultivar Columbia; BAC clone M3E9
C:Genetics:
A:Map position: 4
A:Introns: 19/2; 80/2; 180/2; 314/3; 349/3
A:Note: M3E9.20

Query Match 64.7%; Score 33; DB 2; Length 385;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
|:|:|:|
Db 154 EGGSGFGFDI 163

RESULT 33

B71249

hypothetical protein PH0249 - *Pyrococcus horikoshii*C:Species: *Pyrococcus horikoshii*

C:Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 05-Oct-2004

C:Accession: B71249

R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5: 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: B71249

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-426 <KAW>

A:Cross-references: UNIPROT:O57987; UNIPARC:UPI0000062D67; GB:AP000001; NID:g3236128; PI

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0249

C:Superfamily: conserved hypothetical protein MTH1070

Query Match 64.7%; Score 33; DB 1; Length 426;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
|:|:|:|
Db 275 EGLGSYSFSD 283

RESULT 34

C97188

lysine decarboxylase [imported] - *Clostridium acetobutylicum*C:Species: *Clostridium acetobutylicum*

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 28-Jul-2003

C:Accession: C97188

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: C97188

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-487 <KUR>

A:Cross-references: UNIPARC:UPI00000CA4BA; GB:AE001437; PID:g15025347;

A:Experimental source: *Clostridium acetobutylicum* ATCC824

C:Genetics:

A:Gene: CAC2338

C:Superfamily: lysine decarboxylase

Query Match 64.7%; Score 33; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GSYAFD 9
|:|:|:|
Db 319 GSYAFD 324

RESULT 35

T21701

hypothetical protein F33E2.3 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21701

R;Lennard, N.

submitted to the EMBL Data Library, January 1997

A:Reference number: Z19461

A:Accession: T21701

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-488 <WIL>

A:Cross-references: UNIPROT:O01701; UNIPARC:UPI000007698E; EMBL:Z84574; PIDN:CAB06542.1;

A:Experimental source: clone F33E2

C:Genetics:

A:Gene: CESP:F33E2.3

A:Map position: 1

A:Introns: 94/3; 189/1; 214/3; 241/2; 274/1; 431/1; 458/1

Query Match

64.7%; Score 33; DB 2; Length 488;

Best Local Similarity

50.0%; Pred. No. 1.1e+02;

Matches

5; Conservative

4; Mismatches

1; Indels

0; Gaps

0;

Qy

1 EARGSYAFDI 10

|:|:|:|

Db

116 EANGSYSWEV 125

RESULT 36

T26874

hypothetical protein Y43F8C.14 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T26874

R;Ainscough, R.

submitted to the EMBL Data Library, October 1998

A:Reference number: Z20279

A:Accession: T26874

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-709 <WIL>

A:Cross-references: UNIPROT:Q9XWN6; UNIPARC:UPI00000612A6; EMBL:AL032637; PIDN:CAA21615.

A:Experimental source: clone Y43F8C

C:Genetics:

A:Gene: CESP:Y43F8C.14

A:Introns: 20/3; 80/1; 184/2; 309/3; 427/1; 485/3; 514/1; 603/2; 682/2

Query Match

64.7%; Score 33; DB 2; Length 709;

Best Local Similarity

85.7%; Pred. No. 1.7e+02;

Matches

6; Conservative

1; Mismatches

0; Indels

0; Gaps

0;

Qy

2 ARGSYAF 8

|:|:|:|

Db

426 SRGSYAF 432

RESULT 37

B83540

hemolytic phospholipase C precursor PA0844 [imported] - *Pseudomonas aeruginosa* (strain P

```

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83540
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-730 <S>
A;Cross-references: UNIPROT:P06200; UNIPARC:UPI000013197F; GB:AE004519; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: p1cH; PA0844
C;Superfamily: phospholipase C precursor

Query Match      64.7%; Score 33; DB 2; Length 730;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 EARGSYAFDI 10
Db      :|||:::
          597 DANGRYAFEV 606

RESULT 38
A26391
phospholipase C (EC 3.1.4.3) - Pseudomonas aeruginosa
N;Alternate names: lecithinase C; lipophosphodiesterase I
C;Species: Pseudomonas aeruginosa
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C;Accession: A26391
R;Pritchard, A.E.; Vasil, M.L.
J. Bacteriol. 167, 291-298, 1986
A;Title: Nucleotide sequence and expression of a phosphate-regulated gene encoding a sec
A;Reference number: A26391; MUID:86250607; PMID:3087958
A;Accession: A26391
A;Molecule type: DNA
A;Residues: 1-730 <PRI>
A;Cross-references: UNIPROT:P06200; UNIPARC:UPI000016FCED; GB:M13047; NID:g151492; PIDN:
C;Superfamily: phospholipase C precursor
C;Keywords: phosphoric diester hydrolase

Query Match      64.7%; Score 33; DB 2; Length 730;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 EARGSYAFDI 10
Db      :|||:::
          597 DANGRYAFEV 606

RESULT 39
G64157
probable organic solvent tolerance protein precursor HI0730 - Haemophilus influenzae (str
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: G64157
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: G64157
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-782 <TIGR>
A;Cross-references: UNIPROT:P44846; UNIPARC:UPI0000130ECF; GB:U32756; GB:L42023; NID:g15
C;Superfamily: organic solvent tolerance protein
C;Keywords: periplasmic space
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-782/Product: organic solvent tolerance protein #status predicted <MAT>

```

```

Query Match      64.7%; Score 33; DB 1; Length 782;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      3 RGSYAFD 9
Db      :|||:::
          619 RGSYQFD 625

```

```

RESULT 40
VGBEQH
glycoprotein B precursor - equine herpesvirus 4 (strain 1942)
C;Species: equine herpesvirus 4
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A31880
R;Riggio, M.P.; Cullinane, A.A.; Onions, D.E.
J. Virol. 63, 1123-1133, 1989
A;Title: Identification and nucleotide sequence of the glycoprotein gB gene of equine her
A;Reference number: A31880; MUID:89125704; PMID:2915378
A;Accession: A31880
A;Molecule type: DNA
A;Residues: 1-919 <RIG>
A;Cross-references: UNIPROT:P17472; UNIPARC:UPI000013868D; GB:M26171; NID:g341446; PIDN:
C;Superfamily: herpesvirus glycoprotein B
C;Keywords: glycoprotein; transmembrane protein
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-919/Product: glycoprotein B #status predicted <GPB>
F;740-809/Domain: transmembrane #status predicted <TMN>
F;106,216,321,364,438,456,493,499,666,688/Binding site: carbohydrate (Asn) (covalent) #st

```

```

Query Match      64.7%; Score 33; DB 1; Length 919;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      1 EARGSYAFDI 10
Db      :|||:::
          345 EPRGSYRFTI 354

```

```

Search completed: December 14, 2005, 07:31:51
Job time : 12.8621 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:28 : Search time 53.9655 Seconds
(without alignments)
130.737 Million cell updates/sec

Title: US-10-720-323-3
Perfect score: 51
Sequence: 1 EARGSYAFDI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05_80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	76.5	201	Q3ZFA0_9ACTO	Q3ZFA0 streptomyc
2	38	74.5	284	Q8ITC4_ACIJU	Q8ITC4 acinetobact
3	38	74.5	309	1 FABH_AQUAE	Q67185 aquifex aeo
4	38	74.5	348	2 Q84YU9_ORYSA	Q84YU9 oryza sativ
5	38	74.5	348	2 Q8VPR9_ACIRA	Q8VPR9 acinetobact
6	38	74.5	368	2 Q9LAJ4_ACISP	Q9LAJ4 acinetobact
7	38	74.5	374	2 Q4NO47_9DELT	Q4NO47 acinetobact
8	38	74.5	378	2 Q8TI78_METAC	Q8TI78 anaeromyxob
9	38	74.5	461	2 Q7NGJ5_GLOVI	Q8TI78 methanosarc
10	38	74.5	466	2 Q8H8M5_ORYSA	Q7NGJ5 gloeobacter
11	38	74.5	585	1 NEPU2_THEVU	Q8H8M5 oryza sativ
12	38	74.5	585	2 Q7DI93_THEVU	Q8H751 thermoactin
13	37	72.5	223	2 Q9K6X2_BACHD	Q7DI93 thermoactin
14	37	72.5	378	2 Q8PYK0_METMA	Q9K6X2 bacillus ha
15	37	72.5	586	2 Q9JRP5_THETY	Q8PYK0 methanosarc
16	37	72.5	589	2 Q8ZV65_NITEU	Q9JRP5 thermoanaer
17	37	72.5	942	2 Q5Y8G7_BRARE	Q8ZV65 nitrosomona
18	37	72.5	942	2 Q5Y8G7_BRARE	Q5Y8G7 brachydanio
19	37	72.5	1634	2 Q7XK93_ORYSA	Q5Y8G7 brachydanio
20	37	72.5	2076	2 Q8RL74_PSEFL	Q7XK93 oryza sativ
21	36	70.6	76	2 Q5XB18_STRP6	Q8RL74 pseudomonas
22	36	70.6	76	2 Q8E172_STRAS	Q5XB18 streptococc
23	36	70.6	76	2 Q8E6M7_STRAS	Q8E172 streptococc
24	36	70.6	76	2 Q9Y9W7_STRPY	Q8E6M7 streptococc
25	36	70.6	76	2 Q5M004_STRTI	Q9Y9W7 streptococc
26	36	70.6	76	2 Q5M590_STRTI	Q5M004 streptococc
27	36	70.6	76	2 Q7CN12_STRP8	Q5M590 streptococc
28	36	70.6	76	2 Q7CEY6_STRP3	Q7CN12 streptococc
29	36	70.6	228	2 Q9FJG8_ARATH	Q7CEY6 streptococc
30	36	70.6	230	2 Q5MDG1_BACSK	Q9FJG8 arabidopsis
31	36	70.6	262	2 Q5BPF3_ARATH	Q5MDG1 bacillus cl
					Q5BPF3 arabidopsis

ALIGNMENTS

32	36	70.6	262	2	Q5Q098_ARATH	Q5Q098 arabidopsis
33	36	70.6	479	2	Q9LA62_9CAUD	Q9LA62 prophage p-
34	36	70.6	555	2	Q8BQD4_MOUSE	Q8BQD4 mus musculus
35	36	70.6	558	2	Q9YMQ7_NPVLD	Q9YMQ7 lymantria d
36	36	70.6	571	2	Q4VXL3_HUMAN	Q4VXL3 homo sapien
37	36	70.6	575	2	Q4VXL4_HUMAN	Q4VXL4 homo sapien
38	36	70.6	575	2	Q99K06_MOUSE	Q99K06 mus musculus
39	36	70.6	659	2	Q7MTS1_PORGI	Q7MTS1 porphyromon
40	36	70.6	667	1	YKY1_SCHPO	YKY1 schizosacch
41	36	70.6	807	2	Q8TCR9_HUMAN	Q8TCR9 homo sapien
42	36	70.6	832	2	Q4VXL5_HUMAN	Q4VXL5 homo sapien
43	36	70.6	906	2	Q4VXL6_HUMAN	Q4VXL6 homo sapien
44	36	70.6	930	2	Q6ABA5_PROAC	Q6ABA5 propionibac
45	36	70.6	996	2	Q5US77_HUMAN	Q5US77 homo sapien
46	36	70.6	1026	1	TACC2_HUMAN	Q95359 homo sapien
47	36	70.6	1026	2	Q4VXL7_HUMAN	Q4VXL7 homo sapien
48	36	70.6	1035	1	TACC2_MOUSE	Q91J90 mus musculus
49	36	70.6	1038	2	Q4VXL8_HUMAN	Q4VXL8 homo sapien
50	36	70.6	1094	2	Q86WG7_HUMAN	Q86WG7 homo sapien
51	36	70.6	1149	2	Q811U0_MOUSE	Q811U0 mus musculus
52	36	70.6	1697	2	Q6E7J9_9CYAN	Q6E7J9 lyngbya maj
53	36	70.6	2675	2	Q4VXL2_HUMAN	Q4VXL2 homo sapien
54	36	70.6	2948	2	Q86WG6_HUMAN	Q86WG6 homo sapien
55	36	70.6	2948	2	Q4VXL0_HUMAN	Q4VXL0 homo sapien
56	35	68.6	80	2	Q8TL98_METAC	Q8TL98 methanosarc
57	35	68.6	103	2	Q854D7_9CAUD	Q854D7 mycobacteri
58	35	68.6	208	2	Q5LCM5_BACFN	Q5LCM5 bacteroides
59	35	68.6	208	2	Q64TS4_ASPFU	Q64TS4 bacteroides
60	35	68.6	236	2	Q4WD34_ASPFU	Q4WD34 aspergillus
61	35	68.6	290	2	Q70JY7_BACAM	Q70JY7 bacillus am
62	35	68.6	316	2	Q759D3_ASHGO	Q759D3 ashbya gos
63	35	68.6	344	2	Q4LRZ3_9BURK	Q4LRZ3 burkholderi
64	35	68.6	383	2	Q50ZN2_ENTHI	Q50ZN2 entamoeba h
65	35	68.6	387	2	Q7Q8K7_ANOGA	Q7Q8K7 anopheles g
66	35	68.6	400	2	Q8UIM3_AGR75	Q8UIM3 agrobacteri
67	35	68.6	400	2	Q986F8_RHIL0	Q986F8 rhizobium l
68	35	68.6	410	2	Q7DI76_AGR75	Q7DI76 agrobacteri
69	35	68.6	460	2	Q74ER4_GEOSP	Q74ER4 geobacter s
70	35	68.6	466	2	Q5MZW1_SYNPP	Q5MZW1 vibrio vuln
71	35	68.6	539	1	OXAA_VIBVU	Q84DI2 vibrio vuln
72	35	68.6	539	1	OXAA_VIBVU	Q7MQK5 vibrio vuln
73	35	68.6	542	2	Q4WK65_ASPFU	Q4WK65 aspergillus
74	35	68.6	559	2	Q7X5L9_9BACL	Q7X5L9 paenibacill
75	35	68.6	603	2	Q5B5X2_EMENI	Q5B5X2 aspergillus
76	35	68.6	680	2	Q89UJ2_BRAJA	Q89UJ2 bradyrhizob
77	35	68.6	724	2	Q7TFK1_RHCM6	Q7TFK1 rhesus cyto
78	35	68.6	928	1	KINH_NEUCR	P48467 neurospora
79	35	68.6	929	2	P787I8_NECHE	P787I8 nectria hae
80	35	68.6	931	1	KINH_GIBMO	Q86Z98 gibberella
81	35	68.6	939	2	Q41CH0_GIBZE	Q41CH0 gibberella
82	35	68.6	948	2	Q592Z1_BRARE	Q592Z1 brachydanio
83	35	68.6	949	2	Q592Y9_BRARE	Q592Y9 brachydanio
84	35	68.6	1070	2	Q52F79_MAGGR	Q52F79 magnaporthe
85	35	68.6	1244	2	Q5TW25_ANOGA	Q5TW25 anopheles g
86	35	68.6	1288	2	Q96XM6_SULTO	Q96XM6 sulfolobus
87	35	68.6	2282	2	Q6SNP9_MOUSE	Q6SNP9 mus musculus
88	35	68.6	2405	2	Q5TIR5_HUMAN	Q5TIR5 homo sapien
89	35	68.6	2406	2	Q9BZS0_HUMAN	Q9BZS0 homo sapien
90	35	68.6	2406	2	Q5TIR4_HUMAN	Q5TIR4 homo sapien
91	35	68.6	2414	2	Q9HCL7_HUMAN	Q9HCL7 homo sapien
92	34	66.7	71	2	Q9M3Q4_HORBU	Q9M3Q4 hordeum bul
93	34	66.7	71	2	Q9M3Q6_9FOAL	Q9M3Q6 hordeum mur
94	34	66.7	74	2	Q9M3Q3_HORBU	Q9M3Q3 hordeum bul
95	34	66.7	103	2	Q69K26_ORYSA	Q69K26 oryza sativ
96	34	66.7	188	1	RL5_AQUAE	Q67568 aquifex aeo
97	34	66.7	188	1	RL5_AQUAE	Q92I40 aquifex pyr
98	34	66.7	223	2	P91906_MOUSE	P91906 caenorhabdi
99	34	66.7	240	2	Q8BX61_MOUSE	Q8BX61 mus musculus
100	34	66.7	260	2	Q8G8S7_CAMJE	Q8G8S7 campylobact

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RESULT 1
Q92FA0_9ACTO
ID Q92FA0_9ACTO PRELIMINARY; PRT; 201 AA.
AC Q92FA0;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protocatechuate 3,4-dioxygenase alpha subunit (EC 1.13.11.3).
GN Name=pcag;
OS Streptomyces sp. 2065.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=86383;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2065;
RX DOI=10.1128/AEM.66.4.1499-1508.2000;
RA Iwagami S.G., Yang K., Davies J.;
RT "Characterization of the protocatechuic acid catabolic gene cluster
from Streptomyces sp. strain 2065.";
RL Appl. Environ. Microbiol. 66:1499-1508(2000).
DR EMBL; AF109386; AAD05270.1; -; Genomic_DNA.
DR PIR; T47113; T47113.
DR HSSP; P20371; 1EOA.
DR GO; GO:0008199; F:feric iron binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0018578; F:protocatechuic 3,4-dioxygenase activity; IEA.
DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
DR InterPro; IPR000627; Idiol dioxygenase.
DR Pfam; PF00775; Dioxygenase C; 1.
DR DIOXGENASE; Oxidoreductase.
KW DIOXGENASE; Oxidoreductase.
SQ SEQUENCE 201 AA; 21768 MW; A9DFA3ECAEB3B9D9 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 201;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
DB 178 EGRGTVRFDI 187

RESULT 2
Q6ITC4_ACIJU
ID Q6ITC4_ACIJU PRELIMINARY; PRT; 284 AA.
AC Q6ITC4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HMP-like outer membrane protein (Fragment).
OS Acinetobacter junii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40215;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ZN3859;
RA Zhang Y., Tang Y.C., Mo X.N., Song W., Lu J., Pan X.X., Zhu J.X.,
RA Tan S.Q.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY626903; AAT42489.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR InterPro; IPR006664; Bac OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/MotB; 1.
DR NON TER 1 284
DR NON TER 284 284
SQ SEQUENCE 284 AA; 31024 MW; 3B5C71FEC0C286DE CRC64;

Query Match 74.5%; Score 38; DB 1; Length 309;

QY 1 EARGSYAFD 9
DB 138 EARGTYNFD 146

RESULT 3
FABH_AQUAE
ID FABH_AQUAE STANDARD; PRT; 309 AA.
AC O67185;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 3-oxoacyl-[acyl-carrier-protein] synthase III (EC 2.3.1.41) (Beta-
ketoacyl-ACP synthase III) (KAS III).
GN Name=fabh; OrderedLocusNames=AQ_1099;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Anjay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.W.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
RL Nature 392:353-358(1998).
CC -1- FUNCTION: Catalyzes the condensation reaction of fatty acid
synthesis by the addition to an acyl acceptor of two carbons from
malonyl-ACP. Catalyzes the first condensation reaction which
governing the total rate of fatty acid production. Possesses both
acetoacetyl-ACP synthase and acetyl transacylase activities. Its
substrate specificity determines the biosynthesis of branched-
chain and/or straight-chain of fatty acids (By similarity).
CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
[acyl-carrier protein].
CC -1- PATHWAY: Fatty acid biosynthesis.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- DOMAIN: The last Arg residue of the ACP-binding site is essential
for the weak association between ACP/acpp and fabH (By
similarity).
CC -1- SIMILARITY: Belongs to the fabH family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
DR EMBL; AE000723; AAC07144.1; -; Genomic_DNA.
DR PIR; F70394; F70394.
DR HSSP; P24249; 1HNK.
DR HAMAP; MF 01815; -; 1.
DR InterPro; IPR004655; FabH synth.
DR TIGRfam; TIGR00747; fabH; 1.
KW Acyltransferase; Complete proteome; Fatty acid biosynthesis;
Lipid synthetase; Multifunctional enzyme; Transferase.
FT ACT_SITE 111 111 By similarity.
FT ACT_SITE 236 236 By similarity.
FT ACT_SITE 266 266 By similarity.
FT SITE 237 241 ACE-binding (By similarity).
SQ SEQUENCE 309 AA; 33925 MW; EB97518DE168140D CRC64;

Query Match 74.5%; Score 38; DB 1; Length 309;

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Best Local Similarity 70.0%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
Db 98 KAKGVYAFDI 107

RESULT 4
Q84YU9_ORYSA
ID Q84YU9_ORYSA PRELIMINARY; PRT; 348 AA.
AC Q84YU9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine kinase-like protein.
GN Name=P0045A07.108;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactroideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
RT clone:P0045A07.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005479; BACS7795.1; -; Genomic_DNA.
DR Gramine; Q84YU9; -;
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank. 3.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SMO0248; ANK. 3.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase.
SQ SEQUENCE 348 AA; 37583 MW; B714A50FE16C9176 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFD 9
Db 300 RGSYAFD 306

RESULT 5
Q8VPR9_ACIRA
ID Q8VPR9_ACIRA PRELIMINARY; PRT; 348 AA.
AC Q8VPR9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE OmpA-like protein precursor.
OS Acinetobacter radioresistens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=40216;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=21617377; PubMed=11741856; DOI=10.1128/JB.184.1.165-170.2002;
RA Toren A., Orr E., Paitan Y., Ron E.Z., Rosenberg E.;
RT "The active component of the bioemulsifier alasean from Acinetobacter
RT radioresistens KA53 is an OmpA-like protein.";
RL J. Bacteriol. 184:165-170(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Toren A. Jr., Rosenberg E. Sr.;
RA Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY033946; AAK57731.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/MotB; 1.
KW Signal.
FT SIGNAL. 1 21 Potential.
SQ SEQUENCE 348 AA; 37853 MW; 814793F07F4777A7 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 348;
Best Local Similarity 77.8%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
Db 168 EARGTYHFD 176

RESULT 6
Q9LAJ4_ACISP
ID Q9LAJ4_ACISP PRELIMINARY; PRT; 368 AA.
AC Q9LAJ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Outer membrane protein.
GN Name=OmpA;
OS Acinetobacter sp.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=472;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20278159; PubMed=10816525;
RX DOI=10.1128/IAI.68.6.3657-3666.2000;
RA Ofori-Darko E., Zavros Y., Rieder G., Tarle S.A., Van Antwerp M.,
RA Merchant J.L.;
RT "An OmpA-like protein from Acinetobacter spp. stimulates gastrin and
RT interleukin-8 promoters.";
RL Infect. Immun. 68:3657-3666(2000).
DR EMBL; AF132598; AAF63228.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR006664; Bac_OmpA.
DR InterPro; IPR006665; OmpA/MotB.
DR Pfam; PF00691; OmpA; 1.
DR PRINTS; PR01021; OMPADOMAIN.
DR ProDom; PD000930; OmpA/MotB; 1.
SQ SEQUENCE 368 AA; 40069 MW; E21F540BA3E01519 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 368;
Best Local Similarity 77.8%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
Db 188 EARGTYHFD 196

RESULT 7
Q4NQ47_9DELT
ID Q4NQ47_9DELT PRELIMINARY; PRT; 374 AA.
AC Q4NQ47;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein precursor.
GN ORFNames=AdehDRAFT_078;
OS Anaeromyxobacter dehalogenans 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cyctobacterineae; Myxococcaceae; Anaeromyxobacter.
OX NCBI_TaxID=290397;
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RN  NUCLEOTIDE SEQUENCE.
RC  STRAIN=2CP-C;
RG  US DOE Joint Genome Institute (JGI-PGP);
RA  Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA  Hammon N., Iserani S., Pfluck S., Richardson P.;
RT  "Sequencing of the draft genome assembly of Anaeromyxobacter
RL  dehalogenans 2CP-C.";
RL  Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN  [2]
RN  NUCLEOTIDE SEQUENCE.
RC  STRAIN=2CP-C;
RG  US DOE Joint Genome Institute (JGI-ORNL);
RA  Larimer F., Land M.;
RT  "Annotation of the draft genome assembly of Anaeromyxobacter
RL  dehalogenans 2CP-C.";
RL  Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; AAHD0100038; EAL77666.1; -; Genomic_DNA.
KW  Hypothetical protein; Signal.
FT  SIGNAL 1 25 Potential.
SQ  SEQUENCE 374 AA; 39752 MW; 7365E47B5CC278B1 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 374;
Best Local Similarity 87.5%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFD 9
Db 115 ARGGYAFD 122

RESULT 8
Q8T18 METAC
ID Q8T18 METAC PRELIMINARY; PRT; 378 AA.
AC Q8T18;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN OrderedLocusNames=MA4053;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atncor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The Genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011117; AAM07401.1; -; Genomic DNA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0005875; P:carbohydrate metabolism; IEA.
DR InterPro; IPR004300; Glyco_hydro_57.
DR Pfam; PF03065; Glyco_hydro_57; 1.
KW Complete proteome.
SQ SEQUENCE 378 AA; 43911 MW; 61A14AF51906CAAD CRC64;

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Query Match 74.5%; Score 38; DB 2; Length 378;
Best Local Similarity 70.0%; Pred. No. 58;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
Db 63 EGGGSYAFDL 72

RESULT 9
Q7NGL5 GLOVI
ID Q7NGL5_GLOVI PRELIMINARY; PRT; 461 AA.
AC Q7NGL5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glr3154 protein.
GN OrderedLocusNames=g1r3154;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasanuma Y., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
DR EMBL; BA000045; BAC91095.1; -; Genomic_DNA.
DR InterPro; IPR002510; Peptidase_U62.
DR Pfam; PF01523; PmbA_TldD; 1.
KW Complete proteome.
SQ SEQUENCE 461 AA; 49721 MW; 874900043F365769 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 461;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGSYAFD 9
Db 287 RGSYAFD 293

RESULT 10
Q8H8M5 ORYSA
ID Q8H8M5 ORYSA PRELIMINARY; PRT; 466 AA.
AC Q8H8M5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative kinase.
GN Names=OSJNBa0070N04.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosch D.W., Tallon L.J., Koo H., Ziemann V., Heiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP Buell R.;

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RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AC091494; AAM65028.1; -; Genomic_DNA.
DR Gramine; Q8HBM5; -.
DR GO; GO:0005234; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Chr_Pkin_AS.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-Binding;
KW Serine/threonine-protein kinase; Transferrase.
SQ SEQUENCE 466 AA; 49982 MW; 8E30323B914DFDF CRC64;

Query Match 74.5%; Score 38; DB 2; Length 466;
Best Local Similarity 70.0%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EARGSYAFDI 10
Db 418 EAGSYTFDM 427
||| |||
418 EAGSYTFDM 427

RESULT 11
NEPU2_THEVU
ID NEPU2_THEVU STANDARD; PRT; 595 AA.
AC Q08751;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Neopullulanase 2 (EC 3.2.1.135) (Alpha-amylase II) (TVA II).
GN Name=tvaII;
OS Thermoactinomyces vulgaris.
OC Bacteria; Firmicutes; Bacillales; Thermoactinomycetaceae;
OC Thermoactinomyces.
OX NCBI_TaxID=2026;
RN [1];
RP NUCLEOTIDE SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=R-47;
RX MEDLINE=93222535; PubMed=7763540;
RA Tonozuka T., Ohtsuka M., Mogi S.-I., Sakai H., Ohta T., Sakano Y.;
RT "A neopullulanase-type alpha-amylase gene from Thermoactinomyces
vulgaris R-47.";
RL Biosci. Biotechnol. Biochem. 57:395-401(1993).
RN [2];
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=R-47;
RX MEDLINE=99241045; PubMed=10222200; DOI=10.1006/jmbi.1999.2647;
RA Kamitori S., Kondo S., Okuyama K., Yokota T., Shimura Y., Tonozuka T.,
RA Sakano Y.;
RT "Crystal structure of Thermoactinomyces vulgaris R-47 alpha-amylase II
(TVAII) hydrolyzing cyclodextrins and pullulan at 2.6-A resolution.";
RL J. Mol. Biol. 287:907-921(1999).
RN [3];
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=22047855; PubMed=12051850; DOI=10.1016/S0022-2836(02)00111-0;
RA Kamitori S., Abe A., Ohtaki A., Kaji A., Tonozuka T., Sakano Y.;
RT "Crystal structures and structural comparison of Thermoactinomyces
vulgaris R-47 alpha-amylase I (TVAI) at 1.6 A resolution and alpha-
amylase 2 (TVAII) at 2.3 A resolution.";
RL J. Mol. Biol. 318:443-453(2002).
CC -1- FUNCTION: Hydrolyzes pullulan efficiently but only a small amount
of starch. Endohydrolysis of 1,4-alpha-glucosidic linkages in
pullulan to form panose. Cleaves also (1-6)-alpha-glucosidic
linkages to form maltotriose.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of pullulan to panose (6-alpha-D-
glucosylmaltose).
CC -1- COFACTOR: Binds 1 calcium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; D13178; BAA02473.1; -; Genomic_DNA.
DR PIR; JCI486; JCI486.
DR PDB; 1BV2; X-ray; A/B=1-585.
DR PDB; 1G1Y; X-ray; A/B=1-585.
DR PDB; 1JF5; X-ray; A/B=1-585.
DR PDB; 1JF6; X-ray; A/B=1-585.
DR PDB; 1J12; X-ray; A/B=1-585.
DR PDB; 1J1B; X-ray; A/B=1-585.
DR PDB; 1JL8; X-ray; A/B=1-585.
DR PDB; 1VB9; X-ray; A/B=1-585.
DR PDB; 1VFX; X-ray; A/B=1-585.
DR PDB; 1VFN; X-ray; A/B=1-585.
DR PDB; 1VFO; X-ray; A/B=1-585.
DR PDB; 1VFU; X-ray; A/B=1-585.
DR PDB; 1WZK; X-ray; A/B=1-585.
DR PDB; 1WZL; X-ray; A/B=1-585.
DR PDB; 1WZN; X-ray; A/B=1-585.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR004185; Glyco_hydro_13ig.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF02903; Alpha-amylase N; 1.
DR 3D-structure; Calcium; Carbohydrate metabolism; Glycosidase;
KW Hydrolase; Metal-binding.
FT ACT_SITE 325 325 Nucleophile.
FT ACT_SITE 354 354 Proton donor.
FT ACT_SITE 421 421
FT METAL 143 143 Calcium.
FT METAL 145 145 Calcium (via carbonyl oxygen).
FT METAL 148 148 Calcium.
FT METAL 149 149 Calcium.
FT METAL 169 169 Calcium.
FT METAL 171 171 Calcium.
FT HELIX 3 5
FT STRAND 7 7
FT TURN 12 14
FT STRAND 15 19
FT TURN 20 21
FT STRAND 22 30
FT TURN 31 32
FT STRAND 36 42
FT TURN 44 45
FT TURN 48 49
FT STRAND 53 62
FT STRAND 66 74
FT TURN 76 77
FT STRAND 80 87
FT STRAND 93 97
FT TURN 98 99
FT STRAND 100 102
FT HELIX 105 108
FT STRAND 111 113
FT TURN 119 120
FT HELIX 126 130
FT STRAND 133 136
FT HELIX 138 141
FT TURN 146 147
FT TURN 151 152
FT STRAND 153 153
FT TURN 158 159
FT TURN 164 165
FT STRAND 167 167
FT HELIX 172 185
FT TURN 186 186
FT STRAND 189 192
FT STRAND 196 196
FT STRAND 212 212

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FT TURN 214 216
FT HELIX 219 230
FT TURN 231 233
FT STRAND 236 240
FT TURN 242 244
FT STRAND 244 244
FT TURN 247 248
FT HELIX 250 258
FT HELIX 259 261
FT TURN 263 264
FT HELIX 265 267
FT STRAND 268 268
FT STRAND 270 270
FT STRAND 283 283
FT STRAND 285 285
FT TURN 291 292
FT STRAND 294 296
FT TURN 298 299
FT HELIX 301 317
FT TURN 318 318
FT STRAND 321 324
FT TURN 325 326
FT HELIX 327 329
FT TURN 332 345
FT HELIX 347 348
FT STRAND 350 353
FT TURN 360 366
FT STRAND 370 373
FT HELIX 374 384
FT TURN 385 386
FT HELIX 391 402
FT TURN 403 404
FT HELIX 407 410
FT TURN 411 412
FT STRAND 414 416
FT TURN 420 421
FT HELIX 425 428
FT TURN 429 431
FT HELIX 433 443
FT TURN 444 445
FT STRAND 449 453
FT TURN 454 455
FT HELIX 456 458
FT TURN 459 459
FT TURN 465 468
FT HELIX 476 478
FT TURN 481 496
FT TURN 498 498
FT HELIX 499 502
FT STRAND 504 511
FT TURN 512 515
FT STRAND 516 523
FT TURN 524 525
FT STRAND 526 533
FT STRAND 539 544
FT STRAND 553 555
FT STRAND 561 561
FT STRAND 564 565
FT TURN 566 567
FT STRAND 568 573
FT TURN 575 576
FT STRAND 578 582
SQ SEQUENCE 585 AA; 67467 MW; E311813A05A7791A CRC64;

Query Match 74.5%; Score 38; DB 1; Length 585;
Best Local Similarity 70.0%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFDI 10
Db 9 EAKGSYAYPI 18

RESULT 12
Q7DI93 THEVU
ID Q7DI93 THEVU PRELIMINARY; PRT; 585 AA.
AC Q7DI93;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Alpha-amylase TVA II.
GN Name-tva II; Synonyms=tvaII;
OS Thermoactinomyces vulgaris;
OC Bacteria; Firmicutes; Bacilliales; Thermoactinomycetaceae;
OC Thermoactinomyces.
OX NCBI_TaxID=2026;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R-47;
RX MEDLINE=93222535; PubMed=7763540;
RA Tonozuka T., Ohtsuka M., Mogi S.-I., Sakai H., Ohta T., Sakano Y.;
RT "A neopullulanase-type alpha-amylase gene from Thermoactinomyces
vulgaris R-47.";
RL Biosci. Biotechnol. Biochem. 57:395-401(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R-47;
RX MEDLINE=96001349; PubMed=7548164; DOI=10.1016/0167-4838(95)00101-Y;
RA Tonozuka T., Mogi S., Shimura Y., Ibuka A., Sakai H., Matsuzawa H.,
RA Sakano Y., Ohta T.;
RT "Comparison of primary structures and substrate specificities of two
pullulan-hydrolyzing alpha-amylases, TVA I and TVA II, from
Thermoactinomyces vulgaris R-47.";
RL Biochim. Biophys. Acta 1252:35-42(1995).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R-47;
RA Pi Y.;
RN Submitted (AUG-2000) to the EMBL/GenBank/DBDJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R-47;
RX MEDLINE=21432651; PubMed=11549021; DOI=10.1007/s002530100609;
RA Uotsu-Tomita R., Tonozuka T., Sakai H., Sakano Y.;
RT "Novel glucoamylase-type enzymes from Thermoactinomyces vulgaris and
Methanococcus jannaschii whose genes are found in the flanking region
of the alpha-amylase genes.";
RL Appl. Microbiol. Biotechnol. 56:465-473(2001).
DR EMBL; AB047926; BAB40638.1; -; Genomic_DNA.
DR EMBL; AB029554; BAA97040.1; -; Genomic_DNA.
SQ SEQUENCE 585 AA; 67467 MW; E311813A05A7791A CRC64;
Query Match 74.5%; Score 38; DB 2; Length 585;
Best Local Similarity 70.0%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EARGSYAFDI 10
Db 9 EAKGSYAYPI 18
RESULT 13
Q9K6X2 BACHD
ID Q9K6X2 BACHD PRELIMINARY; PRT; 223 AA.
AC Q9K6X2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Call-division ATP-binding protein.
GN Name-ftsB; OrderedLocusNames=BH3602;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-125 / JCM 9153;

<p> RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317; RA Takami H., Nakasone K., Takaki Y., Maeno G., Sagaki R., Masui N., RA Fuji F., Hirano C., Nakamura Y., Ogasawara N., Kuhara S., RA Horikoshi K.; RT "Complete genome sequence of the alkaliphilic bacterium Bacillus RT halodurans and genomic sequence comparison with Bacillus subtilis."; RL Nucleic Acids Res. 28:4317-4331(2000). CC -1- SIMILARITY: Belongs to the ABC transporter family. DR ENBL; BAB000004; BAB07321.1; -, Genomic_DNA. DR PIR; B84100; B84100. DR HSSP; QS8206; 1L2T. DR GO; GO:0005524; P:ATP binding; IEA. DR GO; GO:0016887; F:ATPase activity; IEA. DR GO; GO:0000166; F:nucleotide binding; IEA. DR GO; GO:0006810; P:transport; IEA. DR InterPro; IPR003593; AAA ATPase. DR InterPro; IPR003439; ABC_transp_like. DR Pfam; PF00005; ABC_tran; 1. DR ProDom; PD000006; ABC_transporter; 1. DR SMART; SM00382; AAA; 1. DR PROSITE; PS00211; ABC_TRANSPORTER 1; 1. DR PROSITE; PS00993; ABC_TRANSPORTER 2; 1. KW ATP-binding; Complete_proteome; Nucleotide-binding; Transport. SQ SEQUENCE 223 AA; 25219 MW; 0A47398E378497A4 CRC64; </p>	<p> Query Match 72.5%; Score 37; Length 223; Best Local Similarity 60.0%; Pred.No. 54; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps </p>	
<p> QY 1 EARGSYAFDI 10 :: :: Db 214 EARGNYGYEI 223 </p>		
<p> RESULT 14 ID Q8PYKO METWA PRELIMINARY; PRT; 378 AA. OC Q8PYKO; DT 01-OCT-2002 (TReMBLrel. 22, Created) DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update) DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update) DE Alpha-amylase (EC 3.2.1.1). GN OrderedLocusNames=MM0861; OS Methanosarcina mazei (Methanosarcina frisia). OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; OC Methanosarcinaceae; Methanosarcina. OX NCBI_TaxId=2209; RN [1] RP NUCLEOTIDE SEQUENCE. RC STRAIN=Goe1 / Goe1 / ATCC BAA-199 / DSM 3647 / OCM 88; RC MEDLINE=22120827; PubMed=12125824; RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A., RA Martinez-Arias R., Henne A., Wieser A., Baumeister S., Jacob C., RA Bruggemann H., Lienard T., Christmann A., Boemcke M., Steckel S., RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P. RA Fritz H.-J., Gottschalk G.; RT "The genome of Methanosarcina mazei: evidence for lateral gene RT transfer between Bacteria and Archaea"; RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002). DR ENBL; AB013311; AAM30557.1; -, Genomic DNA. DR GO; GO:0004556; F:alpha-amylase activity; IEA. DR GO; GO:0003824; F:catalytic activity; IEA. DR GO; GO:0005975; P:carbohydrate metabolism; IEA. DR InterPro; IPR004300; Glyco_hydro_57. DR Pfam; PF03065; Glyco_hydro_57; 1. KW Complete proteome. SQ SEQUENCE 378 AA; 43594 MW; 1B90FAD5F739FD69 CRC64; </p>		<p> Query Match 72.5%; Score 37; DB 2; Length 378; Best Local Similarity 70.0%; Pred.No. 92; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps </p>
<p> QY 1 EARGSYAFDI 10 </p>		

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QY 1 EARGSVAFDI 9
Db 712 EKGGSVAYD 720

RESULT 17
Q6Y8G7 BRARE PRELIMINARY; PRT; 942 AA.
AC Q6Y8G7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Transforming acidic coiled coil 3 protein.
GN Name=tacc3; ORFNames=sb:cb500;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15207008; DOI=10.1186/1471-2148-4-16;
RA Still I.H., Vettaikorumkankav A.K., Dimatteo A., Liang P.;
RT "Structure-function evolution of the transforming acidic coiled coil
RL BMC Evol. Biol. 4:16-16(2004).
DR EMBL; AY170618; A0403163.1; -; mRNA.
DR ZFIN; ZDB-GENE-030131-9871; sb:cb500.
DR InterPro; IPR007707; TACC.
DR Pfam; PF05010; TACC; 1.
SQ SEQUENCE 942 AA; 103764 MW; A9A7F6B3811A6228 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 942;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EARGSVAFDI 10
Db 127 QSRGVSFDL 136

RESULT 18
Q502S8 BRARE PRELIMINARY; PRT; 942 AA.
AC Q502S8;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Transforming acidic coiled coil 3 protein.
GN Name=tacc3;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095573; AAH95573.1; -; mRNA.
DR Ensembl; ENSDARG00000005454; Danio rerio.
DR ZFIN; ZDB-GENE-050522-327; tacc3.
DR InterPro; IPR007707; TACC.
DR Pfam; PF05010; TACC; 1.
SQ SEQUENCE 942 AA; 103668 MW; 8C2581B276E7FF35 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 942;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 EARGSVAFDI 10
Db 127 QSRGVSFDL 136

RESULT 19
Q7XK93 ORYSA PRELIMINARY; PRT; 1634 AA.
AC Q7XK93;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE OSJNB0020J19.17 protein.
GN Name=OSJNB0020J19.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183;
RA Peng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
CAI Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL606556; CAE05788.2; -; Genomic_DNA.
DR Gramene; Q7XK93; -
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0008026; F-ATP-dependent helicase activity; IEA.
DR GO; GO:0003677; F-DNA binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00271; Helicase_C; 2.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00487; DEXDC; 2.
DR SMART; SM00490; HELIC; 2.
SQ SEQUENCE 1634 AA; 183558 MW; 660C063BD79DF471 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 1634;
Best Local Similarity 66.7%; Pred. No. 4e+02;

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Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
Db 200 KAGGAYAFD 208

RESULT 20
Q8RL74_PSEFL PRELIMINARY; PRT; 2076 AA.
ID Q8RL74_PSEFL PRELIMINARY; PRT; 2076 AA.
AC Q8RL74;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2004 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MmpII.
GN Name=mmpII;
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCIMB 10386;
RA El-Sayed A.K., Hothersall J., Cooper S.M., Stephens E., Thomas C.M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF318063; AM12911.1; -; Genomic DNA.
DR GO: 0003824; F: catalytic activity; IEA.
DR GO: 0048037; F: cofactor binding; IEA.
DR GO: 0016788; F: hydrolase activity, acting on ester bonds; IEA.
DR GO: 0009058; P: biosynthesis; IEA.
DR GO: 0006633; P: fatty acid biosynthesis; IEA.
DR InterPro: IPR009081; ACP_like.
DR InterPro: IPR002198; ADH_short.
DR InterPro: IPR000794; Ketoacyl synth.
DR InterPro: IPR008262; Lipase A5.
DR InterPro: IPR006163; Phappanteth_bind.
DR InterPro: IPR006162; Ppantne_S_.
DR InterPro: IPR001031; Thioesterase.
DR Pfam: PF00106; adh_short; 1.
DR Pfam: PF00109; ketoacyl-synt; 1.
DR Pfam: PF02801; Ketoacyl-synt C; 1.
DR Pfam: PF00550; pp-binding; 3.
DR Pfam: PF00975; Thioesterase; 1.
DR PROSITE: PS00075; ACP DOMAIN; 3.
DR PROSITE: PS00120; LIPASE_SER; UNKNOWN 1.
DR PROSITE: PS00012; PHOSPHOPANTHETINE; UNKNOWN 3.
SQ SEQUENCE 2076 AA; 221658 MW; A7C03F8D65E49A81 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 2076;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RGSYAFDI 10
Db 883 RGSFAFDV 890

RESULT 21
Q5XB18_STRP6 PRELIMINARY; PRT; 76 AA.
ID Q5XB18_STRP6 PRELIMINARY; PRT; 76 AA.
AC Q5XB18;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical cytosolic protein.
GN OrderedLocusNames=M6 SPY1260;
OS Streptococcus pyogenes (serotype M6).
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=301450;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MGAS10394;
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RX PubMed=15272401; DOI=10.1086/422697;
RA Banks D.J., Porcella S.F., Barbian K.D., Beres S.B., Phillips L.E.,
RA Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;
RT "Progress toward characterization of the group A Streptococcus
RT metagenome: complete genome sequence of a macrolide-resistant serotype
RT M6 strain.";
RL J. Infect. Dis. 190:727-738(2004).
DR EMBL: CP000003; AAT87395.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 76 AA; 8738 MW; B79C51F207DDF95 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 76;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
Db 54 EARESYSFD 62

RESULT 22
Q8E172_STRAS PRELIMINARY; PRT; 76 AA.
ID Q8E172_STRAS PRELIMINARY; PRT; 76 AA.
AC Q8E172;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SAG0490.
GN OrderedLocusNames=SAG0490;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacilliales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2603 V/R / Serotype V;
RC MEDLINE=22222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Neilson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL: AE014214; AAW99392.1; -; Genomic DNA.
DR TIGR: SAG0490; -.
KW Complete proteome.
SQ SEQUENCE 76 AA; 8712 MW; DA03E86F376ADP84 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 76;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EARGSYAFD 9
Db 54 EARESYSFD 62

RESULT 23
Q8E6M7_STRAS3 PRELIMINARY; PRT; 76 AA.
ID Q8E6M7_STRAS3 PRELIMINARY; PRT; 76 AA.
AC Q8E6M7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein gbs0536.
GN OrderedLocusNames=gbs0536;
OS Streptococcus agalactiae (serotype III).
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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=2242508; PubMed=12354221;
RA Glaser P., Rusniok K., Buchrieser C., Chevallier F., Frangeul L.,
RA Maadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunst F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
DR EMBL; AL766845; CAB46180.1; -; Genomic_DNA.
DR Sagaliet; gb0536; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 76 AA; 8712 MW; DA03E86F376ADF84 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 76;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFD 9
Db 54 EARESYSFD 62

RESULT 24
Q99YW7_STRPY PRELIMINARY; PRT; 76 AA.
AC Q99YW7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SpY1508.
GN OrderedLocNames=SPY1508;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferratti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006584; AAK34305.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 76 AA; 8710 MW; 3513FE1F207DDF8B CRC64;

Query Match 70.6%; Score 36; DB 2; Length 76;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFD 9
Db 54 EARESYSFD 62

RESULT 25
Q5M0Q4_STRT1 PRELIMINARY; PRT; 76 AA.
AC Q5M0Q4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=atr0604;
OS Streptococcus thermophilus (strain CNR2 1066).

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OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=299768;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goldsman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
RA Goffeau A., Hols P.;
RT "Complete sequence and comparative genome analysis of the dairy
RT bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000024; AAV62200.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 76 AA; 8702 MW; 8A1D46DE56339B CRC64;

Query Match 70.6%; Score 36; DB 2; Length 76;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFD 9
Db 54 EARESYSFD 62

RESULT 26
Q5M590_STRT2 PRELIMINARY; PRT; 76 AA.
AC Q5M590;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=stu0604;
OS Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=264199;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15543133; DOI=10.1038/nbt1034;
RA Bolotin A., Quinquis B., Renault P., Sorokin A., Ehrlich S.D.,
RA Kulakauskas S., Lapidus A., Goldsman E., Mazur M., Pusch G.D.,
RA Fonstein M., Overbeek R., Kyprides N., Purnelle B., Prozzi D.,
RA Ngui K., Masuy D., Hancy F., Burteau S., Boutry M., Delcour J.,
RA Goffeau A., Hols P.;
RT "Complete sequence and comparative genome analysis of the dairy
RT bacterium Streptococcus thermophilus.";
RL Nat. Biotechnol. 22:1554-1558(2004).
DR EMBL; CP000023; AAV60310.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 76 AA; 8702 MW; 8A1D46DE56339B CRC64;

Query Match 70.6%; Score 36; DB 2; Length 76;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFD 9
Db 54 EARESYSFD 62

RESULT 27
Q7CN12_STRP8 PRELIMINARY; PRT; 76 AA.
AC Q7CN12;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein spyM18_1526.
GN OrderedLocNames=spyM18_1526;

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OS Streptococcus pyogenes (serotype M18).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=301451;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108; DOI=10.1073/pnas.062526099;
 RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 group A Streptococcus strains associated with acute rheumatic fever
 outbreaks";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 DR EMBL; AB010067; AAL98095.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 76 AA; 8710 MW; 3513FE1F207DDF8B CRC64;
 Query Match 70.6%; Score 36; DB 2; Length 76;
 Best Local Similarity 77.8%; Pred. No. 29;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 EARGSYAFD 9
 DB 54 EARESYSFD 62
 RESULT 28
 O7CEY6_STRP3 PRELIMINARY; PRT; 76 AA.
 AC Q7CEY6; Q79XP9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein SpvM3_1162 (Hypothetical protein SpvM3_1162).
 GN OrderedLocusNames=SP0700, SpvM3_1162;
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=301448;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
 RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
 RA Mamarelli N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 phage-encoded toxins, the high-virulence phenotype, and clone
 emergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SSI-1 / Serotype M3;
 RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
 RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
 RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
 RA Hayashi H., Hattori M., Hamada S.;
 RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
 large-scale genomic rearrangement in invasive strains and new insights
 into phage evolution";
 RL Genome Res. 13:1042-1055(2003).
 DR EMBL; AB014159; AAM79789.1; -; Genomic_DNA.
 DR EMBL; BA000034; BAC63795.1; -; Genomic_DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 76 AA; 8710 MW; 3513FE1F207DDF8B CRC64;
 Query Match 70.6%; Score 36; DB 2; Length 76;
 Best Local Similarity 77.8%; Pred. No. 29;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 EARGSYAFD 9
 DB 54 EARESYSFD 62

RESULT 29
 Q9FUG8_ARATH PRELIMINARY; PRT; 228 AA.
 AC Q9FUG8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Arabidopsis thaliana genomic DNA, chromosome 5, PI clone:MAE1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
 RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:297-308(1998).
 DR EMBL; AB015472; BAB10108.1; -; Genomic_DNA.
 DR EMBL; AB008269; BAB10108.1; JOINED; Genomic_DNA.
 SQ SEQUENCE 228 AA; 25330 MW; A7B08C687E45F3D5 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 228;
 Best Local Similarity 70.0%; Pred. No. 88;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 EARGSYAFDI 10
 DB 184 EGRGSFAPPI 193

RESULT 30
 Q5WDG1_BACSK PRELIMINARY; PRT; 230 AA.
 AC Q5WDG1;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Cell-division ATP-binding protein.
 GN Name=ftsB; OrderedLocusNames=ABC3065;
 OS Bacillus clausii (strain KSM-K16).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=66692;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
 RA Kawai S., Ito S., Horikoshi K.;
 RT "The complete genome sequence of the alkaliphilic Bacillus clausii
 KSM-K16.";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AP006627; BAD65599.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.

KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 230 AA; 25811 MW; 67A70BC364A2329C CRC64;

Query Match 70.6%; Score 36; DB 2; Length 230;

Best Local Similarity 50.0%; Pred. No. 89; Mismatches 4; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
| | | | |
DB 221 EARGNYGYEV 230

RESULT 31

ID Q5BP3 ARATH PRELIMINARY; PRT; 262 AA.
AC Q5BP3 ARATH PRELIMINARY; PRT; 262 AA.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AT5G60880;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Underwood B.A., Xiao Y., Moskal W., Monaghan E., Wang W., Redman J.,
RA Wu H.C., Utterback T., Town C.D.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY924875; AX23950.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 29123 MW; 11EF8972A4AB97E2 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 262;

Best Local Similarity 70.0%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
| | | | |
DB 218 EGRGSFAFPI 227

RESULT 32

ID Q5Q098 ARATH PRELIMINARY; PRT; 262 AA.
AC Q5Q098 ARATH PRELIMINARY; PRT; 262 AA.
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AT5G60880;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xiao Y., Underwood B., Moskal W., Wang W., Redman J., Wu H.C.,
RA Utterback T., Town C.D.;
RT "Reconstruction of cDNA sequences for hypothetical genes in
Arabidopsis thaliana from 5' and 3' RACE products."
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY80653; XAV6889.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 29127 MW; 4C52521A43329FCB CRC64;

Query Match 70.6%; Score 36; DB 2; Length 262;

Best Local Similarity 70.0%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
| | | | |
DB 218 EGRGSFAFPI 227

RESULT 33

ID Q9LA62_9CAUD PRELIMINARY; PRT; 479 AA.
AC Q9LA62_9CAUD PRELIMINARY; PRT; 479 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ORF-401-like protein.
GN Name=orf-401;
OS Prophage P-EiBa.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=120167;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20187497; PubMed=10722621;
RX DOI=10.1128/IAI.68.4.2205-2214.2000;
RA Sandt C.H., Hill C.W.;
RT "Four different genes responsible for nonimmune immunoglobulin-binding
activities within a single strain of *Escherichia coli*.";
RL Infect. Immun. 68:2205-2214(2000).
DR EMBL; AF151091; AAF63232.1; -; Genomic_DNA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR005088; Phage_fiber_2.
DR Pfam; PF01391; Collagen; 3.
DR Pfam; PF03406; Phage_fiber_2; 1.
SQ SEQUENCE 479 AA; 47476 MW; 4632F483C8046FDA CRC64;

Query Match 70.6%; Score 36; DB 2; Length 479;

Best Local Similarity 60.0%; Pred. No. 1.9e+02; Mismatches 2; Indels 0; Gaps 0;

QY 1 EARGSYAFDI 10
| | | | |
DB 44 EETGSYSFDV 53

RESULT 34

ID Q8BQD4_MOUSE PRELIMINARY; PRT; 555 AA.
AC Q8BQD4_MOUSE PRELIMINARY; PRT; 555 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched
library, clone: D030050D05 product: transforming, acidic coiled-coil
containing protein 2, full insert sequence.
GN Name=Tracc2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaishizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

QY 1 EARGSYAFDI 10
| | | | |
DB 44 EETGSYSFDV 53

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Aeburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao K., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayateu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK050985; BAC34486.1; -, mRNA.
DR MG1; MGI:1928899; Tacc2.
DR InterPro; IPR007707; TACC.
DR Pfam; PF05010; TACC; 1.
SQ SEQUENCE 555 AA; 62403 MW; C1525B59ED9708B5 CRC64;
Query Match 70.6%; Score 36; DB 2; Length 555;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSYAFDI 10
Db 35 AKGTYTFDI 43
RESULT 35
QYQM07 NPVLD PRELIMINARY; PRT; 558 AA.
AC QYQM07;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chitinase.
OS Lymantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10449;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99124785; PubMed=9887315; DOI=10.1006/viro.1998.9459;
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
RA Slavicek J.M., Rohrmann G.F.,
RT "Sequence and analysis of the genome of a baculovirus pathogenic for
RT Lymantria dispar."
RL Virology 253:17-34(1999).
DR EMBL; AF081810; AAC70256.1; -, Genomic_DNA.
DR PIR; T30418; T30418.
DR HSP; O83008; IBDQ.
DR GO; GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR011583; Chitinase_II.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR InterPro; IPR002173; PfKB.
DR InterPro; IPR000601; PKD.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Chitinase_II; 1.
DR SMART; SM00636; Glyco_18; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
DR PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 558 AA; 60634 MW; E9277EDA87BE134B CRC64;
Query Match 70.6%; Score 36; DB 2; Length 558;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 ARGSYAFD 9
Db 492 AKGAYAFD 499
RESULT 36
Q4VXL3 HUMAN
ID Q4VXL3_HUMAN PRELIMINARY; PRT; 571 AA.
AC Q4VXL3;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Transforming, acidic coiled-coil containing protein 2.
GN Name=TACC2; ORFNames=RP11-296H2.1-016;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Howden P.,
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL135793; CA195131.1; -, Genomic_DNA.

SQ SEQUENCE 571 AA; 64155 MW; 0C89A2D8C537269B CRC64;

Query Match 70.6%; Score 36; DB 2; Length 571;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSAFDDI 10
 Db 35 AKGTTFDI 43

RESULT 37
 Q4VXL4 HUMAN
 ID Q4VXL4 HUMAN PRELIMINARY; PRT; 575 AA.
 AC Q4VXL4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Transforming, acidic coiled-coil containing protein 2.
 GN Name=TACC2; ORFNames=RP11-296H2.1-015;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Howden P.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL135793; CA195130.1; -; Genomic DNA.
 SQ SEQUENCE 575 AA; 64675 MW; BBE9DB56CFA0E479 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 575;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSAFDDI 10
 Db 35 AKGTTFDI 43

RESULT 38
 Q99K06 MOUSE
 ID Q99K06 MOUSE PRELIMINARY; PRT; 598 AA.
 AC Q99K06;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Tacc2 protein.
 GN Name=Tacc2;
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CZECH II;
 RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RA Director MGC Project;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004057; AAH04057.1; -; mRNA.
 DR HSSP; P02649; 1GS9.
 DR Ensembl; ENSMUSG0000030852; Mus musculus.
 DR MGI; MGI:1928899; Tacc2.
 DR InterPro; IPR007707; TACC.
 DR Pfam; PF05010; TACC; 1.
 SQ SEQUENCE 598 AA; 67057 MW; 3624051C22F57997 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 598;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ARGSAFDDI 10
 Db 35 AKGTTFDI 43

RESULT 39
 Q7MTS1 PORGI
 ID Q7MTS1 PORGI PRELIMINARY; PRT; 659 AA.
 AC Q7MTS1;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Urocanate hydratase.
 GN Name=hutU; OrderedLocNames=PG1872;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 RX DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83.";
 RL J. Bacteriol. 185:5591-5601 (2003).
 DR EMBL; AS017178; AAQ66859.1; -; Genomic DNA.
 DR TIGR; PG1872;
 DR GO; GO:0016829; Flyase activity; IEA.
 DR GO; GO:0016153; Furocanate hydratase activity; IEA.
 DR GO; GO:0006548; P-histidine catabolism; IEA.
 DR InterPro; IPR000193; Urocanase.
 DR Pfam; PF01175; Urocanase; 1.
 DR ProDom; PD025423; Urocanase; 1.
 DR TRGFAME; TIGR01228; hutU; 1.
 DR PROSITE; PS01233; UROCANASE; 1.
 KW Complete proteome.
 SQ SEQUENCE 659 AA; 73724 MW; 263B6CB0AF686598 CRC64;

Query Match 70.6%; Score 36; DB 2; Length 659;
 Best Local Similarity 87.5%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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QY      2 ARGSYAFD 9
Db      386 ARGSYFFD 393
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      |||||

RESULT 40
YKY1 SCHPO
ID_YKY1 SCHPO STANDARD; PRT; 667 AA.
AC O13756; Q9P7G1;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Hypothetical protein C1142.01 in chromosome I.
GN ORFNames=SPAC1142.01, SPAC1766.18;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgouras J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer B., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomycetes pombe.";
RL Nature 415:871-880(2002).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Z99162; CAB16229.1; -; Genomic DNA.
CC DR EMBL; AL159951; CAB77008.1; -; Genomic_DNA.
CC PIR; T37850; T37850.
CC DR GenDB Spombe; SPAC1142.01; -.
CC DR InterPro; IPR006994; DUF654.
CC DR Pfam; PF04910; DUF654; 1.
CC DR Complete proteome; Hypothetical protein.
CC FT COMPIAS 94 104 Poly-Lys.
CC FT COMPIAS 107 110 Poly-Lys.
CC SQ SEQUENCE 667 AA; 76364 MW; C8BB75A277504981 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 667;
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 ARGSYAFD 9
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      |||||
```

The Logo Mark (1991)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:11:28 ; Search time 62.5862 Seconds
(without alignments)
77.224 Million cell updates/sec

Title: US-10-720-323-4
Perfect score: 49
Sequence: 1 RASQSVSYLA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	11	4	AA885368
2	49	100.0	11	4	AA885368
3	49	100.0	11	5	AAE28850
4	49	100.0	11	5	AAU76330
5	49	100.0	11	6	ABJ26743
6	49	100.0	11	7	ADD24394
7	49	100.0	11	7	ADD69238
8	49	100.0	11	7	ADD69232
9	49	100.0	11	7	ADD69235
10	49	100.0	11	7	ADD80771
11	49	100.0	11	7	ADD89874
12	49	100.0	11	8	ADH89419
13	49	100.0	11	8	ADH89428
14	49	100.0	11	8	ADK18247
15	49	100.0	11	8	ADM41605
16	49	100.0	11	8	ADS88073
17	49	100.0	11	8	ADS88067
18	49	100.0	11	8	ADS88079
19	49	100.0	11	8	ADS19299
20	49	100.0	11	8	ADS64649
21	49	100.0	11	8	ADS52384
22	49	100.0	11	8	ADS52432
23	49	100.0	11	8	ADW07069
24	49	100.0	11	9	ADW07085

25	49	100.0	11	9	ADM04907	Adw04907 PAPP-A im
26	49	100.0	11	9	ADY26813	Ady26813 Human ant
27	49	100.0	11	9	ADY3860	Ady3860 Anti-SARS
28	49	100.0	11	9	AEA53685	Aea53685 Novel hum
29	49	100.0	11	9	AEA53692	Aea53692 Novel hum
30	49	100.0	11	9	AEA45811	Aea45811 Apolipop
31	49	100.0	11	9	AE01024	Aeb01024 Human IP1
32	49	100.0	11	9	AE01029	Aeb01029 Human IP1
33	49	100.0	11	9	AE028757	Aeb28757 Human CDR
34	49	100.0	11	9	AE028709	Aeb28709 Human CDR
35	49	100.0	94	7	ADD69248	Ad69248 Human lig
36	49	100.0	95	6	ABO27153	ABO27153 Human ger
37	49	100.0	95	7	ADF10195	Adf10195 Antibody
38	49	100.0	95	7	ADF10093	Adf10093 VEGF anti
39	49	100.0	95	7	ADF09988	Adf09988 Antibody
40	49	100.0	95	8	ADJ80273	Adj80273 Vkapppa ge
41	49	100.0	95	8	ADO07342	ADO07342 Human ant
42	49	100.0	95	8	ADU86536	ADU86536 Immunoglo
43	49	100.0	95	9	ADY75447	Ady75447 Human ger
44	49	100.0	95	9	AEA53928	Aea53928 Novel hum
45	49	100.0	95	9	AE013648	Aeb13648 Human var
46	49	100.0	96	9	AEA53874	Aea53874 Novel hum
47	49	100.0	100	5	AAE23989	Aae23989 Human MOG
48	49	100.0	101	9	AE01068	Aeb01068 Human lig
49	49	100.0	102	9	ADY33953	Ady33953 Anti-Tie
50	49	100.0	102	9	ADY33961	Ady33961 Anti-Tie
51	49	100.0	104	9	ADZ42036	Adz42036 Ig L chai
52	49	100.0	104	9	ADZ42035	Adz42035 Ig L chai
53	49	100.0	106	8	ADI22136	Adi22136 Anti-plat
54	49	100.0	106	9	ADW07075	Adw07075 Anti-Psaa
55	49	100.0	107	2	AA838593	Aar38593 Human lam
56	49	100.0	107	2	AAW58493	Aaw58493 Human kap
57	49	100.0	107	4	AA80988	Aab80988 Human ant
58	49	100.0	107	4	AA85350	Aab85350 Antibody
59	49	100.0	107	4	AA866414	Aab66414 Human Fab
60	49	100.0	107	5	AAE28871	Aae28871 Human KDR
61	49	100.0	107	5	ABB07235	Abb07235 Anti-IL-4
62	49	100.0	107	6	ABJ26764	Abj26764 VEGF bind
63	49	100.0	107	6	ABR54917	ABr54917 Light cha
64	49	100.0	107	6	ABR54916	ABr54916 Light cha
65	49	100.0	107	7	ADD24419	Add24419 Human lig
66	49	100.0	107	7	ADD80796	Add80796 Human clo
67	49	100.0	107	8	ADI01155	Adi01155 Human kap
68	49	100.0	107	8	ADI22135	Adi22135 Anti-plat
69	49	100.0	107	8	ADK18272	Adk18272 KDR bindi
70	49	100.0	107	9	ADY34076	Ady34076 Anti-Tie
71	49	100.0	107	9	ADY26776	Ady26776 Anti-NGF-
72	49	100.0	107	9	ADY93871	Ady93871 Anti-SARS
73	49	100.0	107	9	ADY93864	Ady93864 Anti-SARS
74	49	100.0	107	9	AEA08940	Aea08940 Antibody
75	49	100.0	107	9	AE019292	Aeb19292 Igg kappa
76	49	100.0	107	9	AE019293	Aeb19293 Igg kappa
77	49	100.0	107	9	AE047724	Aeb47724 Anti-Pcrv
78	49	100.0	108	4	AA872884	Aab72884 Human ant
79	49	100.0	108	4	AA862751	Aab62751 Human HIV
80	49	100.0	108	5	AA051165	Aam51165 Anti-tumo
81	49	100.0	108	5	AA051173	Aam51173 Human Vg/
82	49	100.0	108	5	AAU76334	Aau76334 Human ant
83	49	100.0	108	6	AD89224	Ada89224 Human ant
84	49	100.0	108	7	ADD69212	Ad69212 Human ant
85	49	100.0	108	7	ADD69214	Ad69214 Human ant
86	49	100.0	108	7	ADD69213	Ad69213 Human ant
87	49	100.0	108	7	ADJ73533	Adj73533 Erythropro
88	49	100.0	108	8	ADJ73534	Adj73534 Erythropro
89	49	100.0	108	8	ADI22138	Adi22138 Anti-plat
90	49	100.0	108	8	ADSI9298	Adsi9298 Light cha
91	49	100.0	108	9	ADW07091	Adw07091 Anti-Psaa
92	49	100.0	108	9	ADW08864	Adw08864 IGF-IR an
93	49	100.0	108	9	ADW08866	Adw08866 IGF-IR an
94	49	100.0	108	9	ADX01832	Adx01832 SARS coro
95	49	100.0	108	9	AE01057	Aeb01057 Human IP1
96	49	100.0	108	9	AE01062	Aeb01062 Human IP1
97	49	100.0	109	4	AA862756	Aab62756 Human HIV

98 49 100.0 109 7 ADF11411 Adf11411 16E1 anti
99 49 100.0 110 9 ADX02205 SARS coro
100 49 100.0 110 9 ADX02049 SARS coro

ALIGNMENTS

RESULT 1

AA885368
ID AAB85368 standard; peptide; 11 AA.
AC AAB85368;
XX
DT 17-SBP-2001 (first entry)
XX
DE Antibody AAL 160 light chain variable domain CDR1 region.
XX
XX Interleukin 1beta; IL-1beta; antibody AAL 160; immunosuppressive;
KW cerebroprotective; antiinflammatory; anti-allergic; antiasthmatic;
KW osteopathic; vasotropic; antiarthritic; dermatological; antithyroid;
KW neuroprotective; vulnerary; immunomodulator; cytostatic; anti-HIV.
XX
XX Homo sapiens.
XX
XX WO200153353-A2.
XX
XX 26-JUL-2001.
XX
XX 19-JAN-2001; 2001WO-EP000591.
XX
XX 21-JAN-2000; 2000GB-00001448.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Gram H, Di Padova FE;
XX
XX WPI; 2001-451903/48.
XX
XX New anti-IL-beta antibody molecule, comprising at least 1 one
PT immunoglobulin heavy chain variable domain (VH) which comprises
PT hypervariable regions CDR1, CDR2 and CDR3, for treating autoimmune and
PT inflammatory diseases.
XX
XX Claim 2; Page 28; 36pp; English.
XX

CC The invention provides an interleukin 1beta (IL-1beta) binding molecule,
CC in particular a human antibody to human IL-1beta. The IL-1beta binding
CC molecules of the invention are used to treat IL-1 mediated diseases or
CC disorders e.g. septicemia, septic or endotoxic shock, allergies, asthma,
CC bone loss, ischemia, stroke, rheumatoid arthritis, autoimmune diseases
CC (e.g. hemolytic anemia, systemic lupus erythematosus, myasthenia gravis,
CC Crohn's disease, inflammatory bowel syndrome, Graves disease, multiple
CC sclerosis) and inflammatory disorders (e.g. bronchitis and pulmonary
CC emphysema), adult respiratory distress syndrome, meningitis, pneumonia,
CC severe burns, cachexia, cancer, IL-1-dependent tumors and acquired
CC immunodeficiency syndrome (AIDS)-related cachexia. The IL-1beta binding
CC molecules may also be used to prevent graft-versus-host disease in
CC transplant patients. The present sequence represents a complementarity
CC determining region (CDR) of the light chain variable domain of antibody
CC AAL 160, an IL-1beta binding molecule
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
Db |||||
1 RASQSVSSSYLA 11

RESULT 2

AA856416
ID AAB66416 standard; peptide; 11 AA.
XX
AC AAB66416;
XX
DT 04-APR-2001 (first entry)
XX
DE Human Fab clone LD9 VL CDR1.
XX
XX Human; VH; heavy chain variable region; VL; light chain variable region;
KW cytostatic; antiarthritic; antipsoriatic; antidiabetic; antirheumatic;
KW opthalmological; vasotropic; gynaecological; gene therapy;
KW epithelial glycoprotein-2; EGP-2; cancer; leukaemia; haemangioma;
KW acoustic neuroma; rheumatoid arthritis; psoriasis; angiogenesis;
KW telangiectasia; diabetes; vasculogenesis; reproductive disorder; LD9;
KW complementarity determining region 1; CDR1.
XX
XX Homo sapiens.
XX
XX WO200069914-A2.
XX
XX 23-NOV-2000.
XX
XX 18-MAY-2000; 2000WO-GB0001910.
XX
XX 18-MAY-1999; 99GB-00011569.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Hoogenboom HRJM, Reurs A, Beiboer SHWB;
XX
XX WPI; 2001-016213/02.
DR N-PSDB; AAF29507.
XX
XX Novel human antibody that recognizes the epithelial glycoprotein-2
PT antigen useful for diagnosis, prevention and/or treatment of cancer-
PT related diseases.
XX
XX Disclosure; Fig 9; 86pp; English.

XX The present sequence is given in a specification relating to a novel
CC human antibody that is capable of recognising the Epithelial Glycoprotein
CC -2 (EGP-2) antigen. The antibody is useful for prevention and/or
CC treatment of conditions associated with cancer. Such conditions include
CC solid tumours, blood born tumours such as leukaemia, tumour metastasis,
CC benign tumours, for e.g. haemangiomas, acoustic neuromas, rheumatoid
CC arthritis, psoriasis, ocular angiogenesis, diabetic retinopathy,
CC myocardial angiogenesis, telangiectasia, wound granulation, angiogenesis,
CC diabetic neovascularisation, vasculogenesis, ovulation, menstruation and
CC placentation. The antibody is useful for in vivo imaging of cancer and
CC for adjuvant treatment of cancer. Vectors expressing the antibody are
CC useful for inducing an immunological response in a mammal in vivo. The
CC vector is selected from fowl pox virus (FPV), canary pox (ALVAC),
CC entomopox virus, vaccinia virus such as modified virus ankara (MVA) and
CC NYVAC or other non-replicating viral vector systems in order to provide a
CC dual immunotherapeutic approach
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
Db |||||
1 RASQSVSSSYLA 11

RESULT 3

AAE28850
ID AAE28850 standard; peptide; 11 AA.

XX AC AAE28850;

XX DT 27-DEC-2002 (first entry)

XX DE Human KDR (VEGFR-2) Fab light chain CDR1 from D2C6 clone.

XX KW Human; tumour; vascular endothelial growth factor receptor; metastasis;

XX KW epidermal growth factor receptor; non-small cell lung carcinoma; NSCLC;

XX KW breast; VEGFR; Heart; EGFR; complementarity determining region; therapy;

XX KW invasiveness; CDR.

XX OS Homo sapiens.

XX XX

XX PN WO200270008-A1.

XX PD 12-SEP-2002.

XX PF 04-MAR-2002; 2002WO-US006762.

XX PR 02-MAR-2001; 2001US-00798689.

XX XX (IMCL-) IMCLONE SYSTEMS INC.

XX PA (ROCK/) ROCKWELL P.

XX PA (GOLD/) GOLDSTEIN N I.

XX XX

XX DR WPI; 2002-691738/74.

XX XX

XX PT Inhibiting tumor growth in humans involves administering vascular

XX PT endothelial growth factor receptor antagonists in combination with

XX PT radiation, chemotherapeutic agents, or epidermal growth factor receptor

XX PT antagonists.

XX PS Example 9; Page 78; 151pp; English.

XX CC The invention relates to a method of inhibiting tumour growth which

XX CC involves administering, vascular endothelial growth factor receptor

XX CC (VEGFR) antagonists in combination with radiation, chemotherapeutic

XX CC agent, or epidermal growth factor receptor (EGFR) antagonist. The method

XX CC is useful for inhibiting tumour growth in a human, where the tumour (e.g.

XX CC tumour of the breast, heart, lung, small intestine, colon, spleen, bone,

XX CC kidney, bladder, head and neck, ovary, prostate, brain, pancreas, skin,

XX CC bone marrow, blood, thymus, uterus, testicles, cervix or liver) over

XX CC expresses VEGFR. It is also useful for inhibiting growth of colon tumour

XX CC or non-small cell lung carcinoma (NSCLC) and tumour overexpressing EGFR.

XX CC It is preferably useful for treating subjects with both solid tumours,

XX CC preferably high vascular tumours and non-solid tumours. The inhibition or

XX CC reduction of tumour growth includes prevention or inhibition of the

XX CC progression of tumour, including cancerous and non-cancerous tumours,

XX CC where the progression of tumours includes the invasiveness, metastasis,

XX CC recurrence and increase in size of the tumour. The present sequence is

XX CC human KDR (VEGFR-2) Fab antibody light chain complementarity determining

XX CC region (CDR) peptide

XX XX

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11

Db 1 RASQSVSSYLA 11

RESULT 4

AAU76330

ID AAU76330 standard; peptide; 11 AA.

XX AC AAU76330;

XX XX

XX DT 21-MAY-2002 (first entry)

XX XX

Human anti-dual integrin antibody light chain variable region CDR1.

Human; antibody; dual integrin; CDR; light chain variable region; LC CDR;

medical device; immune related disease; rheumatoid arthritis;

gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;

sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;

atherosclerosis; restenosis; angina pectoris; myocardial infarction;

infectious disease; pneumonia; leprosy; malaria; malignant disease;

leukaemia; chronic myelocytic leukaemia; multiple myeloma;

neurological disease; multiple sclerosis; Parkinson's disease;

Alzheimer's disease; Creutzfeldt-Jakob disease.

OS Homo sapiens.

XX XX

XX PN WO200212501-A2.

XX PD 14-FEB-2002.

XX PF 07-AUG-2001; 2001WO-US024784.

XX PR 07-AUG-2000; 2000US-0223363P.

XX PR 01-AUG-2001; 2001US-00920267.

XX PA (CENZ) CENTOCOR INC.

XX XX

XX PI Giles-Komar J, Heavner G, Snyder L, Trikha M;

XX XX

XX DR WPI; 2002-217193/27.

XX DR N-PSDB; ABK10117.

XX XX

XX PT Novel isolated mammalian anti-dual integrin antibody, useful for

XX PT diagnosing or treating dual integrin related condition such as rheumatoid

XX PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

XX PS Claim 29; Page 133; 144pp; English.

XX CC The invention relates to an isolated mammalian anti-dual integrin

XX CC antibody having at least one of the human heavy chain or light chain

XX CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also

XX CC included are the nucleic acids encoding the CDRs, a vector comprising the

XX CC nucleic acids, a host cell comprising the vector, an anti-idiotypic

XX CC antibody that binds to the anti-dual integrin, a medical device comprising

XX CC the antibody suitable for administration by parenteral, subcutaneous,

XX CC intramuscular, intravenous, intrarticular, intrabronchial,

XX CC intradominal, intracapsular, intracartilaginous, intracavitary,

XX CC intracerebellar, or other routes as given in specification. The antibody

XX CC is useful for diagnosing or treating a dual integrin related condition in

XX CC an animal for example, immune related disease such as rheumatoid

XX CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,

XX CC sickle cell anaemia, diabetes, cardiovascular disease such as

XX CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,

XX CC myocardial infarction, infectious disease in a cell such as bacterial,

XX CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant

XX CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's

XX CC lymphoma, multiple myeloma; neurological disease such as multiple

XX CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,

XX CC Creutzfeldt-Jakob disease and many other diseases given in the

XX CC specification. The present sequence is an anti-dual integrin human light

XX CC chain CDR

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 5; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11

Db 1 RASQSVSSYLA 11

RESULT 5

ABJ26743

XX WPI; 2003-618360/58.
XX
XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
XX Claim 3; SEQ ID NO 42; 136pp; English.
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention or
CC demonstrating cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as during gene therapy procedures. The current sequence is that of
CC the human light chain variable region CDR1 peptide of the invention.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSYLA 11
Db 1 RASQSVSSYLA 11
|||||
RESULT 8
ADD69232
ID ADD69232 standard; peptide; 11 AA.
XX
XX ADD69232;
XX
XX 15-JAN-2004 (first entry)
XX Human light chain variable region CDR1 peptide - SEQ ID 36.
XX
XX monoclonal antibody; heavy chain variable region; light; framework;
XX complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
XX prostate specific membrane antigen; PSMA; cytostatic; tumour;
XX colon cancer; renal carcinoma; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2003064606-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002448.
XX
XX 28-JAN-2002; 2002US-00059989.
XX (MEDA-) MEDAREX INC.
XX
XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX WPI; 2003-618360/58.
XX
XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
XX Claim 3; SEQ ID NO 36; 136pp; English.
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention or
CC demonstrating cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as during gene therapy procedures. The current sequence is that of
CC the human light chain variable region CDR1 peptide of the invention.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSYLA 11
Db 1 RASQSVSSYLA 11
|||||
RESULT 9
ADD69235
ID ADD69235 standard; peptide; 11 AA.
XX
XX ADD69235;
XX
XX 15-JAN-2004 (first entry)
XX Human light chain variable region CDR1 peptide - SEQ ID 39.
XX
XX monoclonal antibody; heavy chain variable region; light; framework;
XX complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
XX prostate specific membrane antigen; PSMA; cytostatic; tumour;
XX colon cancer; renal carcinoma; gene therapy; human.
XX
XX Homo sapiens.
XX
XX WO2003064606-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002448.
XX
XX 28-JAN-2002; 2002US-00059989.
XX (MEDA-) MEDAREX INC.
XX
XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX WPI; 2003-618360/58.
XX
XX New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
XX Claim 3; SEQ ID NO 39; 136pp; English.
XX
XX The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention or
CC demonstrating cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as during gene therapy procedures. The current sequence is that of
CC the human light chain variable region CDR1 peptide of the invention.
XX
SQ Sequence 11 AA;

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Query Match      100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
   |||||
Db 1 RASQSVSSYLA 11

RESULT 10
ADD80771
ID ADD80771 standard; peptide; 11 AA.
XX AC
XX AC
XX AC
DT 29-JAN-2004 (first entry)
DE Human variable light chain CDR1 KDR antibody SEQ ID NO:1.
XX KW human; antibody; KDR; cytostatic; gene therapy; anti-KDR antibody;
XX KW tumour; angiogenesis.
XX OS Homo sapiens.
XX PN WO2003075840-A2.
XX PD 18-SEP-2003.
XX PF 04-MAR-2003; 2003WO-US006459.
XX PR 04-MAR-2002; 2002US-0361783P.
XX PA (IMCL-) IMCLONE SYSTEMS INC.
XX PI Zhu 2;
XX WPI; 2003-779032/73.
XX PT New human anti-KDR antibody, useful for preparing a composition for
XX PT reducing tumor growth and inhibiting angiogenesis.
XX PS Claim 4; SEQ ID NO 1; 49pp; English.
XX CC The invention relates to a novel isolated human antibody or its fragment
XX CC binds selectively to KDR. An antibody of the invention has cytostatic
XX CC activity, and may have a use in gene therapy. The antibody is anti-KDR
XX CC antibody. The antibody is useful for preparing a composition for reducing
XX CC tumour growth and inhibiting angiogenesis. The present sequence is used
XX CC in the exemplification of the invention.
XX SQ Sequence 11 AA;

Query Match      100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
   |||||
Db 1 RASQSVSSYLA 11

RESULT 11
ADD89874
ID ADD89874 standard; peptide; 11 AA.
XX AC
XX AC
XX AC
DT 29-JAN-2004 (first entry)
DE Human anti-tumour necrosis factor antibody light chain CDR1.
XX KW Human; Tumour necrosis factor; TNF; antibody;
XX KW complementarity determining region; cytostatic; anabolic;

Query Match      100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
   |||||
Db 1 RASQSVSSYLA 11

RESULT 12
ADD89419
ID ADH89419 standard; peptide; 11 AA.
XX AC
XX AC
XX AC
DT 15-APR-2004 (first entry)
DE Human transferrin fusion protein-related CDR1 peptide SeqID63.
XX KW fusion protein; transferrin protein; glycosylation;
XX KW antibody variable region; cytostatic; antibacterial; virucide;
XX KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
XX KW septic shock; endotoxin shock; cachexia syndrome; bacterial infection;
XX KW viral infection; parasitic infection; neoplasm; autoimmune disease;
XX KW arthritis; graft rejection.
XX OS Unidentified.
XX PN US2003226155-A1.
XX
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eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen; neuroprotective.
 Homo sapiens.
 WO2003083061-A2.
 09-OCT-2003.
 24-MAR-2003; 2003WO-US009072.
 26-MAR-2002; 2002US-0367903P.
 (CENZ) CENTOCOR INC.
 Giles-Komar J, Scallion BJ, Carton JW;
 WPI; 2003-804040/75.
 New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful for diagnosing or treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia, or bacterial infection.
 Claim 2; Page 85; 87pp; English.
 The present sequence is that of complementarity determining region 1 (CDR1) of the light chain variable region of claimed mammalian anti-tumour necrosis factor (TNF) antibodies of the invention. The CDR is derived from a human TNF reactive IGG monoclonal antibody generated by cloning variable and constant region DNA in vector pC4 and expression in CHO cells. The invention provides isolated human, primate, rodent, mammalian, chimeric, humanized and/or CDR-grafted anti-TNF antibodies, immunoglobulins, their cleavage products, other specified portions and variants, as well as anti-TNF antibody compositions, nucleic acids encoding these, vectors, host cells, methods for producing the antibodies using a host cell, transgenic animal or transgenic plant or plant cell, and therapeutic compositions, methods and devices. The antibody, nucleic acid, protein, composition and methods are useful for diagnosing or treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia, or an immune, cardiovascular, infectious, and/or neurological disease.
 Sequence 11 AA;

Query Match 100.0%; Score 49; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSYLA 11
 |||||
 Db 1 RASQSVSSYLA 11

RESULT 12
 ADD89419
 ID ADH89419 standard; peptide; 11 AA.
 XX ADH89419;
 XX 15-APR-2004 (first entry)
 XX Human transferrin fusion protein-related CDR1 peptide SeqID63.
 XX fusion protein; transferrin protein; glycosylation;
 XX antibody variable region; cytostatic; antibacterial; virucide;
 XX antiparasitic; immunosuppressive; antiarthritic; gene therapy;
 XX septic shock; endotoxin shock; cachexia syndrome; bacterial infection;
 XX viral infection; parasitic infection; neoplasm; autoimmune disease;
 XX arthritis; graft rejection.
 OS Unidentified.
 XX US2003226155-A1.

PD 04-DEC-2003.
 XX 10-MAR-2003; 2003US-00384060.
 PF 30-AUG-2001; 2001US-0315745P.
 XX 30-NOV-2001; 2001US-0334059P.
 PR 30-AUG-2002; 2002US-00231494.
 PR 30-AUG-2002; 2002US-0406977P.
 XX (BIOR-) BIOREXIS PHARM CORP.
 PA Sadeghi H, Prior CP, Turner A;
 XX WPI; 2004-022093/02.
 XX New fusion protein comprising a transferrin protein exhibiting reduced glycosylation fused to at least one antibody variable region, useful for preparing a composition for treating e.g., septic shock, neoplasm or autoimmune disease.
 PT Example 2; SEQ ID NO 63; 82pp; English.
 XX This invention relates to a novel fusion protein which comprises a transferrin protein exhibiting reduced glycosylation fused to at least one antibody variable region. The invention may be useful for the development of compounds with cytostatic, antibacterial, virucide, antiparasitic, immunosuppressive or antiarthritic activity. In addition, the sequences disclosed may be useful for gene therapy. The fusion protein is useful for preparing a composition for treating a disease or disease symptom in a patient for example septic shock, endotoxic shock, cachexia syndromes associated with bacterial, viral or parasitic infections, neoplasm, autoimmune disease, arthritis or adverse effects associated with treatment for preventing graft rejection. The present sequence is that of a CDR 1 peptide which was used in the exemplification of the invention.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 49; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSYLA 11
 Db |||||
 1 RASQSVSSYLA 11
 RESULT 13
 ADH89428
 ID ADH89428 standard; peptide; 11 AA.
 XX AC ADH89428;
 XX 15-APR-2004 (first entry)
 DT Human transferrin fusion protein-related CDR1 peptide SeqID72.
 DE fusion protein; transferrin protein; glycosylation;
 XX antibody variable region; cytostatic; antibacterial; virucide;
 KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
 KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
 KW viral infection; parasitic infection; neoplasm; autoimmune disease;
 KW arthritis; graft rejection.
 XX Unidentified.
 OS US2003226155-A1.
 XX 04-DEC-2003.
 XX 10-MAR-2003; 2003US-00384060.
 PF 30-AUG-2001; 2001US-0315745P.
 XX 30-NOV-2001; 2001US-0334059P.
 PR 30-AUG-2002; 2002US-00231494.
 PR 30-AUG-2002; 2002US-0406977P.
 XX (BIOR-) BIOREXIS PHARM CORP.
 PA Sadeghi H, Prior CP, Turner A;
 XX WPI; 2004-022093/02.
 XX New fusion protein comprising a transferrin protein exhibiting reduced glycosylation fused to at least one antibody variable region, useful for preparing a composition for treating e.g., septic shock, neoplasm or autoimmune disease.
 PT Example 2; SEQ ID NO 72; 82pp; English.
 XX This invention relates to a novel fusion protein which comprises a transferrin protein exhibiting reduced glycosylation fused to at least one antibody variable region. The invention may be useful for the development of compounds with cytostatic, antibacterial, virucide, antiparasitic, immunosuppressive or antiarthritic activity. In addition, the sequences disclosed may be useful for gene therapy. The fusion protein is useful for preparing a composition for treating a disease or disease symptom in a patient for example septic shock, endotoxic shock, cachexia syndromes associated with bacterial, viral or parasitic infections, neoplasm, autoimmune disease, arthritis or adverse effects associated with treatment for preventing graft rejection. The present sequence is that of a CDR 1 peptide which was used in the exemplification of the invention.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 49; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSYLA 11
 Db |||||
 1 RASQSVSSYLA 11
 RESULT 14
 ADK18247
 ID ADK18247 standard; peptide; 11 AA.
 XX AC ADK18247;
 XX 06-MAY-2004 (first entry)
 DT KDR binding human Fabs light chain CDR1 peptide, SEQ ID 53.
 DE antibody; antigen binding site; vascular endothelial growth factor;
 KW VEGF receptor; immunoglobulin; tumour; angiogenesis; cytostatic;
 KW immunostimulant; vaccine; kinase insert domain-containing receptor; KDR;
 KW human; CDR; complementarity determining region.
 XX Homo sapiens.
 OS WO2004003211-A1.
 XX 08-JAN-2004.
 XX 24-DEC-2002; 2002WO-US041372.
 XX 26-JUN-2002; 2002WO-US020332.
 PR (IMCL-) IMCLONE SYSTEMS INC.
 XX Zhu Z;
 PI WPI; 2004-083065/08.
 XX

PT New antibody having a first and second binding sites specific for a first
PT and second vascular endothelial growth factor (VEGF) receptor, useful for
PS reducing tumor growth in a mammal and for inhibiting angiogenesis.

PS Claim 14; SEQ ID NO 53; 99pp; English.

XX The invention relates to a novel antibody having a first antigen binding
CC site specific for a first vascular endothelial growth factor (VEGF)
CC receptor and a second antigen specific for a second VEGF receptor. The
CC invention further relates to: an antibody that specifically binds to an
CC extracellular domain of a first VEGF receptor and an extracellular domain
CC of a second VEGF receptor, where binding of the antibody to the first and
CC second VEGF receptor neutralizes activation of that VEGF receptor; a
CC method for making the antibody by co-expressing in a host cell a
CC recombinant DNA construct encoding a first polypeptide having the first
CC immunoglobulin heavy chain domain located to the N-terminus of the second
CC immunoglobulin light chain variable domain; a recombinant DNA construct
CC encoding a second polypeptide having the second immunoglobulin heavy
CC chain variable domain located to the N-terminus of the first
CC immunoglobulin light chain variable domain, for time and in a manner
CC sufficient to allow expression of the polypeptides and formation of the
CC antibody; a method for neutralizing activation of a first VEGF receptor
CC and the second VEGF receptor in a cell by treating a cell with the
CC antibody cited above; a method for reducing tumor growth in a mammal by
CC treating the mammal with the antibody cited above; and a method for
CC inhibiting angiogenesis in a mammal by treating the mammal with the
CC antibody cited above. The antibody has cytostatic and immunostimulant
CC activities. The VEGF receptor antigen can be used to create a vaccine.
CC The antibody is useful for reducing tumor growth in a mammal and for
CC inhibiting angiogenesis. This sequence represents a human kinase insert
CC domain-containing receptor binding Fab complementary determining
CC region (CDR) peptide of the invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 49; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
| | | | | | | | | |
DB 1 RASQSVSSYLA 11

RESULT 15

ID ADW41605
AC ADW41605 standard; peptide; 11 AA.

XX ADW41605;

XX 03-JUN-2004 (first entry)

XX Interleukin-1 receptor type 1 antibody light chain variable region CDR1.

XX Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
KW anticonvulsant; dermatological; antigout; antiparkinsonian; antidiabetic;
KW cytostatic; complementarity determining region.

OS Homo sapiens.

XX WO2004022718-A2.

PN 18-MAR-2004.

XX 05-SEP-2003; 2003WO-US027978.

XX 06-SEP-2002; 2002US-0408719P.

XX (AMGE-) AMGEN INC.

XX

PI Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
PI Elliott G;

XX WPI; 2004-248462/23.

XX Isolated human antibody that specifically binds interleukin-1 receptor
PT type 1 (IL-1RI) useful for treating IL-1 mediated diseases such as
PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.

XX Claim 48; SEQ ID NO 70; 179pp; English.

XX The present sequence is that of complementarity determining region 1
CC (CDR1) of the human anti-interleukin-1 receptor type 1 (IL-1RI)
CC monoclonal antibody (MAb) 26F5 and 27F2 light chain variable region
CC ADW41547. Anti-IL-1RI antibodies of the invention may comprise this CDR.
CC These antibodies inhibit IL-1 signalling by competing with IL-1beta and
CC IL-1alpha binding to IL-1R. Monoclonal antibodies, as well as single
CC chain antibodies single chain Fv antibodies, Fab antibodies, Fab'
CC antibodies and (Fab')2 antibodies, are used in methods of treating IL-1
CC mediated diseases or for detecting the amount of IL-1RI in a sample. IL-1
CC mediated diseases include acute pancreatitis, anorexia, asthma,
CC scleroderma, Alzheimer's disease, cachexia, chronic fatigue syndrome,
CC atherosclerosis, autoimmune vasculitis, coronary conditions, cancer including
CC Clostridium associated illnesses, diabetes, endometriosis, fever,
CC leukaemia and tumour metastasis, graft versus host disease,
CC fibromyalgia, glomerulonephritis, inflammatory eye disease,
CC osteoarthritis, rheumatoid arthritis, inflammatory lung diseases,
CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,
CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,
CC septic shock, side effects of radiation therapy, temporal mandibular
CC joint disease, sleep disturbance, uveitis, or an inflammatory condition
CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic
CC surgery, infection or other disease processes.

XX Sequence 11 AA;

Query Match 100.0%; Score 49; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
| | | | | | | | | |
DB 1 RASQSVSSYLA 11

RESULT 16

ID ADS88073
AC ADS88073 standard; peptide; 11 AA.

XX ADS88073;

XX 18-NOV-2004 (first entry)

XX Human CD20 antibody-related CDR peptide SeqID22.

XX human monoclonal antibody; CD20;
KW human B-lymphocyte-restricted differentiation antigen; Bp35; cytostatic;
KW antipsoriatic; antiinflammatory; neuroprotective; ophthalmological;
KW nephrotropic; antiasthmatic; antiarthritic; arteriosclerotic; antianaemic;
KW antirheumatic; antidiabetic; antithyroid; anti-HIV; gene therapy;
KW cancer; psoriasis; inflammatory bowel disease; meningitis; uveitis;
KW glomerulonephritis; asthma; atherosclerosis; multiple sclerosis;
KW haemolytic anaemia; myasthenia gravis; rheumatoid arthritis;
KW Graves' disease; HIV; CDR; complementarity determining region; human.

OS Homo sapiens.

XX WO2004035607-A2.

XX 29-APR-2004.

XX 17-OCT-2003; 2003WO-US033057.

```

XX 17-OCT-2002; 2002US-0419163P.
PR 02-APR-2003; 2003US-0460028P.
XX (GENM-) GENMAB AS.
XX
XX Teeling J, Ruuls S, Glennie M, Van De Winkel JGJ, Parren P;
PI Petersen J, Baadsgaard OMS, Huang H;
XX WPI; 2004-348434/32.
XX
XX New human monoclonal antibodies against CD20, useful for diagnosing,
PT preventing or treating diseases involving cells expressing CD20, e.g.
PT cancer, psoriasis, HIV, glomerulonephritis, asthma, atherosclerosis or
PT anemia.
XX
XX Claim 34; SEQ ID NO 22; 201pp; English.
XX
XX This invention relates to a novel isolated human monoclonal antibody
CC which binds to human CD20 (human B-lymphocyte-restricted differentiation
CC antigen or Bp35). The invention may be useful for the production of
CC compositions with a cytostatic, antipsoriatic, antiinflammatory,
CC neuroprotective, ophthalmological, nephrotropic, antiasthmatic,
CC antiarteriosclerotic, antianaemic, antirheumatic, antiarthritic,
CC antithyroid or anti-HIV activity. In addition the invention may be useful
CC for gene therapy. The invention is useful for diagnosing, preventing or
CC treating diseases or disorders involving cells expressing CD20, such as
CC cancer, psoriasis, inflammatory bowel disease, meningitis, uveitis,
CC glomerulonephritis, asthma, atherosclerosis, multiple sclerosis,
CC haemolytic anaemia, myasthenia gravis, rheumatoid arthritis, Graves'
CC disease or HIV. The anti-idiotypic antibody is used for detecting the
CC level of human monoclonal antibody against CD20 in a sample. The present
CC sequence is that of a human complementarity determining peptide (CDR)
CC peptide which was used in the exemplification of the invention.
XX
XX SQ Sequence 11 AA;
XX
XX Query Match 100.0%; Score 49; DB 8; Length 11;
XX Best Local Similarity 100.0%; Pred. NO. 0.0046;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RASQSVSSYLA 11
XX |||||
XX Db 1 RASQSVSSYLA 11
XX
XX RESULT 17
XX ADS88067
XX ID ADS88067 standard; peptide; 11 AA.
XX
XX AC ADS88067;
XX
XX 18-NOV-2004 (first entry)
XX
XX DE Human CD20 antibody-related CDR peptide SeqID16.
XX
XX human monoclonal antibody; CD20;
XX human B-lymphocyte-restricted differentiation antigen; Bp35; cytostatic;
XX antipsoriatic; antiinflammatory; neuroprotective; ophthalmological;
XX nephrotropic; antiasthmatic; antiarteriosclerotic; antianaemic;
XX antirheumatic; antiarthritic; antithyroid; anti-HIV; gene therapy;
XX cancer; psoriasis; inflammatory bowel disease; meningitis; uveitis;
XX glomerulonephritis; asthma; atherosclerosis; multiple sclerosis;
XX haemolytic anaemia; myasthenia gravis; rheumatoid arthritis;
XX Graves' disease; HIV; CDR; complementarity determining region; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004035607-A2.
XX
XX PD 29-APR-2004.
XX
XX PF 17-OCT-2003; 2003WO-US033057.
XX
XX Query Match 100.0%; Score 49; DB 8; Length 11;
XX Best Local Similarity 100.0%; Pred. NO. 0.0046;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RASQSVSSYLA 11
XX |||||
XX Db 1 RASQSVSSYLA 11
XX
XX RESULT 18
XX ADS88079
XX ID ADS88079 standard; peptide; 11 AA.
XX
XX AC ADS88079;
XX
XX 18-NOV-2004 (first entry)
XX
XX DE Human CD20 antibody-related CDR peptide SeqID28.
XX
XX human monoclonal antibody; CD20;
XX human B-lymphocyte-restricted differentiation antigen; Bp35; cytostatic;
XX antipsoriatic; antiinflammatory; neuroprotective; ophthalmological;
XX nephrotropic; antiasthmatic; antiarteriosclerotic; antianaemic;
XX antirheumatic; antiarthritic; antithyroid; anti-HIV; gene therapy;
XX cancer; psoriasis; inflammatory bowel disease; meningitis; uveitis;
XX glomerulonephritis; asthma; atherosclerosis; multiple sclerosis;
XX haemolytic anaemia; myasthenia gravis; rheumatoid arthritis;
XX Graves' disease; HIV; CDR; complementarity determining region; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004035607-A2.
XX
XX PD 29-APR-2004.
XX
XX PF 17-OCT-2003; 2003WO-US033057.
XX

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XX 17-OCT-2002; 2002US-0419163P.
 PR 02-APR-2003; 2003US-0460028P.
 XX (GENM-) GENNAB AS.
 PA Teeling J, Ruuls S, Glennie M, Van De Winkel JGJ, Parren P;
 PI Petersen J, Baadsgaard OMS, Huang H;
 XX WPI; 2004-348434/32.
 DR New human monoclonal antibodies against CD20, useful for diagnosing,
 XX PT preventing or treating diseases involving cells expressing CD20, e.g.
 PT cancer, psoriasis, HIV, glomerulonephritis, asthma, atherosclerosis or
 PT anemia.
 XX Claim 37; SEQ ID NO 28; 201pp; English.
 PS This invention relates to a novel isolated human monoclonal antibody
 XX which binds to human CD20 (human B-lymphocyte-restricted differentiation
 CC antigen or Bp35). The invention may be useful for the production of
 CC compositions with a cytostatic, antiproliferative, antiinflammatory,
 CC neuroprotective, ophthalmological, antiproliferative, antiasthmatic,
 CC antiarthritic, antiangiogenic, antirheumatic, antiarthritic,
 CC antithyroid or anti-HIV activity. In addition the invention may be useful
 CC for gene therapy. The invention is useful for diagnosing, preventing or
 CC treating diseases or disorders involving cells expressing CD20, such as
 CC cancer, psoriasis, inflammatory bowel disease, meningitis, uveitis,
 CC glomerulonephritis, asthma, atherosclerosis, multiple sclerosis,
 CC haemolytic anaemia, myasthenia gravis, rheumatoid arthritis, Graves'
 CC disease or HIV. The anti-idiotypic antibody is used for detecting the
 CC level of human monoclonal antibody against CD20 in a sample. The present
 CC sequence is that of a human complementarity determining peptide (CDR)
 CC peptide which was used in the exemplification of the invention.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 49; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 11
 DB |||||
 1 RASQSVSSSYLA 11
 RESULT 19
 ADS19299
 XX ADS19299 standard; peptide; 11 AA.
 AC ADS19299;
 XX 18-NOV-2004 (first entry)
 DT Light chain CDR1 peptide of human mAb 3G6 antibody SeqID 10.
 XX human; antibody; mAb 3G6; lymphocyte migration;
 DE inflammatory bowel disease; Crohn's disease; gastroenteritis;
 XX pulmonary inflammatory disease; asthma; chronic bronchitis;
 KW graft rejection; psoriasis; eczema; urticaria; scleroderma;
 KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;
 KW antidiabetic; Behcet's syndrome; viral infection; cancer;
 KW immunosuppressive; antiproliferative; dermatological; neuroprotective;
 KW alphaE integrin; CD103; alphaE-beta7.
 XX Homo sapiens.
 OS US2003232387-A1.
 XX 18-DEC-2003.
 PD ,XX

PF 14-JUN-2002; 2002US-00173551.
 XX 14-JUN-2002; 2002US-00173551.
 PR (MILL-) MILLENNIUM PHARM INC.
 PA Lu C;
 PI WPI; 2004-178738/17.
 DR Novel antibody which binds activated alpha-E integrin, specifically to
 XX PT activation-induced epitope on integrin alpha-E chain (CD103), useful for
 PT treating inflammatory bowel diseases e.g., Crohn's disease,
 PT gastroenteritis.
 XX Claim 8; SEQ ID NO 10; 67pp; English.
 PS This invention relates to novel antibody and antigen-binding fragments of
 XX antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically,
 CC it refers to the binding of activation induced epitopes present on
 CC activated alphaE integrins, where these integrins are activated by
 CC exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable
 CC growth factors and/or mitogens. The present invention describes the
 CC alphaE-beta7 integrin as a homing receptor that mediates lymphocyte
 CC migration to mucosal epithelium. As such, compositions of this invention
 CC are useful for treating a subject having an inflammatory bowel disease
 CC such as Crohn's disease or gastroenteritis or pulmonary inflammatory
 CC diseases such as asthma and chronic bronchitis. Furthermore, such
 CC compositions can be used for inhibiting graft rejection, psoriasis,
 CC eczema, urticaria, scleroderma, autoimmune diseases such as multiple
 CC sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's
 CC syndrome, viral infections, cancer and/or neoplastic diseases such as
 CC leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory,
 CC antiasthmatic, immunosuppressive, antiproliferative, dermatological,
 CC neuroprotective, antidiabetic, nephrotropic, virucide, cytostatic and
 CC vasotropic activities. This peptide sequence is a human antibody heavy
 CC chain complementarity determining region (CDR) that binds the integrin
 CC alphaE chain of the invention.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 49; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RASQSVSSSYLA 11
 DB |||||
 1 RASQSVSSSYLA 11
 RESULT 20
 ADS64649
 ID ADS64649 standard; peptide; 11 AA.
 XX ADS64649;
 AC 16-DEC-2004 (first entry)
 XX Human anti-TNF antibody light chain CDR1 peptide #2.
 DE Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;
 XX obesity; immune related disease; rheumatoid arthritis;
 KW cardiovascular disease; stroke; malignant disease; leukaemia;
 KW neurological disease; multiple sclerosis; infection; hepatitis;
 KW anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;
 KW neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;
 KW anti-TNF antibody; CDR; complementarity determining region; human;
 KW light chain.
 XX Homo sapiens.
 OS US2004185047-A1.
 XX 18-DEC-2003.
 PD ,XX

PD 23-SEP-2004.
 XX
 PF 21-MAR-2003; 2003US-00394471.
 XX
 PR 21-MAR-2003; 2003US-00394471.
 XX
 PA (GILE/) GILES-KOMAR J.
 PA (SCAL/) SCALLON B J.
 PA (CART/) CARTON J M.
 XX
 PI Giles-Komar J, Scallion BJ, Carton JM;
 XX WPI; 2004-676151/66.
 DR
 XX Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody
 PT capable of inhibiting binding of TNF alpha to TNF receptor, useful for
 PT treating TNF-related diseases such as obesity or rheumatoid arthritis.
 XX
 PS Claim 2; SEQ ID NO 12; 45pp; English.
 XX
 CC The present invention relates to a mammalian anti-tumor necrosis factor
 CC (TNF) antibody capable of inhibiting binding of TNF alpha to TNF
 CC receptor. The invention is useful for diagnosing or treating an anti-TNF
 CC related condition in a cell, tissue, organ or animal and in
 CC immunotherapy. The invention is also useful for treating TNF related
 CC diseases chosen from obesity, immune related disease such as rheumatoid
 CC arthritis, cardiovascular disease such as stroke, malignant disease such
 CC as leukaemia, neurological disease such as multiple sclerosis and
 CC bacterial or viral infections such as hepatitis. The present sequence is
 CC the human anti-TNF antibody light chain complementarity determining
 CC region 1 (CDRL) peptide.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 49; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSYLA 11
 Db 1 RASQSVSSYLA 11
 RESULT 21
 ADS52384
 ID ADS52384 standard; peptide; 11 AA.
 AC
 XX ADS52384;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Fab targeting HLA-A2/Tax11-19, T3D3, light chain CDR 1.
 XX
 KW Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KW major histocompatibility complex; MHC class I; viral infection;
 KW human T lymphotropic virus-1 infection; viral oncoprotein;
 KW mycoplasma infection; bacterial infection; fungal infection;
 KW protozoal infection; phage display; light chain; CDR;
 KW complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 XX US2004191260-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 26-MAR-2003; 2003US-00396578.
 XX
 PR 26-MAR-2003; 2003US-00396578.
 XX
 PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 PI Reiter Y, Cohen C;
 XX WPI; 2004-735863/72.
 DR
 XX New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 XX
 PS Claim 5; SEQ ID NO 35; 68pp; English.
 XX
 CC The invention relates to a composition-of-matter comprising (a multimeric
 CC form of) an antibody or antibody fragment including an antigen-binding
 CC region capable of specifically binding an antigen-presenting portion of a
 CC complex composed of a human antigen-presenting molecule and an antigen
 CC derived from a pathogen. Also included are an isolated polynucleotide
 CC comprising a nucleic acid sequence encoding an antibody fragment (the
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule and an antigen derived from a
 CC pathogen), a nucleic acid construct comprising the isolated
 CC polynucleotide above (and a promoter sequence for directing transcription
 CC of the isolated polynucleotide in a host cell), a host cell comprising
 CC the nucleic acid construct above, a host virus comprising the nucleic
 CC acid construct above, a virus comprising a coat protein fused to the
 CC antibody fragment, detecting an antigen-presenting portion of a complex
 CC composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen, a method of diagnosing an infection by a pathogen in an
 CC individual, a method of killing or damaging a target cell
 CC expressing/displaying an antigen-presenting molecule and an antigen derived
 CC (composed of) a human antigen-presenting molecule, a method of detecting
 CC (from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polyhistidine tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC Pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
 CC The antigen derived from a pathogen is restricted by the antigen-
 CC presenting molecule and is a polypeptide selected from a segment of a
 CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
 CC composition comprising as an active ingredient the composition-of-matter
 CC is useful in a method for treating a disease associated with a pathogen
 CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
 CC protozoans. The composition-of-matter or the methods are useful for
 CC diagnosing an infection by a pathogen in an individual and for killing or
 CC damaging a target cell expressing or displaying an antigen-presenting
 CC portion of a complex composed of a human antigen-presenting molecule and
 CC an antigen derived from a pathogen. A phage displayed library of human
 CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC sequences compared. The present sequence is a CDR from the light chain of
 CC an isolated Fab clone.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 49; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RASQSVSSYLA 11
 Db 1 RASQSVSSYLA 11
 RESULT 22

ADSS2432
ID ADSS2432 standard; peptide; 11 AA.
AC ADSS2432;
XX
DT 16-DEC-2004 (first entry)
DE Fab targeting HLA-A2/Tax11-19, T4B7, light chain CDR 1.
XX
XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
KW major histocompatibility complex; MHC class I; viral infection;
KW human T lymphotropic virus-1 infection; viral oncoprotein;
KW mycoplasma infection; bacterial infection; fungal infection;
KW protozoal infection; phage display; light chain; CDR;
KW Complementarity determining region.
XX
OS Homo sapiens.
XX
PN US2004191260-A1.
PN
PD 30-SEP-2004.
PD
XX
PF 26-MAR-2003; 2003US-00396578.
PF
PR 26-MAR-2003; 2003US-00396578.
PR
XX (TECR) TECHNION RES & DEV FOUND LTD.
PA
XX Reiter Y, Cohen C;
PI
XX WPI; 2004-735863/72.
DR
XX
XX New composition comprising a multimeric form of an antibody or fragment
PT which specifically binds an antigen-presenting portion of a complex,
PT useful for treating pathogen-associated diseases e.g., HIV.
XX
XX Claim 5; SEQ ID NO 83; 68pp; English.
PS
CC The invention relates to a composition-of-matter comprising (a multimeric
CC form of) an antibody or antibody fragment including an antigen-binding
CC region capable of specifically binding an antigen-presenting portion of a
CC complex composed of a human antigen-presenting molecule and an antigen
CC derived from a pathogen. Also included are an isolated polynucleotide
CC comprising a nucleic acid sequence encoding an antibody fragment (the
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule and an antigen derived from a
CC pathogen), a nucleic acid construct comprising the isolated
CC polynucleotide above (and a promoter sequence for directing transcription
CC of the isolated polynucleotide in a host cell), a host cell comprising
CC the nucleic acid construct above, a host virus comprising the nucleic
CC acid construct above, a virus comprising a coat protein fused to the
CC antibody fragment, detecting an antigen-presenting portion of a complex
CC composed of a human antigen-presenting molecule and an antigen derived
CC from a pathogen, a method of diagnosing an infection by a pathogen in an
CC individual, a method of killing or damaging a target cell
CC expressing/displaying an antigen-presenting portion of a complex
CC (composed of a human antigen-presenting molecule and an antigen derived
CC from a pathogen) and a method of detecting in a biological sample an
CC antigen-presenting portion of a complex as described above. The target
CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
CC or a dendritic cell. The composition-of-matter further comprises a
CC detectable moiety attached to the antibody or antibody fragment. The
CC detectable moiety is a recognition sequence of a biotin protein ligase, a
CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
CC polyhistidine tag. The biotin protein ligase is BirA, the fluorophore is
CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
CC pseudomonas exotoxin A or its portion, which is a translocation domain
CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
CC is a major histocompatibility complex (MHC), preferably MHC class I
CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
CC preferably a retrovirus, more preferably human T lymphotropic virus-1.

CC The antigen derived from a pathogen is restricted by the antigen-
CC presenting molecule and is a polypeptide selected from a segment of a
CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
CC composition comprising as an active ingredient the composition-of-matter
CC is useful in a method for treating a disease associated with a pathogen
CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
CC protozoans. The composition-of-matter or the methods are useful for
CC diagnosing an infection by a pathogen in an individual and for killing or
CC damaging a target cell expressing or displaying an antigen-presenting
CC portion of a complex composed of a human antigen-presenting molecule and
CC an antigen derived from a pathogen. A phage displayed library of human
CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
CC were then sequenced and their CDR (complementarity determining region)
CC sequences compared. The present sequence is a CDR from the light chain of
CC an isolated Fab clone.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSYLA 11
Db |||||
1 RASQSVSSYLA 11
RESULT 23
ADW07069
ID ADW07069 standard; peptide; 11 AA.
XX
AC ADW07069;
XX
DT 07-APR-2005 (first entry)
XX
DE Anti-PsAA-antibody 1-1585 VK CDR1.
KW antibacterial; antiinflammatory; immunosuppressive; antibody engineering;
KW pharmaceutical; infection; pneumonia; meningitis; sepsis;
KW pneumococcal surface adhesin A; PsAA; light chain variable region;
KW complementarity determining region 1; CDR1; ds.
OS Homo sapiens.
XX
PN WO2005003174-A1.
XX
PD 13-JAN-2005.
XX
PF 08-JUL-2004; 2004WO-DK000492.
PF
PR 08-JUL-2003; 2003DK-00001044.
PR
XX 11-JUL-2003; 2003US-0486647P.
XX
PA (GENE-) GENESTO AS.
XX
PI Sorensen AP, Benfield TL, Lundgren JD, Kempe TD;
XX
DR WPI; 2005-101476/11.
DR
XX N-PSDB; ADW07068.
XX
PT New binding member towards Streptococcus pneumoniae surface adhesin A
PT protein, useful for treating or preventing pneumonia, meningitis and/or
PT sepsis.
XX
XX Disclosure; SEQ ID NO 18; 137pp; English.
XX
XX The invention describes an isolated binding member comprising at least
XX one binding domain capable of specifically binding Streptococcus
CC pneumoniae surface adhesin A (Psaa) protein, the binding domain having a
CC dissociation constant Kd for Psaa which is less than 1 x10 -6 M. Also
CC described are: an isolated nucleic acid molecule encoding at least a part
CC of the binding member described above; a vector comprising the nucleic

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
|||||

Db 1 RASQSVSSYLA 11
|||||

RESULT 26
ADY26813
ID ADY26813 standard; protein; 11 AA.
XX
AC ADY26813;
XX
DT 19-MAY-2005 (first entry)
XX
DE Human anti-NGF-antibody light chain CDR1 SEQ ID NO 128.
XX
KW analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
KW neurological disease; NGF; nerve growth factor; heavy chain; CDR1.
XX
OS Homo sapiens.
XX
FN WO2005019266-A2.
XX
PD 03-MAR-2005.
XX
PF 15-JUL-2004; 2004WO-US022876.
XX
PR 15-JUL-2003; 2003US-0487431P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
XX
DR WPI; 2005-202606/21.
XX
XX New human anti-nerve growth factor (NGF) neutralizing antibodies useful
PT for manufacturing a medicament for treating painful disorders (e.g. acute
PT pain) or conditions associated with increased expression or sensitivity
PT to NGF.
XX
PS Claim 38; SEQ ID NO 128; 190pp; English.
XX
XX The invention describes an isolated human antibody that interacts with or
CC binds specifically to human nerve growth factor (NGF) and neutralize the
CC function of NGF. Also described are: methods of treating a condition
CC caused by increased expression of NGF or increased sensitivity to NGF in
CC a patient; methods for detecting NGF in a biological sample; an NGF
CC specific binding agent comprising any of the 59 amino acid sequences
CC comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
CC specification, and where the binding agent can bind to NGF; a
CC pharmaceutical composition comprising a pharmaceutical carrier and a
CC therapeutic amount of the antibody or binding agent cited above; or a
CC medicament for treating a painful disorder or condition associated with
CC increased expression of NGF or increased sensitivity to NGF, the
CC medicament comprising a pharmaceutical amount of a monoclonal antibody or
CC its immunologically functional immunoglobulin fragment, or pharmaceutical
CC salts of the monoclonal antibody or the fragment, where the monoclonal
CC antibody is at least one of the monoclonal antibody cited above, and a
CC pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
CC polynucleotide that encodes the above antibody or binding agent; an
CC isolated cell line that produces the above antibody or binding agent; an
CC expression vector comprising the above polynucleotide; and a host cell
CC comprising the nucleic acid or expression vector. The composition
CC (including the antibody) and methods are useful for manufacturing a
CC medicament for treating a painful disorder (e.g. acute pain, dental pain,
CC or pain from trauma or cancer), or a condition associated with increased
CC expression of NGF or increased sensitivity to NGF. This is the amino acid
CC sequence of a human NGF antibody heavy chain complementarity determining
CC region 1 (CDR1).
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
|||||

Db 1 RASQSVSSYLA 11
|||||

RESULT 27
ADY93860
ID ADY93860 standard; peptide; 11 AA.
XX
AC ADY93860;
XX
DT 16-JUN-2005 (first entry)
XX
DE Anti-SARS 201.2 antibody VK CDR1 SEQ ID NO:10.
XX
KW glycoprotein; respiratory-gen.; virucide; sars coronavirus infection;
KW antibody; light chain variable region.
XX
OS SARS coronavirus.
XX
FN US2005069869-A1.
XX
PD 31-MAR-2005.
XX
PF 04-AUG-2004; 2004US-00911838.
XX
PR 04-AUG-2003; 2003US-0492529P.
PR 09-OCT-2003; 2003US-0510251P.
PR 18-FEB-2004; 2004US-0545670P.
PR 26-APR-2004; 2004US-0565595P.
XX
XX (AMBR/) AMBROSINO D.
PA (HERN/) HERNANDEZ H.
PA (GREE/) GREENOUGH T.
PA (LUZU/) LUZURIAGA K.
PA (SOMA/) SOMASUNDARAN M.
PA (BABC/) BABCOCK G J.
PA (THOM/) THOMAS W D.
PA (SULL/) SULLIVAN J.
XX
XX Ambrosino D, Hernandez H, Greenough T, Luzuriaga K;
PI Somasundaran M, Babcock GJ, Thomas WD, Sullivan J;
XX
XX WPI; 2005-252952/26.
XX
XX New isolated nucleic acid encoding a SARS-Cov spike glycoprotein
PT polypeptide, and optimized for expression in a human host, useful for
PT diagnosing, preventing and/or treating SARS-Cov infection.
XX
PS Claim 49; SEQ ID NO 10; 138pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising a sequence
CC encoding a SARS coronavirus (SARS-Cov) spike glycoprotein (S protein), or
CC its fragment, where the sequence has been optimized for expression in a
CC human host. Also described: (1) a nucleic acid expression vector
CC comprising the above nucleic acid; (2) an isolated cell comprising the
CC expression vector of (1); (3) a polypeptide encoded by the above nucleic
CC acid; (4) an isolated polypeptide comprising an extracellular portion of
CC the SARS-Cov S polypeptide located between amino acids 15-1190 of
CC ADY9385, or its fragment; (5) an isolated antibody, or its antigen
CC binding fragment, that specifically binds to the polypeptide of (3); (6)
CC an isolated antibody, or its antigen binding fragment, that specifically
CC binds to an antigen binding fragment of an anti-S protein antibody; (7) a
CC composition comprising a polypeptide of (4) or an antibody, or its
CC antigen binding fragment, and a pharmaceutical carrier; (8) making an S
CC protein, or its fragment, of SARS-Cov; (9) making an antibody, or its
CC antigen binding fragment, that specifically binds to an S protein of SARS
CC -Cov; (10) evaluating a biological sample for the presence of SARS-Cov;
CC (11) evaluating an antibody, or its antigen binding fragment, for

CC inhibition of infection by SARS-Cov; (12) treating a subject at risk for,
 CC or exposed to SARS-Cov; (13) an immunoconjugate comprising the antibody
 CC of (5) linked to a therapeutic agent; (14) an isolated nucleic acid
 CC molecule encoding the antibody, its antigen-binding portion, variable
 CC heavy chain or variable light chain of (5); (15) an expression vector
 CC comprising the nucleic acid molecule of (14); (16) a host cell comprising
 CC the expression vector of (15); (17) a transgenic mammal comprising human
 CC immunoglobulin heavy and light chain transgenes, where the mouse
 CC expresses the antibody of (5); (18) a hybridoma prepared from the mammal
 CC of (17), where the hybridoma produces the antibody; and (19) preparing an
 CC anti-S protein antibody. The methods and compositions of the present
 CC invention are useful for the diagnosis, prevention and/or treatment of
 CC SARS-Cov infection. The present sequence represents the CDR1 amino acid
 CC sequence from the anti-SARS 201.2 antibody light chain variable region
 CC from the present invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RASQSVSSYLA 11
 |||||
 Db 1 RASQSVSSYLA 11

RESULT 28

AEA53685
 ID AEA53685 standard; peptide; 11 AA.

XX AC AEA53685;

XX DT 11-AUG-2005 (first entry)

XX DE Novel human MMP26-binding antibody-related CDR1 peptide #482.

XX antibody engineering; cytostatic; antiinflammatory; osteopathic;
 KW antiarthritic; gene therapy; cancer; breast tumor; prostate tumor;
 KW lung tumor; inflammation; rheumatoid arthritis; restenosis;
 KW graft versus host disease; multiple sclerosis; gingivitis;
 KW osteoarthritis.

XX OS Unidentified.

XX PN WO2005051299-A2.

XX PD 09-JUN-2005.

XX PF 19-NOV-2004; 2004WO-US039052.

XX PR 19-NOV-2003; 2003US-0523745P.

XX PA (DYAX-) DYAX CORP.

XX PI Dransfield DT, Rookey K, Ladner RC;

XX DR WPI; 2005-417817/42.

XX New protein comprising heavy and light chain immunoglobulin variable
 PT domain sequences, useful in preparing a composition for treating or
 PT preventing neoplastic or inflammatory disorders.

XX Example; Page 129; 192pp; English.

XX This invention relates to novel proteins, comprising a heavy chain
 CC immunoglobulin variable domain sequence and a light chain immunoglobulin
 CC variable domain sequence, which bind to matrix metalloproteinase (MMP)-26
 CC and comprise at least one human complementarity determining region or
 CC framework region. The invention may be useful for the development of
 CC compounds with a cytostatic, antiinflammatory, osteopathic or
 CC antiarthritic activity whilst the disclosed sequences may prove useful
 CC for gene therapy. The protein is useful in preparing a composition for

CC treating or preventing neoplastic disorders, for example breast,
 CC prostate, or lung cancer or inflammatory disorders, for example
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
 CC multiple sclerosis or a disorder characterized by excessive or undesired
 CC MMP-26 activity, for example periodontitis, rheumatoid arthritis or
 CC osteoarthritis. The present sequence is that of a CDR peptide which was
 CC used during the development of the novel MMP26-binding antibodies of the
 CC invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 49; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0046;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RASQSVSSYLA 11
 |||||
 Db 1 RASQSVSSYLA 11

RESULT 29

AEA53692
 ID AEA53692 standard; peptide; 11 AA.

XX AC AEA53692;

XX DT 11-AUG-2005 (first entry)

XX DE Novel human MMP26-binding antibody-related CDR1 peptide #489.

XX antibody engineering; cytostatic; antiinflammatory; osteopathic;
 KW antiarthritic; gene therapy; cancer; breast tumor; prostate tumor;
 KW lung tumor; inflammation; rheumatoid arthritis; restenosis;
 KW graft versus host disease; multiple sclerosis; gingivitis;
 KW osteoarthritis.

XX OS Unidentified.

XX PN WO2005051299-A2.

XX PD 09-JUN-2005.

XX PF 19-NOV-2004; 2004WO-US039052.

XX PR 19-NOV-2003; 2003US-0523745P.

XX PA (DYAX-) DYAX CORP.

XX PI Dransfield DT, Rookey K, Ladner RC;

XX DR WPI; 2005-417817/42.

XX New protein comprising heavy and light chain immunoglobulin variable
 PT domain sequences, useful in preparing a composition for treating or
 PT preventing neoplastic or inflammatory disorders.

XX Example; Page 129; 192pp; English.

XX This invention relates to novel proteins, comprising a heavy chain
 CC immunoglobulin variable domain sequence and a light chain immunoglobulin
 CC variable domain sequence, which bind to matrix metalloproteinase (MMP)-26
 CC and comprise at least one human complementarity determining region or
 CC framework region. The invention may be useful for the development of
 CC compounds with a cytostatic, antiinflammatory, osteopathic or
 CC antiarthritic activity whilst the disclosed sequences may prove useful
 CC for gene therapy. The protein is useful in preparing a composition for
 CC treating or preventing neoplastic disorders, for example breast,
 CC prostate, or lung cancer or inflammatory disorders, for example
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
 CC multiple sclerosis or a disorder characterized by excessive or undesired
 CC MMP-26 activity, for example periodontitis, rheumatoid arthritis or
 CC osteoarthritis. The present sequence is that of a CDR peptide which was
 CC used during the development of the novel MMP26-binding antibodies of the

```
CC invention.
XX
SQ Sequence 11 AA;
    Query Match      100.0%; Score 49; DB 9; Length 11;
    Best Local Similarity 100.0%; Pred. No. 0.0046;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSYLA 11
   |||||
Db 1 RASQSVSSSYLA 11
   |||||

RESULT 31
AEA45811
ID AEA45811 standard; peptide; 11 AA.
XX
AC AEA45811;
XX
DT 11-AUG-2005 (first entry)
DE Apolipoprotein E C-terminal domain antibody VL-CDR1 peptide #64.
XX
KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen.; Apolipoprotein E;
KW Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
KW motor neurone disease; chronic obstructive pulmonary disease.
XX
OS Homo sapiens.
XX
PN GB2408508-A.
XX
PD 01-JUN-2005.
XX
PF 26-NOV-2004; 2004GB-00026043.
XX
PR 28-NOV-2003; 2003US-0525174P.
XX
PA (ASTR ) ASTRAZENECA AB.
PA (DYAX-) DYAX CORP.
XX
PI Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
PI Hufton S, Anderseon CV, Lindquist J, Sunnemark D, Leonov S;
XX
DR WPI; 2005-408785/42.
XX
PT New human antibody or antibody fragment which binds to a sequence of the
PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
PT manufacturing a medicament for treating or preventing an amyloid disorder
PT e.g. Alzheimers disease.
XX
PS Example 21; Page 103; 392pp; English.
XX
CC The present invention relates to a human antibody or antibody fragment,
CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD;
CC AEA44803) and also to human plaques. The antibody or its fragment is
CC useful for manufacturing a medicament for treating or preventing an
CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.
```

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XX
SQ Sequence 11 AA;
    Query Match      100.0%; Score 49; DB 9; Length 11;
    Best Local Similarity 100.0%; Pred. No. 0.0046;
    Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RASQSVSSSYLA 11
   |||||
Db 1 RASQSVSSSYLA 11
   |||||

RESULT 31
AEB01024
ID AEB01024 standard; peptide; 11 AA.
XX
AC AEB01024;
XX
DT 08-SEP-2005 (first entry)
DE Human IP10 antibody light chain variable region, CDR1, SEQ ID NO 52.
XX
KW antibody; IP-10; inflammation; immune disorder; dermatological disease;
KW respiratory disease; neurological disease; degeneration; infection;
KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;
KW Gastrointestinal-Gen.; Antiulcer; Dermatological; Immunosuppressive;
KW Antidiabetic; Antipsoriatic; Antichyroid; Antiasthmatic;
KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Virucide;
KW Antibacterial.
XX
OS Homo sapiens.
XX
PN WO2005058815-A2.
XX
PD 30-JUN-2005.
XX
PF 10-DEC-2004; 2004WO-US041506.
XX
PR 10-DEC-2003; 2003US-0529180P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
PI Pasemore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
XX
DR WPI; 2005-467095/47.
XX
PT Isolated human monoclonal antibody or an antigen-binding portion, which
PT specifically binds to human interferon gamma inducible protein 10 (IP-
PT 10), useful for treating viral or bacterial infection, or inflammatory or
PT autoimmune diseases.
XX
PS Claim 17; SEQ ID NO 52; 179pp; English.
XX
CC The invention relates to an isolated human monoclonal antibody or an
CC antigen-binding portion, which specifically binds to human IP-10 and
CC exhibits at least one property selected from: inhibits binding of IP-10
CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
CC react with mouse IP-10; does not cross-react with human MIG; or does not
CC cross-react with human IPAC. The isolated human monoclonal antibody is
CC useful for treating an inflammatory or autoimmune disease including
CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,
CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
```



```
XX SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
   |||||
Db 1 RASQSVSSSYLA 11

RESULT 34
AEB28709
ID AEB28709 standard; peptide; 11 AA.
XX
AC AEB28709;
XX
DT 22-SEP-2005 (first entry)
XX
DE Human CDR1 of T3D3 Fab specifically binding HLA-A2/Tax11-19, SEQ: 35.
XX
KW Diagnosis; therapeutic; infection; antimicrobial; light chain; T3D3.
XX
OS Homo sapiens.
XX
PN US2005152912-A1.
XX
PD 14-JUL-2005.
XX
PF 09-MAR-2005; 2005US-00074803.
XX
PR 26-MAR-2003; 2003US-00396578.
XX
PA (TECR ) TECHNION RES & DEV FOUND LTD.
XX
PI Reiter Y, Cohen C;
XX
DR WPI; 2005-496781/50.
XX
PT New composition-of-matter capable of specifically binding an antigen-
PT presenting molecule and a pathogen-derived antigen complexes, useful for
PT treating diseases associated with a pathogen.
XX
PS Claim 5; SEQ ID NO 35; 65pp; English.
XX
CC The present invention relates to a composition-of-matter which comprises
CC an antibody or antibody fragment or a multimeric form of an antibody or
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule (APM) and an antigen derived from
CC a pathogen. The invention is useful for the specific detection of the
CC antigen-presenting portion of the complex and for diagnosing/creating
CC various types of diseases associated with a pathogen infection by
CC killing/damaging pathogen infected cells. The present sequence is a
CC complementarity determining regions (CDR) of Fab light chain antibody
CC specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex.
CC Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-
CC 1).
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 49; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
   |||||
Db 1 RASQSVSSSYLA 11

RESULT 35
,ADD69248
```

```
ID ADD69248 standard; protein; 94 AA.
XX
AC ADD69248;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human light chain L6 protein.
XX
KW monoclonal antibody; heavy chain variable region; light; framework;
KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
KW colon cancer; renal carcinoma; gene therapy; human; L6.
XX
OS Homo sapiens.
XX
PN WO2003064606-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002448.
XX
PR 28-JAN-2002; 2002US-00059989.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;
XX
DR WPI; 2003-618360/58.
XX
DR N-PSDB; ADD69251.
XX
PT New isolated human monoclonal antibody comprising a human heavy chain and
PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
PT cancer.
XX
PS Disclosure; SEQ ID NO 52; 136pp; English.
XX
CC The invention relates to a novel isolated human monoclonal antibody
CC comprising a human heavy chain variable region and a human light chain
CC variable region both comprising FR (framework region)-1, CDR
CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
CC sequences. The antibody is directed against the human prostate specific
CC membrane antigen (PSMA). The monoclonal antibody of the invention
CC demonstrates cytostatic activity and may be useful for treating or
CC preventing a disease characterised by the growth of tumour cells such as
CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
CC well as during gene therapy procedures. The current sequence is that of
CC the human light chain L6 protein of the invention.
XX
SQ Sequence 94 AA;
Query Match 100.0%; Score 49; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
   |||||
Db 24 RASQSVSSSYLA 34

RESULT 36
ABO27153
ID ABO27153 standard; protein; 95 AA.
XX
AC ABO27153;
XX
DT 10-SEP-2003 (first entry)
XX
DE Human germline light chain variable region gene segment #33.
XX
KW Human; light chain variable region; VK; humanised antibody;
KW chimeric antibody; complementarity determining region; CDR;
KW canonical CDR structure type.
```


CC antibody than the selected antibody; and (ix) operatively linking the
 CC selected framework sequences to one or more complementarity determining
 CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
 CC hybrid antibody fragment. The method is useful for producing a hybrid
 CC antibody or hybrid antibody fragment (claimed). The antibody and
 CC fragments are useful for therapeutic and diagnostic purposes. The method
 CC uses entire framework regions from a single antibody variable heavy or
 CC variable light chain to receive the CDRs. This produces antibodies that
 CC are highly homologous and exhibit reduced immunogenicity while
 CC maintaining an optimum binding profile. This sequence represents the
 CC amino acid sequence of an antibody from the V kappa gene locus.

xx

SQ Sequence 95 AA;

Query Match 100.0%; Score 49; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11

|||||||

Db 24 RASQSVSSYLA 34

Search completed: December 14, 2005, 07:25:28
 Job time : 65.5862 secs

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:38 ; Search time 16.1207 Seconds
(without alignments)
56.414 Million cell updates/sec

Title: US-10-720-323-4

Perfect score: 49

Sequence: 1 RASQSVSYLA 11

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	49	100.0	100	2	US-09-899-896-4
3	49	100.0	107	1	US-08-107-669D-14
4	49	100.0	107	1	US-08-472-788A-14
5	49	100.0	107	1	US-08-477-531B-14
6	49	100.0	107	1	US-08-082-842A-14
7	49	100.0	107	2	US-09-438-954-40
8	49	100.0	107	2	US-08-434-870-2
9	49	100.0	115	1	US-08-053-131-179
10	49	100.0	115	1	US-08-096-762-179
11	49	100.0	115	2	US-09-042-353-42
12	49	100.0	115	2	US-08-758-417A-307
13	49	100.0	139	2	US-09-472-087-16
14	49	100.0	139	2	US-09-472-087-90
15	49	100.0	142	2	US-08-472-087-91
16	49	100.0	146	2	US-09-472-087-21
17	49	100.0	146	2	US-09-472-087-93
18	49	100.0	224	2	US-09-456-090A-46
19	49	100.0	224	2	US-09-456-090A-82
20	49	100.0	224	2	US-09-456-090A-84
21	49	100.0	224	2	US-09-456-090A-88
22	49	100.0	224	2	US-09-456-090A-90
23	49	100.0	224	2	US-09-453-234-46
24	49	100.0	224	2	US-09-453-234-82
25	49	100.0	224	2	US-09-453-234-84
26	49	100.0	224	2	US-09-453-234-88
27	49	100.0	224	2	US-09-453-234-90
28	49	100.0	234	2	US-09-472-087-17
29	49	100.0	234	2	US-09-472-087-69
30	48	98.0	109	2	US-09-157-370-3
31	45	91.8	95	2	US-10-194-975-87
32	45	91.8	107	1	US-07-934-373C-18
33	45	91.8	107	2	US-08-437-642B-18
34	45	91.8	107	2	US-08-146-206C-18
35	45	91.8	107	2	US-09-648-067A-14
36	45	91.8	107	2	US-09-705-686-18
37	45	91.8	107	2	US-09-705-392A-18
38	45	91.8	107	2	US-09-705-398-18
39	45	91.8	107	2	US-09-602-812A-5
40	45	91.8	107	4	PCT-US93-07832-18
41	45	91.8	108	2	US-08-974-899-3
42	45	91.8	108	2	US-09-157-370-4
43	45	91.8	108	2	US-09-795-798-3
44	45	91.8	108	2	US-08-908-469-12
45	45	91.8	109	1	US-07-934-373C-3
46	45	91.8	109	2	US-08-437-642B-3
47	45	91.8	109	2	US-08-146-206C-3
48	45	91.8	109	2	US-09-705-686-3
49	45	91.8	109	2	US-09-705-392A-3
50	45	91.8	109	2	US-09-705-398-3
51	45	91.8	109	4	PCT-US93-07832-3
52	45	91.8	115	1	US-08-053-131-181
53	45	91.8	115	1	US-08-096-762-181
54	45	91.8	115	2	US-09-042-353-44
55	45	91.8	115	2	US-08-758-417A-309
56	45	91.8	224	2	US-09-456-090A-36
57	45	91.8	224	2	US-09-453-234-36
58	44	89.8	11	2	US-09-192-854-6
59	44	89.8	11	2	US-09-511-939-10
60	44	89.8	11	2	US-09-511-939-16
61	44	89.8	11	2	US-09-511-939-22
62	44	89.8	11	2	US-09-511-939-28
63	44	89.8	11	2	US-09-511-939-34
64	44	89.8	11	2	US-09-511-939-40
65	44	89.8	11	2	US-09-511-939-46
66	44	89.8	11	2	US-09-511-939-52
67	44	89.8	11	2	US-09-511-939-64
68	44	89.8	11	2	US-09-511-939-100
69	44	89.8	11	2	US-09-511-939-106
70	44	89.8	11	2	US-09-511-939-112
71	44	89.8	11	2	US-09-511-939-118
72	44	89.8	11	2	US-09-511-939-124
73	44	89.8	11	2	US-09-511-939-136
74	44	89.8	11	2	US-09-511-939-154
75	44	89.8	11	2	US-09-511-939-160
76	44	89.8	11	2	US-09-511-939-166
77	44	89.8	11	2	US-09-511-939-172
78	44	89.8	11	2	US-09-511-939-178
79	44	89.8	11	2	US-09-511-939-202
80	44	89.8	11	2	US-09-511-939-208
81	44	89.8	11	2	US-09-511-939-226
82	44	89.8	11	2	US-09-511-939-232
83	44	89.8	11	2	US-09-511-939-244
84	44	89.8	11	2	US-09-511-939-250
85	44	89.8	11	2	US-09-511-939-256
86	44	89.8	11	2	US-09-511-939-280
87	44	89.8	11	2	US-09-511-939-292
88	44	89.8	11	2	US-09-511-939-304
89	44	89.8	76	2	US-08-851-362B-21
90	44	89.8	88	2	US-09-905-243-32
91	44	89.8	95	2	US-09-472-087-94
92	44	89.8	95	2	US-10-194-975-54
93	44	89.8	95	2	US-10-194-975-55
94	44	89.8	95	2	US-10-194-975-67
95	44	89.8	95	2	US-10-194-975-69
96	44	89.8	95	2	US-10-330-613A-43
97	44	89.8	99	2	US-09-899-896-6
98	44	89.8	99	2	US-09-899-896-10
99	44	89.8	103	2	US-09-240-274-42
100	44	89.8	103	2	US-09-848-798-42

Sequence 17, Appl
Sequence 69, Appl
Sequence 3, Appl
Sequence 87, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 14, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 5, Appl
Sequence 18, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 12, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 44, Appl
Sequence 12, Appl
Sequence 94, Appl
Sequence 54, Appl
Sequence 55, Appl
Sequence 69, Appl
Sequence 43, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 42, Appl

ALIGNMENTS

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RESULT 1
US-10-194-975-86
; Sequence 86, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-86

Query Match      100.0%; Score 49; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
      |||||
Db      24 RASQSVSSYLA 34

RESULT 2
US-09-899-896-4
; Sequence 4, Application US/09899896
; Patent No. 6569431
; GENERAL INFORMATION:
; APPLICANT: von Bdingen, Hans-Christian
; APPLICANT: Hauser, Stephen L.
; TITLE OF INVENTION: Recombinant Antibody Fragments as Autoantibody
; FILE REFERENCE: SF01-025-2
; CURRENT APPLICATION NUMBER: US/09/899,896
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 09/691,654
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 100
; TYPE: PRT
; ORGANISM: human
US-09-899-896-4

Query Match      100.0%; Score 49; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
      |||||
Db      24 RASQSVSSYLA 34

RESULT 3
US-08-107-669D-14
; Sequence 14, Application US/08107669D
; Patent No. 5766886
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
```

```
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,669D
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-107-669D-14

Query Match      100.0%; Score 49; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
      |||||
Db      24 RASQSVSSYLA 34

RESULT 4
US-08-472-788A-14
; Sequence 14, Application US/08472788A
; Patent No. 5770196
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,788A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/082,842
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; FILING DATE: 23-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-788A-14

Query Match 100.0%; Score 49; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | |
Db 24 RASQSVSSYLA 34

RESULT 5
US-08-477-531B-14
; Sequence 14, Application US/08477531B
; Patent No. 5821123
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,531B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Michele A. Cimbala
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; INFORMATION FOR SEQ ID NO: 14:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-531B-14

Query Match 100.0%; Score 49; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | |
Db 24 RASQSVSSYLA 34

RESULT 6
US-08-082-842A-14
; Sequence 14, Application US/08082842A
; Patent No. 5869619
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,842A
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0610.1000002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/371-2600
; TELEFAX: 202/371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-082-842A-14

Query Match 100.0%; Score 49; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | |
Db 24 RASQSVSSYLA 34

RESULT 7
US-09-438-954-40

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; Sequence 40, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of human antibody (X82934)
US-09-438-954-40

Query Match      100.0%; Score 49; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
Db      24 RASQSVSSSYLA 34

RESULT 8
US-09-434-870-2
; Sequence 2, Application US/09434870
; Patent No. 6849425
; GENERAL INFORMATION:
; APPLICANT: Huse, William
; APPLICANT: Watkins, Jeffrey
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-06352
; CURRENT APPLICATION NUMBER: US/09/434,870
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/159,689
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-434-870-2

Query Match      100.0%; Score 49; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
Db      24 RASQSVSSSYLA 34

RESULT 9
US-08-053-131-179
; Sequence 179, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
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; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-131-179

Query Match      100.0%; Score 49; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
Db      44 RASQSVSSSYLA 54

RESULT 10
US-08-096-762-179
; Sequence 179, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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, APPLICATION NUMBER: US/08/096,762
, FILING DATE: 22-JUL-1993
, CLASSIFICATION: 800
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/053,131
, FILING DATE: 26-APR-1993
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/990,860
, FILING DATE: 16-DEC-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/904,068
, FILING DATE: 23-JUN-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/853,408
, FILING DATE: 18-MAR-1992
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/810,279
, FILING DATE: 17-DEC-1991
, ATTORNEY/AGENT INFORMATION:
, NAME: Smith, William M.
, REGISTRATION NUMBER: 30,223
, REFERENCE/DOCKET NUMBER: 14643-9-4
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 415-326-2400
, TELEFAX: 415-326-2422
, INFORMATION FOR SEQ ID NO: 179:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 115 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-096-762-179

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Query Match 100.0%; Score 49; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels

Qy 1 RASQSVSSYLA 11
|||
Db 44 RASQSVSSYLA 54

RESULT 11
US-09-042-353-42
; Sequence 42, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408

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? FILING DATE: 18-MAR-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/904,068
? FILING DATE: 23-JUN-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/990,860
? FILING DATE: 16-DEC-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/053,131
? FILING DATE: 26-APR-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/096,762
? FILING DATE: 22-JUL-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/155,301
? FILING DATE: 18-NOV-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/161,739
? FILING DATE: 03-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/165,699
? FILING DATE: 10-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/209,741
? FILING DATE: 09-MAR-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/352,322
? FILING DATE: 07-DEC-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/544,404
? FILING DATE: 10-OCT-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/728,463
? FILING DATE: 10-OCT-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/US96/16433
? FILING DATE: 10-OCT-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/758,417
? FILING DATE: 02-DEC-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/US97/21803
? FILING DATE: 01-DEC-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Apple, Randolph T.
? REGISTRATION NUMBER: 36,429
? REFERENCE/DOCKET NUMBER: 014643-009040US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 42:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 115 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-09-042-353-42

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Query Match      100.0%; Score 49; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels
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Qy 1 RASQSVSSYLA 11
Db 44 RASQSVSSYLA 54

RESULT 12
US-08-758-417A-307
; Sequence 307, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lomberg, Nils

;/ Kay, Robert M.
;/ TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;/ Producing Heterologous Antibodies
;/ NUMBER OF SEQUENCES: 417
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew LLP
;/ STREET: Two Embarcadero Center, Eighth Floor
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94111-3834
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/758,417A
;/ FILING DATE: 02-Dec-1996
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/728,463
;/ FILING DATE: 10-OCT-1996
;/ APPLICATION NUMBER: US 08/544,404
;/ FILING DATE: 10-OCT-1995
;/ APPLICATION NUMBER: US 08/352,322
;/ FILING DATE: 07-DEC-1994
;/ APPLICATION NUMBER: US 08/209,741
;/ FILING DATE: 09-MAR-1994
;/ APPLICATION NUMBER: US 08/165,699
;/ FILING DATE: 10-DEC-1993
;/ APPLICATION NUMBER: US 08/161,739
;/ FILING DATE: 03-DEC-1993
;/ APPLICATION NUMBER: US 08/155,301
;/ FILING DATE: 18-NOV-1993
;/ APPLICATION NUMBER: US 08/096,762
;/ FILING DATE: 22-JUL-1993
;/ APPLICATION NUMBER: US 08/053,131
;/ FILING DATE: 26-APR-1993
;/ APPLICATION NUMBER: US 07/990,860
;/ FILING DATE: 16-DEC-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Serafini, Andrew T.
;/ REGISTRATION NUMBER: 41,303
;/ REFERENCE/DOCKET NUMBER: 014643-009030US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 576-0200
;/ TELEFAX: (415) 576-0300
;/ INFORMATION FOR SEQ ID NO: 307:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 115 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 307:
;/ US-08-758-417A-307

Query Match 100.0%; Score 49; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
Db 44 RASQSVSSYLA 54
|||||

RESULT 13
US-09-472-087-16
; Sequence 16, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: GILMAN, STEVEN H.
; APPLICANT: HANKE, JEFFREY H.

;/ APPLICANT: MUELLER, EILLEN E.
;/ APPLICANT: HANKE, JEFFREY H.
;/ APPLICANT: GILMAN, STEVEN C.
;/ APPLICANT: DAVIS, C. GEOFFREY
;/ APPLICANT: CORVALAN, JOSE R.
;/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;/ FILE REFERENCE: ABX-PF1
;/ CURRENT APPLICATION NUMBER: US/09/472,087
;/ CURRENT FILING DATE: 1999-12-23
;/ PRIOR APPLICATION NUMBER: 60/113,647
;/ PRIOR FILING DATE: 1998-12-23
;/ NUMBER OF SEQ ID NOS: 147
;/ SOFTWARE: PatentIn Ver. 2.1
;/ SEQ ID NO 16
;/ LENGTH: 139
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ US-09-472-087-16

Query Match 100.0%; Score 49; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
Db 16 RASQSVSSYLA 26
|||||

RESULT 14
US-09-472-087-90
; Sequence 90, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-90

Query Match 100.0%; Score 49; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
Db 16 RASQSVSSYLA 26
|||||

RESULT 15
US-09-472-087-91
; Sequence 91, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.

```
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-91

Query Match      100.0%; Score 49; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
Db      19 RASQSVSSSYLA 29

RESULT 16
US-09-472-087-21
; Sequence 21, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-21

Query Match      100.0%; Score 49; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
Db      19 RASQSVSSSYLA 29

RESULT 17
US-09-472-087-93
; Sequence 93, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
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; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-93

Query Match      100.0%; Score 49; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
Db      19 RASQSVSSSYLA 29

RESULT 18
US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-456-090A-46

Query Match      100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
Db      24 RASQSVSSSYLA 34

RESULT 19
US-09-456-090A-82
; Sequence 82, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
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US-09-456-090A-82

Query Match 100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
|||||

Db 24 RASQSVSSSYLA 34

RESULT 20

US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84

Query Match 100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
|||||

Db 24 RASQSVSSSYLA 34

RESULT 21

US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match 100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
|||||

Db 24 RASQSVSSSYLA 34

RESULT 22

US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match 100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
|||||

Db 24 RASQSVSSSYLA 34

RESULT 23

US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match 100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
|||||

Db 24 RASQSVSSSYLA 34

RESULT 24

US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars


```
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match      100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
      |||||
Db      24 RASQSVSSSYLA 34

RESULT 25
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84

Query Match      100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
      |||||
Db      24 RASQSVSSSYLA 34

RESULT 26
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: 020015-000110US
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match      100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
      |||||
Db      24 RASQSVSSSYLA 34

RESULT 27
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match      100.0%; Score 49; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
      |||||
Db      24 RASQSVSSSYLA 34

RESULT 28
US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
```

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; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-17

Query Match      100.0%; Score 49; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
DB      44 RASQSVSSYLA 54

RESULT 29
US-09-472-087-69
; Sequence 69, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-69

Query Match      100.0%; Score 49; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
DB      44 RASQSVSSYLA 54

RESULT 30
US-09-157-370-3
; Sequence 3, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157,370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7

; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-157-370-3

Query Match      98.0%; Score 48; DB 2; Length 109;
Best Local Similarity 90.9%; Pred. No. 0.03;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
DB      24 RASQSVSSYLA 34

RESULT 31
US-10-194-975-87
; Sequence 87, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-87

Query Match      91.8%; Score 45; DB 2; Length 95;
Best Local Similarity 90.9%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
DB      24 RASQSVSSYLA 34

RESULT 32
US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-18

Query Match          91.8%; Score 45; DB 1; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
      |||||:|:|
Db      24 RASQSIISNYLA 34

RESULT 33
US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-18

Query Match          91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
      |||||:|:|
Db      24 RASQSIISNYLA 34

RESULT 34
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-18

Query Match          91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSSYLA 11
      |||||:|:|
Db      24 RASQSIISNYLA 34

RESULT 35
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven

```

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; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
US-09-648-067A-14

Query Match          91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSIISNYLA 34

RESULT 36
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESTA, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-No. 6639055-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match          91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSIISNYLA 34

RESULT 37
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESTA, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-No. 6719971-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18

Query Match          91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSIISNYLA 34

RESULT 38
US-09-705-398-18
; Sequence 18, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; PRESTA, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-No. 6639055-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match          91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
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;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatin (Genentech)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/705,398
;; FILING DATE: 02-NOV-1993
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146206
;; FILING DATE: 17-NOV-1993
;; APPLICATION NUMBER: 07/715272
;; FILING DATE: 14-JUN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709P1D2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;;
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18

Query Match 91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
|||||:|:
Db 24 RASQSIISNYLA 34

RESULT 39
US-09-602-812A-5
; Sequence 5, Application US/09602812A
; Patent No. 6949245
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
; FILE REFERENCE: P1467R2
; CURRENT APPLICATION NUMBER: US/09/602,812A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 5
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain consensus sequence
US-09-602-812A-5

Query Match 91.8%; Score 45; DB 2; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
|||||:|:
Db 24 RASQSIISNYLA 34

RESULT 40
PCT-US93-07832-18
; Sequence 18, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-18

Query Match 91.8%; Score 45; DB 4; Length 107;
Best Local Similarity 81.8%; Pred. No. 0.12;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
|||||:|:
Db 24 RASQSIISNYLA 34

Search completed: December 14, 2005, 07:33:21
Job time : 17.1207 secs

11/15/2017 (10:10)

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:54 ; Search time 50.4483 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-720-323-4

Perfect score: 49

Sequence: 1 RASQSVSSYLA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
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4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	11	3	US-09-920-267C-4
2	49	100.0	11	4	US-10-091-300-1
3	49	100.0	11	4	US-10-384-060-63
4	49	100.0	11	4	US-10-384-060-72
5	49	100.0	11	4	US-10-173-551-10
6	49	100.0	11	4	US-10-656-769-70
7	49	100.0	11	4	US-10-687-799-16
8	49	100.0	11	4	US-10-687-799-22
9	49	100.0	11	4	US-10-687-799-28
10	49	100.0	11	4	US-10-394-471B-12
11	49	100.0	11	4	US-10-720-323-4
12	49	100.0	11	4	US-10-396-578-35
13	49	100.0	11	4	US-10-396-578-83
14	49	100.0	11	5	US-10-482-630-53
15	49	100.0	11	5	US-10-783-311-232
16	49	100.0	11	5	US-10-911-838-10
17	49	100.0	11	5	US-10-891-658-128
18	49	100.0	11	5	US-10-506-997-1
19	49	100.0	11	6	US-11-074-803-35
20	49	100.0	11	6	US-11-074-803-83
21	49	100.0	11	6	US-11-009-731-52
22	49	100.0	11	6	US-11-009-731-57
23	49	100.0	11	6	US-11-102-403-43
24	49	100.0	95	4	US-10-194-975-86
25	49	100.0	95	4	US-10-308-817-33
26	49	100.0	95	4	US-10-453-658-33
27	49	100.0	95	4	US-10-379-392-93
28	49	100.0	95	4	US-10-379-392-93
29	49	100.0	95	4	US-10-379-392-93
30	49	100.0	95	4	US-10-379-392-93
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70	49	100.0	95	4	US-10-379-392-93
71	49	100.0	95	4	US-10-379-392-93
72	49	100.0	95	4	US-10-379-392-93
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74	49	100.0	95	4	US-10-379-392-93
75	49	100.0	95	4	US-10-379-392-93
76	49	100.0	95	4	US-10-379-392-93
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81	49	100.0	95	4	US-10-379-392-93
82	49	100.0	95	4	US-10-379-392-93
83	49	100.0	95	4	US-10-379-392-93
84	49	100.0	95	4	US-10-379-392-93
85	49	100.0	95	4	US-10-379-392-93
86	49	100.0	95	4	US-10-379-392-93
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91	49	100.0	95	4	US-10-379-392-93
92	49	100.0	95	4	US-10-379-392-93
93	49	100.0	95	4	US-10-379-392-93
94	49	100.0	95	4	US-10-379-392-93
95	49	100.0	95	4	US-10-379-392-93
96	49	100.0	95	4	US-10-379-392-93
97	49	100.0	95	4	US-10-379-392-93
98	49	100.0	95	4	US-10-379-392-93
99	49	100.0	95	4	US-10-379-392-93
100	49	100.0	95	4	US-10-379-392-93

Sequence 4, Appli
Sequence 96, Appl
Sequence 36, Appl
Sequence 38, Appl
Sequence 99, Appl
Sequence 69, Appl
Sequence 71, Appl
Sequence 2, Appli
Sequence 40, Appl
Sequence 26, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 142, App
Sequence 143, App
Sequence 143, App
Sequence 78, Appl
Sequence 2, Appli
Sequence 14, Appl
Sequence 21, Appl
Sequence 91, Appl
Sequence 65, Appl
Sequence 157, App
Sequence 26, Appl
Sequence 98, Appl
Sequence 1, Appli
Sequence 3, Appli
Sequence 17, Appl
Sequence 14, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 68, Appl
Sequence 9, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 85, Appl
Sequence 90, Appl
Sequence 101, App
Sequence 9, Appli
Sequence 11, Appl
Sequence 24, Appl
Sequence 66, Appl
Sequence 230, App
Sequence 16, Appl
Sequence 54, Appl
Sequence 30, Appl
Sequence 8, Appli
Sequence 12, Appl
Sequence 57, Appl
Sequence 31, Appl
Sequence 12, Appl
Sequence 34, Appl
Sequence 16, Appl
Sequence 29, Appl
Sequence 25, Appl
Sequence 55, Appl
Sequence 90, Appl
Sequence 16, Appl
Sequence 90, Appl
Sequence 25, Appl
Sequence 51, Appl
Sequence 26, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 28, Appl
Sequence 21, Appl

ALIGNMENTS

```
RESULT 1
US-09-920-267C-4
; Sequence 4, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-4

Query Match      100.0%; Score 49; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      1 RASQSVSSYLA 11
|||||

RESULT 2
US-10-091-300-1
; Sequence 1, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human
US-10-091-300-1

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      1 RASQSVSSYLA 11
|||||

RESULT 3
US-10-384-060-63
; Sequence 63, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 39 CDRI sequence
US-10-384-060-72

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      1 RASQSVSSYLA 11
|||||

RESULT 4
US-10-384-060-72
; Sequence 72, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 39 CDRI sequence
US-10-384-060-72

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      1 RASQSVSSYLA 11
|||||

RESULT 5
US-10-384-060-63
; Sequence 63, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 33 CDRI sequence
US-10-384-060-63

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      1 RASQSVSSYLA 11
|||||
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```
US-10-173-551-10
; Sequence 10, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafan
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173.551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-10

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 6
US-10-656-769-70
; Sequence 70, Application US/10656769
; Publication No. US2004009712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01.1554
; CURRENT APPLICATION NUMBER: US/10/656.769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-70

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 7
US-10-687-799-16
; Sequence 16, Application US/10687799
; Publication No. US20040167319A1
; GENERAL INFORMATION:
; APPLICANT: Teeling, Jessica
; APPLICANT: Ruuls, Sigrid
; APPLICANT: Glennie, Martin
; APPLICANT: van de Winkel, Jan
; APPLICANT: Parren, Paul
; APPLICANT: Petersen, Jorgen
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055
; CURRENT APPLICATION NUMBER: US/10/687.799

US-10-173-551-10
; Sequence 10, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafan
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173.551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-10

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 8
US-10-687-799-22
; Sequence 22, Application US/10687799
; Publication No. US20040167319A1
; GENERAL INFORMATION:
; APPLICANT: Teeling, Jessica
; APPLICANT: Ruuls, Sigrid
; APPLICANT: Glennie, Martin
; APPLICANT: van de Winkel, Jan
; APPLICANT: Parren, Paul
; APPLICANT: Petersen, Jorgen
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055
; CURRENT APPLICATION NUMBER: US/10/687.799
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,163
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/460,028
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-799-22

Query Match      100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 9
US-10-687-799-28
; Sequence 28, Application US/10687799
; Publication No. US20040167319A1
; GENERAL INFORMATION:
; APPLICANT: Teeling, Jessica
; APPLICANT: Ruuls, Sigrid
; APPLICANT: Glennie, Martin
; APPLICANT: van de Winkel, Jan
; APPLICANT: Parren, Paul
; APPLICANT: Petersen, Jorgen
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055
; CURRENT APPLICATION NUMBER: US/10/687.799
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; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055
; CURRENT APPLICATION NUMBER: US/10/687,799
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,163
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/460,028
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-799-28

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 10

US-10-394-471B-12
; Sequence 12, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Cartton, Jill; Scallan, Bernard J.
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-12

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 11

US-10-720-323-4
; Sequence 4, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 C1PNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-4

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 12

US-10-396-578-35
; Sequence 35, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-35

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 13

US-10-396-578-83
; Sequence 83, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-83

Query Match 100.0%; Score 49; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 1 RASQSVSSYLA 11

RESULT 14
US-10-482-630-53
; Sequence 53, Application US/10482630
; Publication No. US20040242851A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors
; FILE REFERENCE: 11245/48502
; CURRENT APPLICATION NUMBER: US/10/482,630
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/US02/20332
; PRIOR FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US 60/301,299
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 53
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human
US-10-482-630-53

Query Match 100.0%; Score 49; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 1 RASQSVSSYLA 11

RESULT 15
US-10-783-311-232
; Sequence 232, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
US-10-783-311-232

Query Match 100.0%; Score 49; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 1 RASQSVSSYLA 11

RESULT 16
US-10-911-838-10
; Sequence 10, Application US/10911838

Publication No. US20050069869A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: LUZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: WJ1-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: SARS-Associated Coronavirus
US-10-911-838-10

Query Match 100.0%; Score 49; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 1 RASQSVSSYLA 11

RESULT 17
US-10-891-658-128
; Sequence 128, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 128
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-128

Query Match 100.0%; Score 49; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 1 RASQSVSSYLA 11

```
RESULT 18
US-10-506-997-1
; Sequence 1, Application US/10506997
; Publication No. US20050234225A1
; GENERAL INFORMATION:
; APPLICANT: Imclone Systems Incorporated
; TITLE OF INVENTION: Human Antibodies Specific To KDR And Uses Thereof
; FILE REFERENCE: 11245/47802
; CURRENT APPLICATION NUMBER: US/10/506,997
; PRIOR FILING DATE: 2004-09-04
; PRIOR APPLICATION NUMBER: PCT/US03/06459
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,783
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human
US-10-506-997-1

Query Match      100.0%; Score 49; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 19
US-11-074-803-35
; Sequence 35, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-11-074-803-35

Query Match      100.0%; Score 49; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 20
US-11-074-803-83
; Sequence 83, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-52

Query Match      100.0%; Score 49; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 21
US-11-009-731-52
; Sequence 52, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vargipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MX1-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-52

Query Match      100.0%; Score 49; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11

RESULT 22
US-11-009-731-57
; Sequence 57, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
```

```
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-57

Query Match      100.0%; Score 49; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      1 RASQSVSSYLA 11

RESULT 23
US-11-102-403-43
; Sequence 43, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PAREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STREIN, PAMELA
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 43
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-43

Query Match      100.0%; Score 49; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      1 RASQSVSSYLA 11

RESULT 24
US-10-194-975-86
; Sequence 86, Application US/10194975
```

```
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-86

Query Match      100.0%; Score 49; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

RESULT 25
US-10-308-817-33
; Sequence 33, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
US-10-308-817-33

Query Match      100.0%; Score 49; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

RESULT 26
US-10-453-698-33
; Sequence 33, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
US-10-453-698-33

Query Match      100.0%; Score 49; DB 4; Length 95;
```

```
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 24 RASQSVSSSYLA 34

RESULT 27
US-10-379-392-93
; Sequence 93, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiya, Basail I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-93

Query Match 100.0%; Score 49; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 24 RASQSVSSSYLA 34

RESULT 28
US-09-899-896-4
; Sequence 4, Application US/09899896
; Patent No. US20020072588A1
; GENERAL INFORMATION:
; APPLICANT: von Bdingen, Hans-Christian
; APPLICANT: Genain, Claude P.
; APPLICANT: Hauser, Stephen L.
; TITLE OF INVENTION: Recombinant Antibody Fragments as Autoantibody
; TITLE OF INVENTION: Antagonists
; FILE REFERENCE: SF01-025-2
; CURRENT APPLICATION NUMBER: US/09/899,896
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 09/691,654
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 100
; TYPE: PRT
; ORGANISM: human
US-09-899-896-4

Query Match 100.0%; Score 49; DB 3; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 24 RASQSVSSSYLA 34

Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 24 RASQSVSSSYLA 34

RESULT 29
US-11-009-731-96
; Sequence 96, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-96

Query Match 100.0%; Score 49; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 24 RASQSVSSSYLA 34

RESULT 30
US-10-916-840-30
; Sequence 30, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
; APPLICANT: Hufton, Simon E.
; APPLICANT: Hoet, Rene
; APPLICANT: Pieters, Henk
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Rokey, Kristen
; TITLE OF INVENTION: TIE1-BINDING LIGANDS
; FILE REFERENCE: 10280-083001
; CURRENT APPLICATION NUMBER: US/10/916,840
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-916-840-30

Query Match 100.0%; Score 49; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
Db 25 RASQSVSSSYLA 35
```

RESULT 31

US-10-916-840-38
; Sequence 38, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
; APPLICANT: Hufton, Simon E.
; APPLICANT: Hoet, Rene
; APPLICANT: Pieters, Henk
; APPLICANT: Kent, Rachel Barbault
; APPLICANT: Rookey, Kristen
; TITLE OF INVENTION: T1E1-BINDING LIGANDS
; FILE REFERENCE: 10280-083001
; CURRENT APPLICATION NUMBER: US/10/916,840
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-916-840-38

Query Match 100.0%; Score 49; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 25 RASQSVSSYLA 35

RESULT 32

US-11-021-715-99
; Sequence 99, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-99

Query Match 100.0%; Score 49; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 24 RASQSVSSYLA 34

RESULT 33

US-09-791-153A-69
; Sequence 69, Application US/09791153A

; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-69

Query Match 100.0%; Score 49; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 24 RASQSVSSYLA 34

RESULT 34

US-09-791-153A-71
; Sequence 71, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-71

Query Match 100.0%; Score 49; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | |
Db 24 RASQSVSSYLA 34

RESULT 35

US-09-982-464-2
; Sequence 2, Application US/09982464
; Publication No. US20030120044A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William
; APPLICANT: Watkins, Jeffery
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-06352
; CURRENT APPLICATION NUMBER: US/09/982,464
; CURRENT FILING DATE: 2002-04-16

```
; PRIOR APPLICATION NUMBER: 09/434,870
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/159,689
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-464-2

Query Match      100.0%; Score 49; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

RESULT 36
US-10-233-996-40
; Sequence 40, Application US/10233996
; Publication No. US20030096976A1
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-YuIl
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODIES LB-00503 AND LB-00506 SPECIFIC FOR HUMAN 4-1
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING SAID HUMANIZED ANTIBODIES
; FILE REFERENCE: 4363-0102P
; CURRENT APPLICATION NUMBER: US/10/233,996
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of human antibody (X82934)
US-10-233-996-40

Query Match      100.0%; Score 49; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

RESULT 37
US-10-091-300-26
; Sequence 26, Application US/10091300
; Publication No. US20030108545A1
; GENERAL INFORMATION:
; APPLICANT: Rockwell, Patricia
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: Combination Methods of Inhibiting Tumor Growth with a Vascular
; TITLE OF INVENTION: Endothelial Growth Factor Receptor Antagonist
; FILE REFERENCE: 11245/46211
; CURRENT APPLICATION NUMBER: US/10/091,300
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 26
; LENGTH: 107
; TYPE: PRT
```

```
; ORGANISM: Human
US-10-091-300-26

Query Match      100.0%; Score 49; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

RESULT 38
US-10-181-324-4
; Sequence 4, Application US/10181324
; Publication No. US20030124617A1
; GENERAL INFORMATION:
; APPLICANT: Gram, Hermann
; APPLICANT: Dipadova, Franco E
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IL-1 BETA
; FILE REFERENCE: 4-31289A
; CURRENT APPLICATION NUMBER: US/10/181,324
; CURRENT FILING DATE: 2002-07-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus/Homo sapiens
US-10-181-324-4

Query Match      100.0%; Score 49; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

RESULT 39
US-10-340-189-14
; Sequence 14, Application US/10340189
; Publication No. US20030229207A1
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 W. Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/340,189
; FILING DATE: 10-Jan-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,202A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/082,842
; FILING DATE: 23-JUN-1993
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
```


ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-340-189-14

Query Match 100.0%; Score 49; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | | | | | | | | | | | |
Db 24 RASQSVSSYLA 34

RESULT 40
US-10-325-696-14
; Sequence 14, Application US/10325696
; Publication No. US20040005630A1
; GENERAL INFORMATION:
; APPLICANT: Studnicka, Gary M.
; TITLE OF INVENTION: Modified Antibody Variable Domains
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/325,696
; FILING DATE: 18-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,980
; FILING DATE: 16-JUN-1998
; APPLICATION NUMBER: 08/107,669
; FILING DATE: 13-AUG-1993
; APPLICATION NUMBER: PCT/US92/10906
; FILING DATE: 14-DEC-1992
; APPLICATION NUMBER: US 07/808,464
; FILING DATE: 13-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Janet M. McNicholas, Ph.D.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9050
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-325-696-14

Query Match 100.0%; Score 49; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | | | | | | | | |
Db 24 RASQSVSSYLA 34

Search completed: December 14, 2005, 07:37:53
Job time : 50.4483 secs

THE 1990s

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:25:44 ; Search time 3.41379 Seconds
(without alignments)
21.698 Million cell updates/sec

Title: US-10-720-323-4

Perfect score: 49

Sequence: 1 RASQSVSSYLA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubaa/US09 NEW PUB pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US06 NEW PUB pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US07 NEW PUB pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US08 NEW PUB pep.*
- 5: /cgn2_6/ptodata/1/pubaa/PCT NEW PUB pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US10 NEW PUB pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US11 NEW PUB pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US60 NEW PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	11	7	US-11-093-274-10
2	49	100.0	11	7	US-11-093-274-11
3	49	100.0	11	7	US-11-093-274-12
4	49	100.0	94	7	US-11-093-274-33
5	49	100.0	95	7	US-11-054-669-86
6	49	100.0	95	7	US-11-084-554-138
7	49	100.0	107	7	US-11-040-159-17
8	49	100.0	107	7	US-11-093-274-24
9	49	100.0	108	7	US-11-093-274-22
10	49	100.0	108	7	US-11-093-274-23
11	49	100.0	128	6	US-10-721-763-31
12	49	100.0	251	7	US-11-054-515-1049
13	45	91.8	95	7	US-11-054-669-87
14	45	91.8	95	7	US-11-084-554-131
15	45	91.8	108	6	US-10-925-366A-233
16	45	91.8	108	7	US-11-120-338-3
17	45	91.8	129	6	US-10-721-763-19
18	45	91.8	129	6	US-10-721-763-23
19	44	89.8	95	7	US-11-054-669-54
20	44	89.8	95	7	US-11-054-669-55
21	44	89.8	95	7	US-11-054-669-67
22	44	89.8	95	7	US-11-054-669-69
23	44	89.8	95	7	US-11-084-554-139
24	44	89.8	95	7	US-11-084-554-140
25	44	89.8	95	7	US-11-084-554-143

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28	44	89.8	105	7	US-11-155-775-52
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36	44	89.8	109	7	US-11-127-677-29
37	44	89.8	240	6	US-10-925-366A-219
38	44	89.8	241	7	US-11-054-515-1932
39	44	89.8	241	7	US-11-054-515-2054
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46	43	87.8	313	7	US-11-000-463-427
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49	41	83.7	95	7	US-11-054-669-58
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81	39	79.6	237	7	US-11-054-515-2019
82	39	79.6	237	7	US-11-054-515-2020
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89	39	79.6	237	7	US-11-054-515-2111
90	39	79.6	237	7	US-11-054-515-2114
91	39	79.6	237	7	US-11-054-515-2115
92	39	79.6	238	7	US-11-054-515-2053
93	39	79.6	242	7	US-11-054-515-1580
94	39	79.6	244	7	US-11-054-515-1881
95	39	79.6	245	7	US-11-054-515-1291
96	39	79.6	248	7	US-11-054-515-1004
97	39	79.6	248	7	US-11-054-515-1385
98	39	79.6	248	7	US-11-054-515-1717

Sequence 146, App
Sequence 42, Appl
Sequence 52, Appl
Sequence 234, App
Sequence 3, Appl
Sequence 6, Appl
Sequence 232, App
Sequence 28, Appl
Sequence 36, Appl
Sequence 61, Appl
Sequence 29, Appl
Sequence 219, App
Sequence 1932, Ap
Sequence 919, App
Sequence 2054, Ap
Sequence 1635, Ap
Sequence 1174, Ap
Sequence 72, Appl
Sequence 124, App
Sequence 69, Appl
Sequence 427, App
Sequence 335, App
Sequence 899, App
Sequence 58, Appl
Sequence 61, Appl
Sequence 111, App
Sequence 121, App
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Sequence 9, Appl
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Sequence 85, Appl
Sequence 127, App
Sequence 130, App
Sequence 288, App
Sequence 39, Appl
Sequence 12, Appl
Sequence 1268, Ap
Sequence 1952, Ap
Sequence 1238, Ap
Sequence 65, Appl
Sequence 66, Appl
Sequence 70, Appl
Sequence 129, App
Sequence 129, App
Sequence 133, App
Sequence 134, App
Sequence 137, App
Sequence 1906, Ap
Sequence 2003, Ap
Sequence 2005, Ap
Sequence 2017, Ap
Sequence 2019, Ap
Sequence 2020, Ap
Sequence 2027, Ap
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Sequence 2043, Ap
Sequence 2104, Ap
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Sequence 2053, Ap
Sequence 1580, Ap
Sequence 1881, Ap
Sequence 1291, Ap
Sequence 1004, Ap
Sequence 1385, Ap
Sequence 1717, Ap

Sequence 1719, Ap
Sequence 1733, Ap

99 39 79.6 248 7 US-11-054-515-1719
100 39 79.6 248 7 US-11-054-515-1733

ALIGNMENTS

RESULT 1

US-11-093-274-10
; Sequence 10, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-10

Query Match 100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11
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RESULT 2

US-11-093-274-11
; Sequence 11, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-11

Query Match 100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11
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RESULT 3

US-11-093-274-12
; Sequence 12, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-12

Query Match 100.0%; Score 49; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
Db 1 RASQSVSSSYLA 11
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RESULT 4

US-11-093-274-33
; Sequence 33, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-33

Query Match 100.0%; Score 49; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
Db 24 RASQSVSSSYLA 34
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RESULT 5

US-11-054-669-86
; Sequence 86, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES

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; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-86

Query Match      100.0%; Score 49; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 24 RASQSVSSYLA 34

RESULT 6
US-11-084-554-138
; Sequence 138, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korvet, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-138

Query Match      100.0%; Score 49; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 24 RASQSVSSYLA 34

RESULT 7
US-11-040-159-17
; Sequence 17, Application US/11040159
; Publication No. US2005025552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehrsén, Kenneth
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Hong
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey T.
; APPLICANT: KaloBios, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; TITLE OF INVENTION: Binding Determinants
; FILE REFERENCE: 021167-00173005
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; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: V-region of
; OTHER INFORMATION: anti-PCrv antibody 1F1 VL
US-11-040-159-17

Query Match      100.0%; Score 49; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 24 RASQSVSSYLA 34

RESULT 8
US-11-093-274-24
; Sequence 24, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-24

Query Match      100.0%; Score 49; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 24 RASQSVSSYLA 34

RESULT 9
US-11-093-274-22
; Sequence 22, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
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; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-22

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Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      24 RASQSVSSYLA 34

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; Sequence 23, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-23

Query Match      100.0%; Score 49; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

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US-10-721-763-31
; Sequence 31, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 31
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-31

Query Match      100.0%; Score 49; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      44 RASQSVSSYLA 54

RESULT 12
US-11-054-515-1049
; Sequence 1049, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1049

Query Match      100.0%; Score 49; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      166 RASQSVSSYLA 176

RESULT 13
US-11-054-669-87
; Sequence 87, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
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; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-87

Query Match          91.8%; Score 45; DB 7; Length 95;
Best Local Similarity 90.9%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQGVSSYLA 34

RESULT 14
US-11-084-554-131
; Sequence 131, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-131

Query Match          91.8%; Score 45; DB 7; Length 95;
Best Local Similarity 90.9%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQGVSSYLA 34

RESULT 15
US-10-925-366A-233
; Sequence 233, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Dewiltd, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Baeran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28

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; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 233
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vx Sequence of Clone E5sd
US-10-925-366A-233

Query Match          91.8%; Score 45; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 10
Db      24 RASQSVSSYLA 33

RESULT 16
US-11-120-338-3
; Sequence 3, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 3
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-3

Query Match          91.8%; Score 45; DB 7; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.0079;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQSVSSYLA 34

RESULT 17
US-10-721-763-19
; Sequence 19, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT

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; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19

Query Match      91.8%; Score 45; DB 6; Length 129;
Best Local Similarity 90.9%; Pred. No. 0.0096;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      44 RASQSVSSFLA 54

RESULT 18
US-10-721-763-23
; Sequence 23, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-23

Query Match      91.8%; Score 45; DB 6; Length 129;
Best Local Similarity 90.9%; Pred. No. 0.0096;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYLA 11
Db      44 RASQSVSSFLA 54

RESULT 19
US-11-054-669-54
; Sequence 54, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-54

Query Match      89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RASQSVSSYL 10
Db      24 RASQSISSYL 33

RESULT 20
US-11-054-669-55
; Sequence 55, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-55

Query Match      89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RASQSVSSYL 10
Db      24 RASQSISSYL 33

RESULT 21
US-11-054-669-67
; Sequence 67, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-67

Query Match      89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 RASQSVSSYLA 11
Db      24 RASQGISSYLA 34

RESULT 22
US-11-054-669-69
; Sequence 69, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 69
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-69

Query Match      89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQGISSYLA 34

RESULT 23
US-11-084-554-139
; Sequence 139, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Larry L.
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-139

Query Match      89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQGISSYLA 34

RESULT 24
US-11-084-554-140
; Sequence 140, Application US/11084554
```

```
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Larry L.
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-140

Query Match      89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RASQSVSSYLA 11
Db      24 RASQGISSYLA 34

RESULT 25
US-11-084-554-143
; Sequence 143, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Larry L.
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-143

Query Match      89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYL 10
Db      24 RASQSISSYL 33

RESULT 26
US-11-084-554-146
; Sequence 146, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
```

; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ARGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/534,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-146

Query Match 89.8%; Score 44; DB 7; Length 95;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 24 RASQSISSYL 33
|||||:||||

RESULT 27
US-11-144-248-42
; Sequence 42, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ASX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-42

Query Match 89.8%; Score 44; DB 7; Length 96;
Best Local Similarity 90.0%; Pred. No. 0.011;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 24 RASQSISSYL 33
|||||:||||

RESULT 28
US-11-155-775-52
; Sequence 52, Application US/11155775
; Publication No. US20050266013A1
; GENERAL INFORMATION:
; APPLICANT: Morell, Andreas
; APPLICANT: Imboden, Martin
; APPLICANT: Stadler, Boda
; APPLICANT: Miescher, Sylvia
; APPLICANT: Vogel, Monique
; APPLICANT: Amstutz, Hanspeter

; TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
; TITLE OF INVENTION: STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
; TITLE OF INVENTION: THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
; FILE REFERENCE: 6816/P63221US0
; CURRENT APPLICATION NUMBER: US/11/155,775
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: US/09/147,443
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: PCT/EP97/03253
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: EP 96810421.6
; PRIOR FILING DATE: 1996-06-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-775-52

Query Match 89.8%; Score 44; DB 7; Length 105;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 22 RASQSISSYL 31
|||||:||||

RESULT 29
US-10-925-366A-234
; Sequence 234, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Demildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Baaran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 234
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:


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; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 232
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vk Sequence of Clone K8
US-10-925-366A-232

Query Match      89.8%; Score 44; DB 6; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYL 10
Db      24 RASQSISSYL 33

RESULT 33
US-11-127-677-28
; Sequence 28, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-28

Query Match      89.8%; Score 44; DB 7; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYL 10
Db      24 RASQSISSYL 33

RESULT 34
US-11-127-677-36
; Sequence 36, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-36

Query Match      89.8%; Score 44; DB 7; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYL 10
Db      24 RASQSISSYL 33

RESULT 35
US-11-127-677-61
; Sequence 61, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-61

Query Match      89.8%; Score 44; DB 7; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RASQSVSSYL 10
Db      24 RASQSISSYL 33

RESULT 36
US-11-127-677-29
; Sequence 29, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
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1 PRIOR APPLICATION NUMBER: PCT/GB03/04942
1 PRIOR FILING DATE: 2003-11-14
1 PRIOR APPLICATION NUMBER: GB 0226729.2
1 PRIOR FILING DATE: 2002-11-15
1 NUMBER OF SEQ ID NOS: 150
1 SOFTWARE: PatentIn version 3.1
1 SEQ ID NO 29
1 LENGTH: 109
1 TYPE: PRT
1 ORGANISM: Artificial sequence
1 FEATURE:
1 OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-29

Query Match 89.8%; Score 44; DB 7; Length 109;
Best Local Similarity 81.8%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | : | | | |
Db 24 RASQGISSYLA 34

RESULT 37
US-10-925-366A-219
1 Sequence 219, Application US/10925366A
1 Publication No. US20050271663A1
1 GENERAL INFORMATION:
1 APPLICANT: Ignatovich, Olga
1 APPLICANT: Dewildt, Rudolph M.T.
1 APPLICANT: Benjamin, Woolven
1 APPLICANT: Grant, Steven
1 APPLICANT: Jones, Philip
1 APPLICANT: Basran, Anrik
1 APPLICANT: Brewis, Neil
1 TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
1 FILE REFERENCE: 8039/2105
1 CURRENT APPLICATION NUMBER: US/10/925.366A
1 CURRENT FILING DATE: 2004-08-24
1 PRIOR APPLICATION NUMBER: US 10/744,774
1 PRIOR FILING DATE: 2003-12-23
1 PRIOR APPLICATION NUMBER: PCT/GB2003/002804
1 PRIOR FILING DATE: 2003-06-30
1 PRIOR APPLICATION NUMBER: PCT/GB2002/03014
1 PRIOR FILING DATE: 2002-06-28
1 PRIOR APPLICATION NUMBER: GB 0230202.4
1 PRIOR FILING DATE: 2002-12-27
1 PRIOR APPLICATION NUMBER: GB 115841.9
1 PRIOR FILING DATE: 2001-06-28
1 PRIOR APPLICATION NUMBER: PCT/GB2004/002829
1 PRIOR FILING DATE: 2004-06-30
1 PRIOR APPLICATION NUMBER: US 60/535,076
1 PRIOR FILING DATE: 2004-01-08
1 PRIOR APPLICATION NUMBER: PCT/GB2003/005646
1 PRIOR FILING DATE: 2003-12-24
1 PRIOR APPLICATION NUMBER: GB 0327706.8
1 PRIOR FILING DATE: 2003-11-28
1 PRIOR APPLICATION NUMBER: US 60/509,613
1 PRIOR FILING DATE: 2003-10-08
1 NUMBER OF SEQ ID NOS: 368
1 SOFTWARE: PatentIn version 3.3
1 SEQ ID NO 219
1 LENGTH: 240
1 TYPE: PRT
1 ORGANISM: Artificial Sequence
1 FEATURE:
1 OTHER INFORMATION: Synthetic Antibody Sequence, VH and VL joined by Gly4Ser Linker
US-10-925-366A-219

Query Match 89.8%; Score 44; DB 6; Length 240;
Best Local Similarity 90.0%; Pred. No. 0.03;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
| | | | : | | | |
Db 156 RASQGISSYL 165

RESULT 38
US-11-054-515-1932
1 Sequence 1932, Application US/11054515
1 Publication No. US2005025532A1
1 GENERAL INFORMATION:
1 APPLICANT: Ruben et al.
1 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
1 FILE REFERENCE: PF523P3
1 CURRENT APPLICATION NUMBER: US/11/054,515
1 CURRENT FILING DATE: 2005-02-10
1 PRIOR APPLICATION NUMBER: 60/543,296
1 PRIOR FILING DATE: 2004-02-11
1 PRIOR APPLICATION NUMBER: 60/580,347
1 PRIOR FILING DATE: 2004-06-18
1 PRIOR APPLICATION NUMBER: 10/293,418
1 PRIOR FILING DATE: 2002-11-14
1 PRIOR APPLICATION NUMBER: 60/331,469
1 PRIOR FILING DATE: 2001-11-16
1 PRIOR APPLICATION NUMBER: 60/340,817
1 PRIOR FILING DATE: 2001-12-19
1 PRIOR APPLICATION NUMBER: 09/880,748
1 PRIOR FILING DATE: 2001-06-15
1 PRIOR APPLICATION NUMBER: 60/293,499
1 PRIOR FILING DATE: 2001-05-25
1 PRIOR APPLICATION NUMBER: 60/277,379
1 PRIOR FILING DATE: 2001-03-21
1 PRIOR APPLICATION NUMBER: 60/276,248
1 PRIOR FILING DATE: 2001-03-16
1 PRIOR APPLICATION NUMBER: 60/240,816
1 PRIOR FILING DATE: 2000-10-17
1 Remaining Prior Application data removed - See File Wrapper or PALM.
1 NUMBER OF SEQ ID NOS: 3247
1 SEQ ID NO 1932
1 LENGTH: 241
1 TYPE: PRT
1 ORGANISM: Homo sapiens
US-11-054-515-1932

Query Match 89.8%; Score 44; DB 7; Length 241;
Best Local Similarity 81.8%; Pred. No. 0.031;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
| | | | : | | | |
Db 157 RASQGISSYLA 167

RESULT 39
US-11-054-515-2054
1 Sequence 2054, Application US/11054515
1 Publication No. US2005025532A1
1 GENERAL INFORMATION:
1 APPLICANT: Ruben et al.
1 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
1 FILE REFERENCE: PF523P3
1 CURRENT APPLICATION NUMBER: US/11/054,515
1 CURRENT FILING DATE: 2005-02-10
1 PRIOR APPLICATION NUMBER: 60/543,296
1 PRIOR FILING DATE: 2004-02-11
1 PRIOR APPLICATION NUMBER: 60/580,347
1 PRIOR FILING DATE: 2004-06-18
1 PRIOR APPLICATION NUMBER: 10/293,418
1 PRIOR FILING DATE: 2002-11-14
1 PRIOR APPLICATION NUMBER: 60/331,469
1 PRIOR FILING DATE: 2001-11-16
1 PRIOR APPLICATION NUMBER: 60/340,817
1 PRIOR FILING DATE: 2001-12-19
1 PRIOR APPLICATION NUMBER: 09/880,748

Search completed: December 14, 2005, 07:38:16
Job time : 4.41379 secs

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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2054
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2054

Query Match 89.8%; Score 44; DB 7; Length 241;
Best Local Similarity 81.8%; Pred. No. 0.031;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 157 RASQGISSYLA 167

RESULT 40
US-11-054-515-919
; Sequence 919, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 919
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-919

Query Match 89.8%; Score 44; DB 7; Length 249;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 165 RASQGISSYLA 175

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:38 ; Search time 11.9483 Seconds
(without alignments)
88.581 Million cell updates/sec

Title: US-10-720-323-4

Perfect score: 49

Sequence: 1 RASQSVSYLA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.80.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	78	2 S34102	Ig kappa chain V r
2	49	100.0	86	2 S16837	Ig kappa chain V r
3	49	100.0	86	2 S16830	Ig kappa chain V r
4	49	100.0	86	2 S16833	Ig kappa chain V-I
5	49	100.0	86	2 S16826	Ig kappa chain V r
6	49	100.0	92	2 S37506	Ig kappa chain V r
7	49	100.0	92	2 S37512	Ig kappa chain V r
8	49	100.0	92	2 S37522	Ig kappa chain V r
9	49	100.0	92	2 S37516	Ig kappa chain V r
10	49	100.0	108	2 G44151	Ig kappa chain V r
11	49	100.0	111	2 S23628	Ig kappa chain V r
12	49	100.0	114	2 S54905	Ig kappa chain V r
13	49	100.0	115	1 K3HUVG	Ig kappa chain pre
14	49	100.0	128	2 A56701	Ig kappa chain V r
15	49	100.0	128	2 S40379	Ig kappa chain V-J
16	49	100.0	129	2 S40363	Ig kappa chain - h
17	49	100.0	144	2 P40106	Ig kappa chain pre
18	46	93.9	106	2 S2482	Ig kappa chain (an
19	46	93.9	107	2 S37444	Ig kappa chain V-J
20	46	93.9	125	2 S40344	Ig kappa chain V-J
21	45	91.8	86	2 S16825	Ig kappa chain V r
22	45	91.8	108	1 K1HUUH	Ig kappa chain V-I
23	45	91.8	115	2 S11697	Ig kappa chain pre
24	45	91.8	129	2 S29627	Ig kappa chain V r
25	44	89.8	82	2 S34090	Ig kappa chain V r
26	44	89.8	86	2 S16832	Ig kappa chain V r
27	44	89.8	86	2 S34086	Ig kappa chain V r
28	44	89.8	87	2 S34084	Ig kappa chain V r
29	44	89.8	87	2 S21523	Ig kappa chain V r

30	44	89.8	87	2 S34083	Ig kappa chain V r
31	44	89.8	88	2 S21522	Ig kappa chain V r
32	44	89.8	88	2 S21528	Ig kappa chain V r
33	44	89.8	88	2 S21520	Ig kappa chain V r
34	44	89.8	88	2 S34104	Ig kappa chain V r
35	44	89.8	88	2 S21524	Ig kappa chain V r
36	44	89.8	91	2 S37521	Ig kappa chain V r
37	44	89.8	107	2 S36284	Ig lambda chain V
38	44	89.8	108	2 S34007	Ig kappa chain V r
39	44	89.8	108	2 S44122	Ig kappa chain V r
40	44	89.8	108	2 S47182	Ig kappa chain - h
41	44	89.8	108	2 B49047	Ig kappa chain V r
42	44	89.8	108	2 S30521	Ig kappa chain V r
43	44	89.8	116	2 A27554	Ig kappa chain pre
44	44	89.8	117	2 S24206	Ig kappa chain V r
45	44	89.8	123	2 S40331	Ig kappa chain - h
46	44	89.8	124	2 S40318	Ig kappa chain V r
47	44	89.8	124	2 S40336	Ig kappa chain V-J
48	44	89.8	128	2 S46372	Ig light chain var
49	44	89.8	132	2 S38646	Ig kappa chain V r
50	43	87.8	43	2 S21065	Ig kappa chain V r
51	43	87.8	86	2 S16840	Ig kappa chain V r
52	43	87.8	92	2 S37504	Ig kappa chain V r
53	43	87.8	98	2 S41813	Ig kappa chain V r
54	43	87.8	110	2 PNO535	Ig kappa chain V r
55	43	87.8	117	1 K1HUI2	Ig kappa chain pre
56	43	87.8	125	2 S40333	Ig kappa chain V-J
57	41	83.7	39	2 PH0878	Ig kappa chain V r
58	41	83.7	71	2 S21526	Ig kappa chain V r
59	41	83.7	88	2 S21525	Ig kappa chain V r
60	41	83.7	95	2 PH0866	Ig kappa chain V r
61	41	83.7	95	2 PH0863	Ig kappa chain V r
62	41	83.7	101	2 S44117	Ig kappa chain V r
63	41	83.7	106	2 PC2397	anti-tetanus toxin
64	41	83.7	106	2 PL0267	Ig kappa chain V r
65	41	83.7	107	2 S36275	Ig lambda chain V
66	41	83.7	107	2 S40366	Ig kappa chain V-J
67	41	83.7	108	2 S19674	Ig kappa chain V r
68	41	83.7	108	2 S31977	Ig kappa chain - h
69	41	83.7	109	2 S31998	Ig kappa chain - h
70	41	83.7	117	2 C21056	Ig kappa chain pre
71	41	83.7	123	2 S35479	Ig kappa chain pre
72	41	83.7	125	2 S40350	Ig kappa chain - h
73	41	83.7	127	2 S40367	Ig kappa chain V-J
74	41	83.7	129	1 K1HUMK	Ig kappa chain pre
75	41	83.7	131	2 S40352	Ig kappa chain V-J
76	41	83.7	132	2 S40334	Ig kappa chain - h
77	40	81.6	83	2 S78489	Ig kappa chain V r
78	40	81.6	84	2 S34099	Ig kappa chain V r
79	40	81.6	86	2 S16834	Ig kappa chain V r
80	40	81.6	86	2 S16834	Ig kappa chain V r
81	40	81.6	86	2 S16836	Ig kappa chain V r
82	40	81.6	86	2 S16839	Ig kappa chain V r
83	40	81.6	86	2 S16828	Ig kappa chain V r
84	40	81.6	86	2 S16829	Ig kappa chain V r
85	40	81.6	86	2 S16835	Ig kappa chain V r
86	40	81.6	87	2 S34098	Ig kappa chain V r
87	40	81.6	91	2 S37525	Ig kappa chain V r
88	40	81.6	91	2 S37527	Ig kappa chain V r
89	40	81.6	92	2 S37523	Ig kappa chain V r
90	40	81.6	96	2 G33750	Ig kappa chain V r
91	40	81.6	98	2 PH1083	Ig light chain V r
92	40	81.6	103	2 S44121	Ig kappa chain V-J
93	40	81.6	103	2 S19975	Ig kappa chain V r
94	40	81.6	106	2 S26345	Ig light chain V r
95	40	81.6	107	1 K1HUAR	Ig kappa chain V-I
96	40	81.6	107	2 S34005	Ig kappa chain V r
97	40	81.6	108	2 S40377	Ig kappa chain - h
98	40	81.6	110	2 S40326	Ig kappa chain V-J
99	40	81.6	117	2 S40362	Ig kappa chain - h
100	40	81.6	127	2 S04574	Ig kappa chain pre

ALIGNMENTS

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RESULT 1
S34102
IG kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C;Accession: S34102
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Molecule type: DNA
A;Status: preliminary
A;Cross-references: UNIPARC:UPI0000176B23; EMBL:X67186
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 49; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
   |||||
Db 15 RASQSVSSSYLA 25

RESULT 2
S16837
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16837
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16837
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPARC:UPI0000176DA6; EMBL:X54835
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
   |||||
Db 15 RASQSVSSSYLA 25

RESULT 3
S16830
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16830
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16830
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPARC:UPI0000176DA9; EMBL:X54828
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
   |||||
Db 15 RASQSVSSSYLA 25

RESULT 4
S16833
IG kappa chain V-III region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16833; S16838
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16833
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54831
A;Experimental source: clone BkV17
A;Accession: S16838
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLM>
A;Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54836
A;Experimental source: clone s1kv14
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11
   |||||
Db 15 RASQSVSSSYLA 25

RESULT 5
S16826
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16826; S34101
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16826
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPARC:UPI0000115E92; EMBL:X54824; NID:g33653; PIDN:CAA38593.1; PID
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34101
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <WAG>
A;Cross-references: UNIPARC:UPI0000115E92; EMBL:X67185
C;Superfamily: immunoglobulin V region; immunoglobulin homology
```


C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11
|||||
Db 15 RASQSVSSSYLA 25

RESULT 6

S37506

Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37506

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A;Reference number: S37501

A;Accession: S37506

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-92 <KLE>

A;Cross-references: UNIPARC:UPI0000116576; EMBL:Z26606; NID:g405653; PIDN:CAA81359.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 49; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11

|||||

Db 7 RASQSVSSSYLA 17

RESULT 7

S37512

Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37512

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A;Reference number: S37501

A;Accession: S37512

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-92 <KLE>

A;Cross-references: UNIPARC:UPI0000116570; EMBL:Z26599; NID:g405666; PIDN:CAA81353.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 49; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11

|||||

Db 7 RASQSVSSSYLA 17

RESULT 8

S37522

Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37522

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A;Reference number: S37501

A;Accession: S37522

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-92 <KLE>

A;Cross-references: UNIPARC:UPI0000116586; EMBL:Z26622; NID:g405686; PIDN:CAA81375.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 49; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11

|||||

Db 7 RASQSVSSSYLA 17

RESULT 9

S37516

Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37516

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A;Reference number: S37501

A;Accession: S37516

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-92 <KLE>

A;Cross-references: UNIPARC:UPI0000116588; EMBL:Z26624; NID:g405674; PIDN:CAA81377.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 49; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11

|||||

Db 7 RASQSVSSSYLA 17

RESULT 10

G44151

Ig kappa chain V region (JM-10) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C;Accession: G44151

R;Zebede, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotien, R.H.; Graff, R.; DeGraw, J.; Pya

Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992

A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.

A;Reference number: A44151; MUID:92228746; PMID:1373487

A;Accession: G44151

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-108 <ZEB>

A;Cross-references: UNIPARC:UPI00001139AC; GB:M88317; NID:g183968; PIDN:AAA35975.1; PID:

A;Note: nucleotide translation not given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-89/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.0077;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSSYLA 11

|||||

Db 23 RASQSVSSSYLA 33

RESULT 11

S23628

IG kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S23628

R:Oltee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992

A>Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23628

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 <OLE>

A:Cross-references: UNIPARC:UPI0000115F96; EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 0.0079;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11

|||||

Db 24 RASQSVSSSYLA 34

RESULT 12

S54905

IG kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S54905

R:Epposito, G.; Traboni, C.

submitted to the EMBL Data Library, November 1994

A:Description: Cloning and sequencing of cDNA coding for the variable domains of a human

A:Reference number: S54905

A:Accession: S54905

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-114 <ESP>

A:Cross-references: UNIPARC:UPI000011620A; EMBL:X82934; NID:g809554; PIDN:CAA58108.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 0.0081;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11

|||||

Db 24 RASQSVSSSYLA 34

RESULT 13

K3HUVG

IG kappa chain precursor V-III region (Vg) - human

C:Species: Homo sapiens (man)

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C:Accession: A01900

R:Pech, M.; Zachau, H.G.

Nucleic Acids Res. 12, 9229-9236, 1984

A>Title: Immunoglobulin genes of different subgroups are interdigitated within the V-K 1

A:Reference number: A93549; MUID:85087932; PMID:6440122

A:Accession: A01900

A:Molecule type: DNA

A:Residues: 1-115 <PEC>

A:Cross-references: UNIPROT:P04433; UNIPARC:UPI0000116D05; GB:X01668; GB:X02768; NID:g33

A>Note: the sequence was determined from the germline gene

C:Genetics:

A:Gene: GDB:IGKV3

A:Cross-references: GDB:136266

A:Map position: 2p12-2p11

A:Introns: 17/1

C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Product: Ig kappa chain V-III region (Vg) #status predicted <MAT>

F:21-43/Region: framework 1

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:55-69/Region: framework 2

F:70-76/Region: complementarity-determining 2

F:77-108/Region: framework 3

F:109-115/Region: complementarity-determining 3

F:43-108/Disulfide bonds: #status predicted

Query Match 100.0%; Score 49; DB 1; Length 115;

Best Local Similarity 100.0%; Pred. No. 0.0082;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11

|||||

Db 44 RASQSVSSSYLA 54

RESULT 14

A56701

IG kappa chain V region precursor (HuA) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000

C:Accession: A56701

R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.

J. Biol. Chem. 270, 12457-12465, 1995

A>Title: Human and mouse monoclonal antibodies to blood group A substance, which are near

A:Reference number: A56701; MUID:95279371; PMID:7759488

A:Accession: A56701

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 <NIC>

A:Cross-references: UNIPARC:UPI0000113B26; GB:I41174; NID:g762823; PIDN:AAA64877.1; PID:5

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 128;

Best Local Similarity 100.0%; Pred. No. 0.0091;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSSYLA 11

|||||

Db 44 RASQSVSSSYLA 54

RESULT 15

S40379

IG kappa chain V-J region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40379

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A>Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40379

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-128 <KLE>

A:Cross-references: UNIPARC:UPI0000116181; EMBL:X72489; NID:g441446; PIDN:CAA51157.1; PFI

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 49; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
|||||
Db 44 RASQSVSSYLA 54

RESULT 16

S40363

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40363

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40363

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <KLE>

A;Cross-references: UNIPARC:UPI0000116171; EMBL:X72473; NID:g441414; PIDN:CAA51141.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-109/Domain: immunoglobulin homology <IMM>

Query Match

100.0%; Score 49; DB 2; Length 129;

Best Local Similarity 100.0%; Pred. No. 0.0092;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11

|||||

Db 43 RASQSVSSYLA 53

RESULT 17

PL0106

Ig kappa chain precursor V-J-C region (LS1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C;Accession: PL0106

R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A;Title: Relationship of variable region genes expressed by a human B cell lymphoma sec

A;Reference number: PL0106; MUID:89235583; PMID:2541221

A;Accession: PL0106

A;Molecule type: mRNA

A;Residues: 1-144 <STIL>

A;Cross-references: UNIPARC:UPI00001767A2

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-115/Domain: V region <VRE>

F;36-110/Domain: immunoglobulin homology <IMM>

F;44-54/Region: complementarity-determining 1

F;70-76/Region: complementarity-determining 2

F;109-115/Region: complementarity-determining 3

F;116-127/Domain: J region <JRG>

F;128-144/Domain: C region (fragment) <CRE>

Query Match

100.0%; Score 49; DB 2; Length 144;

Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11

|||||

Db 44 RASQSVSSYLA 54

RESULT 18

PC4282

Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000

C;Accession: PC4282; PC4284

R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.

Biochem. Biophys. Res. Commun. 232, 101-106, 1997

A;Title: Molecular cloning of anti-SS-A/Ro 60-kDa peptide fab fragments from infiltratin

A;Reference number: PC4279; MUID:97236289; PMID:9125110

A;Accession: PC4282

A;Molecule type: protein

A;Residues: 1-106 <SUZ>

A;Cross-references: UNIPARC:UPI0000176E92

A;Note: E-42

A;Accession: PC4284

A;Residues: 1-106 <SU2>

A;Cross-references: UNIPARC:UPI0000176E92

A;Note: E-56

C;Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjoe

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;14-88/Domain: immunoglobulin homology <IMM>

Query Match

93.9%; Score 46; DB 2; Length 106;

Best Local Similarity 90.9%; Pred. No. 0.032;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11

|||||

Db 22 RASQSVSSYLA 32

RESULT 19

S57444

Ig kappa chain V-J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000

C;Accession: S57444

R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.

submitted to the EMBL Data Library, June 1995

A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuro

A;Reference number: S57408

A;Accession: S57444

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-107 <PAT>

A;Cross-references: UNIPARC:UPI00001137A8; EMBL:X87898; NID:g871275; PIDN:CAA61149.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match

93.9%; Score 46; DB 2; Length 107;

Best Local Similarity 90.9%; Pred. No. 0.032;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11

|||||

Db 24 RASQSVSSYLA 34

RESULT 20

S40344

Ig kappa chain V-J region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40344

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40344

A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-125 <KLE>
 A;Cross-references: UNIPARC:UPI000011615E, EMBL:X72454; NID:G441376; PIDN:CAA51122.1; PID
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 93.8%; Score 46; DB 2; Length 125;
 Best Local Similarity 90.9%; Pred. No. 0.037; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||
 Db 44 RASQSVSTYLA 54

RESULT 21

S16825
 Ig kappa chain V region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S16825
 R;Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
 Eur. J. Immunol. 21, 1221-1227, 1991
 A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
 A;Reference number: S16823; MUID:91243737; PMID:1903706
 A;Accession: S16825
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-86 <BLA>
 A;Cross-references: UNIPARC:UPI0000176D64; EMBL:X54823
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 91.8%; Score 45; DB 2; Length 86;
 Best Local Similarity 90.9%; Pred. No. 0.041; Mismatches 0; Indels 1; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||
 Db 15 RASQSVDSYLA 25

RESULT 22

K1HUHU
 Ig kappa chain V-I region (Hau) - human
 C;Species: Homo sapiens (man)
 C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
 C;Accession: A01868; S02574
 R;Watanabe, S.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 351, 1291-1295, 1970
 A;Title: The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subg
 A;Reference number: A01868; MUID:71032830; PMID:4097974
 A;Accession: A01868
 A;Molecule type: protein
 A;Residues: 1-108 <WAR>
 A;Cross-references: UNIPROT:P01600; UNIPARC:UPI0000012E143
 A;Note: the C region of this chain has the Inv (3) marker
 R;Steiner, V.; Chang, J.Y.
 FEBS Lett. 222, 6-10, 1987
 A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
 A;Reference number: S02572; MUID:88005152; PMID:3115831
 A;Contents: annotation
 C;Comment: This is a Bence Jones protein.
 C;Genetics:

A;Gene: GDB:IGKV1
 A;Cross-references: GDB:136264
 A;Map position: 2p12-2p12

C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
 chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>
 F;23-88/Disulfide bonds: #status predicted

Query Match 91.8%; Score 45; DB 1; Length 108;
 Best Local Similarity 81.8%; Pred. No. 0.052; Mismatches 2; Indels 0; Gaps 0;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||
 Db 24 RASQSISSYLS 34

RESULT 23

S11697
 Ig kappa chain precursor V-III region - human
 C;Species: Homo sapiens (man)
 C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S11697
 R;Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
 J. Mol. Biol. 183, 291-299, 1985
 A;Title: A large section of the gene locus encoding human immunoglobulin variable region;
 A;Reference number: S11697; MUID:85264787; PMID:3927006
 A;Accession: S11697
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-115 <PEC>
 A;Cross-references: UNIPARC:UPI0000115E41; EMBL:X17264; NID:G37898; PIDN:CAA35168.1; PID
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
 C;Genetics:
 A;Introns: 17/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 91.8%; Score 45; DB 2; Length 115;
 Best Local Similarity 90.9%; Pred. No. 0.055; Mismatches 0; Indels 1; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||
 Db 44 RASQGVSSYLA 54

RESULT 24

S29627
 Ig kappa chain V region (60.3 hybridoma) - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C;Accession: S34110; S29627
 R;Walls, M.A.; Hsiao, K.; Harris, L.J.
 Nucleic Acids Res. 21, 2921-2929, 1993
 A;Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains with
 A;Reference number: S34110; MUID:93324379; PMID:8332501
 A;Accession: S34110
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-129 <WA2>
 A;Cross-references: UNIPARC:UPI000011649A; EMBL:Z17330; NID:G38511; PIDN:CAA78978.1; PID
 A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma cells
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
 C;Genetics:

A;Introns: 17/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 91.8%; Score 45; DB 2; Length 129;
 Best Local Similarity 90.9%; Pred. No. 0.062; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||

Db 44 RASQSVGSYLA 54

RESULT 25
S34090

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34090
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34090
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <WAG>
A:Cross-references: UNIPROT:Q9UL79; UNIPARC:UPI0000176DA2; EMBL:X67174
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 82;
Best Local Similarity 81.8%; Pred. No. 0.064;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
||||:||||
Db 15 RASQGISYLA 25

RESULT 26
S16832

Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16832
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16832
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176D68; EMBL:X54830
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 86;
Best Local Similarity 90.9%; Pred. No. 0.067;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
||||:||||
Db 15 RASHSVSSYLA 25

RESULT 27
S34086

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34086
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WAG>

A:Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176D9E; EMBL:X67169
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 86;
Best Local Similarity 90.0%; Pred. No. 0.067;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 10
||||:||||
Db 17 RASQGISYLA 26

RESULT 28
S34084

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34084
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34084
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: UNIPARC:UPI00001198BC; EMBL:X67167
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 87;
Best Local Similarity 90.0%; Pred. No. 0.068;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 10
||||:||||
Db 17 RASQGISYLA 26

RESULT 29
S21523

Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C:Accession: S34079; S21523
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: UNIPARC:UPI000011604C; EMBL:X66039; NID:G33312; PIDN:CAA46838.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 87;
Best Local Similarity 81.8%; Pred. No. 0.068;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
||||:||||
Db 17 RASQGISYLA 27

RESULT 30
S34083

Ig kappa chain V region - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S34083
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993

A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in the germline
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34083
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <WAG>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176D9F; EMBL:X66045
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 89.8%; Score 44; DB 2; Length 87;
Best Local Similarity 90.0%; Pred. No. 0.068;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYL 10
|||||:||||
DB 17 RASQSISSYL 26

RESULT 31

S21522
IG kappa chain V region (patient 10 and 12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34078; S34085; S21522
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in the germline
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34078
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000116052; EMBL:X66046; NID:G33308; PIDN:CAA46845.1; PID
A;Experimental source: patient 10
A;Accession: S34085
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000116052; EMBL:X67168
A;Experimental source: patient 12
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 88;
Best Local Similarity 90.0%; Pred. No. 0.068;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYL 10
|||||:||||
DB 17 RASQSISSYL 26

RESULT 32

S21528
IG kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21528
R;Wagner, S.D.; Luzzatto, L.
submitted to the EMBL Data Library, May 1992
A;Description: V kappa genes rearranged in chronic lymphocytic leukaemia do not show somatic
A;Reference number: S21520
A;Accession: S21528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>

A;Cross-references: UNIPARC:UPI0000116051; EMBL:X66045; NID:G33322; PIDN:CAA46844.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 89.8%; Score 44; DB 2; Length 88;
Best Local Similarity 90.0%; Pred. No. 0.068;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYL 10
|||||:||||
DB 17 RASQSISSYL 26

RESULT 33

S21520
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34077; S21520
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in the germline
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34077
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI000011604A; EMBL:X66037; NID:G33306; PIDN:CAA46836.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 88;
Best Local Similarity 81.8%; Pred. No. 0.068;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSYL 11
|||||:||||
DB 17 RASQGISSYL 27

RESULT 34

S34104
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34104
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in the germline
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34104
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI000011604B; EMBL:X66038; NID:G33310; PIDN:CAA46837.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 88;
Best Local Similarity 81.8%; Pred. No. 0.068;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSYL 11
|||||:||||
DB 17 RASQGISSYL 27

RESULT 35

S21524
IG kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
 C;Accession: S34080; S21524
 R;Wagner, S.D.; Luzzatto, L.
 Eur. J. Immunol. 23, 391-397, 1993
 A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
 A;Reference number: S34076; MUID:93170387; PMID:8436174
 A;Accession: S34080
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-88 <W>
 A;Cross-references: UNIPARC:UPI000011604D; EMBL:X66040; NID:G33314; PIDN:CAA46839.1; PID
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 88;
 Best Local Similarity 81.8%; Pred. No. 0.068;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||
 Db 17 RASQGISSYLA 27

RESULT 36

Ig kappa chain V region (V-kappa 3) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S37521
 R;Klein, U.; Kueppers, R.; Rajewsky, K.
 submitted to the EMBL Data Library, September 1993
 A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
 A;Reference number: S37501
 A;Accession: S37521
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-91 <K>
 A;Cross-references: UNIPARC:UPI0000116587; EMBL:Z26623; NID:G405684; PIDN:CAA81376.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 89.8%; Score 44; DB 2; Length 91;
 Best Local Similarity 90.9%; Pred. No. 0.071;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||
 Db 7 RASQSVSSYLA 17

RESULT 37

Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
 C;Accession: S36264
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.
 A;Reference number: S36256; MUID:93178448; PMID:7679990
 A;Accession: S36264
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-107 <GRI>
 A;Cross-references: UNIPARC:UPI00001180F4; EMBL:Z18845; NID:G33426; PIDN:CAA79297.1; PID
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 107;
 Best Local Similarity 90.0%; Pred. No. 0.083;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 10
 |||||:||||
 Db 24 RASQSISSYLA 33

RESULT 38

S34007
 Ig kappa chain V region - human

C;Species: Homo sapiens (man)
 C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S34007
 R;Mariette, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A;Reference number: S34001; MUID:93209281; PMID:7681398

A;Accession: S34007
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-108 <MAR>
 A;Cross-references: UNIPARC:UPI0000176CC8
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 108;
 Best Local Similarity 81.8%; Pred. No. 0.084;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 |||||:||||
 Db 24 RASQGISSYLA 34

RESULT 39

S44122
 Ig kappa chain V region - human

C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
 C;Accession: S44122
 R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
 submitted to the EMBL Data Library, March 1994

A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
 A;Reference number: S44105
 A;Accession: S44122
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-108 <HAW>
 A;Cross-references: UNIPARC:UPI0000116630; EMBL:Z31390; NID:9472976; PIDN:CAA83265.1; PI
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 108;
 Best Local Similarity 90.0%; Pred. No. 0.084;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 10
 |||||:||||
 Db 24 RASQSISSYLA 33

RESULT 40

S47182
 Ig kappa chain - human

C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C;Accession: S47182
 R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
 submitted to the EMBL Data Library, June 1994

A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patient
 A;Reference number: S47181
 A;Accession: S47182

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
A;Cross-references: UNIPARC:UPI00001161E5; EMBL:X79786; NID:g506422; PIDN:CAA56182.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 44; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.084;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
| | | | |
Db 24 RASQSISSYL 33

Search completed: December 14, 2005, 07:31:51
Job time : 11.9483 secs

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:28 : Search time 59.3621 Seconds
(without alignment)
130.737 Million cell updates/sec

Title: US-10-720-323-4

Perfect score: 49

Sequence: 1 RASQSVSYLA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_trenbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	49	100.0	115	1 KV3I_HUMAN	P04433 homo sapien
2	45	91.8	108	1 KVIH_HUMAN	P01600 homo sapien
3	44	89.8	107	2 Q6S8A9_HUMAN	Q6S8A9 homo sapien
4	44	89.8	108	2 Q9UL77_HUMAN	Q9UL77 homo sapien
5	44	89.8	234	2 Q72473_HUMAN	Q72473 homo sapien
6	44	89.8	236	2 Q6PIH7_HUMAN	Q6PIH7 homo sapien
7	43	87.8	117	1 KVIJ_HUMAN	P01602 homo sapien
8	41	83.7	107	2 Q9UL81_HUMAN	Q9UL81 homo sapien
9	41	83.7	108	2 Q9UL70_HUMAN	Q9UL70 homo sapien
10	41	83.7	129	1 KVIW_HUMAN	P04431 homo sapien
11	41	83.7	236	2 Q72374_HUMAN	Q72374 homo sapien
12	40	81.6	107	1 KVID_HUMAN	P01596 homo sapien
13	40	81.6	108	2 Q9UL83_HUMAN	Q9UL83 homo sapien
14	40	81.6	128	1 Q9UL83_HUMAN	Q9UL83 homo sapien
15	39	79.6	108	2 KVIN_HUMAN	P06311 homo sapien
16	39	79.6	108	2 Q9UL79_HUMAN	Q9UL79 homo sapien
17	39	79.6	236	2 Q6GMX8_HUMAN	Q6GMX8 homo sapien
18	38.5	78.6	100	1 KVIC_HUMAN	P01621 homo sapien
19	38.5	78.6	109	1 KVB3_HUMAN	P01620 homo sapien
20	38.5	78.6	109	2 Q9UL86_HUMAN	Q9UL86 homo sapien
21	38.5	78.6	109	2 Q9UL78_HUMAN	Q9UL78 homo sapien
22	38.5	78.6	129	1 KVB3L_HUMAN	P18135 homo sapien
23	38.5	78.6	129	1 KVB3M_HUMAN	P01621 homo sapien
24	38	77.6	117	1 KVI0_RABIT	P01691 oryctolagus
25	38	77.6	1401	2 Q51PF3_MAGGR	Q51PF3 magnaporthe
26	37.5	76.5	109	1 KVF3F_HUMAN	P01624 homo sapien
27	37	75.5	108	1 KVI1F_HUMAN	P01598 homo sapien
28	37	75.5	108	1 KVI1F_HUMAN	P04430 homo sapien
29	37	75.5	108	1 KVS5K_MOUSE	P01644 mus sapien
30	37	75.5	108	1 KVS5L_MOUSE	P01645 mus sapien
31	37	75.5	108	1 KV5M_MOUSE	P01646 mus sapien

32	37	75.5	129	1 KV3H_HUMAN	P04207 homo sapien
33	37	75.5	916	2 Q7NDD9_GLOVI	Q7NDD9 gloebacter
34	36	73.5	108	1 KV5D_MOUSE	P01636 mus musculus
35	36	73.5	114	2 Q30750_PASMU	Q30750 pasteurella
36	36	73.5	139	2 Q7VPF1_HAEDU	Q7VPF1 haemophilus
37	36	73.5	211	2 Q4PNG6_9BACT	Q4PNG6 uncultured
38	36	73.5	235	2 Q6GMW0_HUMAN	Q6GMW0 homo sapien
39	36	73.5	236	2 Q6GMX9_HUMAN	Q6GMX9 homo sapien
40	36	73.5	262	2 Q6SZ11_MOUSE	Q6SZ11 mus musculus
41	36	73.5	670	1 SC5A2_MOUSE	Q92317 mus musculus
42	36	73.5	670	1 SC5A2_RAT	P33792 rattus norv
43	36	73.5	672	1 SC5A2_RABIT	P26430 oryctolagus
44	36	73.5	673	2 Q6XUI1_BOVIN	Q6XUI1 bos taurus
45	36	73.5	680	2 Q5E9G8_BOVIN	Q5E9G8 bos taurus
46	36	73.5	1185	2 Q53P25_ORISA	Q53P25 oryza sativ
47	36	73.5	3001	2 Q8QXLO_9POTV	Q8QXLO scallion mo
48	35.5	72.4	235	2 Q6GMV9_HUMAN	Q6GMV9 homo sapien
49	35.5	72.4	236	2 Q6PIL8_HUMAN	Q6PIL8 homo sapien
50	35	71.4	115	1 KV5F_MOUSE	P01638 mus musculus
51	35	71.4	236	2 Q6GMX0_HUMAN	Q6GMX0 homo sapien
52	35	71.4	236	2 Q6PIT5_HUMAN	Q6PIT5 homo sapien
53	35	71.4	236	2 Q7TS98_MOUSE	Q7TS98 mus musculus
54	35	71.4	375	2 Q6SQB6_MANSM	Q6SQB6 manheimia
55	35	71.4	471	2 Q994E4_AADEN	Q994E4 porcine ade
56	35	71.4	678	1 LGP2_MOUSE	Q99J87 mus musculus
57	35	71.4	705	2 Q9LVN9_ARATH	Q9LVN9 arabidopsis
58	35	71.4	709	2 Q97FZ1_CLOAB	Q97FZ1 clostridium
59	35	71.4	764	2 Q4UHP6_THEAN	Q4UHP6 theileria a
60	35	71.4	787	2 Q76PT3_VARV	Q76PT3 variola min
61	35	71.4	787	2 Q89093_VARV	Q89093 variola vir
62	35	71.4	6973	2 Q7QXR7_GIALA	Q7QXR7 giardia lam
63	34.5	70.4	109	1 KV3D_HUMAN	P01622 homo sapien
64	34.5	70.4	109	1 KV3E_HUMAN	P01623 homo sapien
65	34.5	70.4	116	1 KV3J_HUMAN	P0434 homo sapien
66	34	69.4	108	1 KV08_RABIT	P01689 oryctolagus
67	34	69.4	108	1 KVI1E_HUMAN	P01597 homo sapien
68	34	69.4	108	1 KVI1L_HUMAN	P01604 homo sapien
69	34	69.4	108	1 KVI1S_HUMAN	P01611 homo sapien
70	34	69.4	108	1 KV5N_MOUSE	P01647 mus musculus
71	34	69.4	108	1 KV5O_MOUSE	P01648 mus musculus
72	34	69.4	108	1 KV5P_MOUSE	P01649 mus musculus
73	34	69.4	109	2 Q9UL85_HUMAN	Q9UL85 homo sapien
74	34	69.4	111	1 KV3H_MOUSE	P01660 mus musculus
75	34	69.4	111	1 KV3J_MOUSE	P01662 mus musculus
76	34	69.4	111	1 KV3K_MOUSE	P01663 mus musculus
77	34	69.4	117	1 KV1I_HUMAN	P01601 homo sapien
78	34	69.4	128	1 KV5E_MOUSE	P01637 mus musculus
79	34	69.4	131	1 KV3I_MOUSE	P01661 mus musculus
80	34	69.4	147	2 Q6SD76_BACLD	Q6SD76 bacillus li
81	34	69.4	209	2 Q8XWU0_RALSO	Q8XWU0 ralstonia s
82	34	69.4	336	1 LEU3_MYCLE	Q33117 mycobacteri
83	34	69.4	381	1 CARA_HALER	Q8R884 halomonas e
84	34	69.4	445	2 Q52293_9RHIZ	Q52293 agrobacteri
85	34	69.4	616	2 Q4HSN4_9DEIO	Q4HSN4 deionococcus
86	34	69.4	678	2 Q4IIQ6_GIBZE	Q4IIQ6 gibberella
87	34	69.4	753	2 Q4N7W0_THEPA	Q4N7W0 theileria p
88	34	69.4	780	2 Q6A5W9_PROAC	Q6A5W9 proptonibac
89	34	69.4	828	2 Q8L274_PROVU	Q8L274 proteus vul
90	33	67.3	50	2 Q6LBV5_HUMAN	Q6LBV5 homo sapien
91	33	67.3	67	2 Q72C91_DESVH	Q72C91 desulfovibr
92	33	67.3	92	1 KV09_RABIT	P01690 oryctolagus
93	33	67.3	118	2 Q60CB6_METCA	Q60CB6 methylococc
94	33	67.3	160	2 Q7U2B0_MYCBO	Q7U2B0 mycobacteri
95	33	67.3	160	2 Q07234_MYCTU	Q07234 mycobacteri
96	33	67.3	162	2 Q933V8_SALTY	Q933V8 salymonella
97	33	67.3	162	2 Q93SZ1_SALET	Q93SZ1 salmonella
98	33	67.3	162	2 Q93SZ2_SALNE	Q93SZ2 salmonella
99	33	67.3	162	2 Q93SZ5_SALDU	Q93SZ5 salmonella
100	33	67.3	162	2 Q93SZ7_SALET	Q93SZ7 salmonella

ALIGNMENTS

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RESULT 1
KV31_HUMAN
ID KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region Vg precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within
RL Nucleic Acids Res. 12:9229-9236 (1984).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X01668; -, NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; A01900; K3HUVG.
DR HSSP; P01625; IBEQ.
DR SMR; P04433; 21-115.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-III region Vg.
FT REGION 21 43 Framework-1.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Framework-2.
FT REGION 70 76 Framework-3.
FT REGION 77 108 Complementarity-determining-2.
FT REGION 109 115 Complementarity-determining-3.
FT DISULFID 43 108 By similarity.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
| | | | |
DB 44 RASQSVSSYLA 54

RESULT 2
KV1H_HUMAN
ID KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.

Query Match 91.8%; Score 45; DB 1; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
| | | | |
DB 24 RASQSVSSYLA 34

RESULT 3
Q96SA9_HUMAN
ID Q96SA9_HUMAN PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mycosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
RT antibody V region genes".
RL J. Immunol. 161:2020-2031 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
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RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal strational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal strational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652(1991).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1903706;
RA Blaison G., Kuntz J.L., Pasquali J.L.;
RT "Molecular analysis of V kappa III variable regions of polyclonal
RT rheumatoid factors during rheumatoid arthritis.";
RL Eur. J. Immunol. 21:1221-1227(1991).
DR EMBL; U96396; AAB68785.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S31977; S31977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSSP; P01607; 1BWW.
DR SMR; Q96SA9; 1-107.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 89.8%; Score 44; DB 2; Length 107;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db |||||:||||
24 RASQSIS5YL 33

RESULT 4
ID Q9UL77 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1516616;
RA Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT "Human monoclonal strational autoantibodies isolated from thymic B
RT lymphocytes of patients with myasthenia gravis use VH and VL gene
RT segments associated with the autoimmune repertoire.";
RL Eur. J. Immunol. 22:2231-2236(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035037; AAD56273.1; -; mRNA.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWW.
DR SMR; Q9UL77; 1-108.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 89.8%; Score 44; DB 2; Length 108;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db |||||:||||
24 RASQSIS5YL 33

RESULT 5
ID Q7Z473 HUMAN PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE IGKC protein.
DE Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berger J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -; mRNA.
DR HSSP; P01834; IHEZ.
DR SNR; Q7Z473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 89.8%; Score 44; DB 2; Length 234;
Best Local Similarity 81.8%; Pred. No. 0.63;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
Db |||||:||||
44 RASQSIGSYLA 54

RESULT 6
Q6PIH7 HUMAN
ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Baha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -; mRNA.
DR HSSP; P01607; IAR2.
DR SNR; Q6PIH7; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 89.8%; Score 44; DB 2; Length 236;
Best Local Similarity 81.8%; Pred. No. 0.63;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
Db |||||:||||
46 RASQGISYLA 56

RESULT 7
KVJQ_HUMAN
ID KVJQ_HUMAN STANDARD; PRT; 117 AA.
AC P01602;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region HKI02 precursor (Fragment).
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RL kappa genes and a pseudogene.";
RL Nature 288:730-733(1990).
CC -----
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CC -----
DR EMBL; J00245; AAA59087.1; -; Genomic DNA.
DR EMBL; Z00001; CAA77292.1; -; Genomic DNA.
DR FRR; A01882; KJH12.
DR HSSP; P01607; 1BWW.
DR SNR; P01602; 23-117.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR HGNC; HGNC:5741; IGKV1-5.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
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DR SMART: SMO0406; IGV: 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 Ig kappa chain V-I region HK102.
FT REGION 23 45 Framework-1.
FT REGION 46 56 Complementarity-determining-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Framework-3.
FT REGION 111 >117 Complementarity-determining-3.
FT DISULFID 45 110 By similarity.
FT NON TER 117
SQ SEQUENCE 117 AA; 12768 MW; AD1DF3A40AF1A9B CRC64;

Query Match 87.8%; Score 43; DB 1; Length 117;
Best Local Similarity 81.8%; Pred. No. 0.47;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 46 RASQSISSYLA 56

RESULT 8
Q9UL81 HUMAN PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCB1_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -; mRNA.
DR HSP; P01607; IBBW.
DR SMR; Q9UL81; 1-107.
DR InterPro; IPR007110; IG-Like.
DR SMART; SMO0406; IGV: 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 83.7%; Score 41; DB 2; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 24 RASQSISSYL 33

RESULT 9
Q9UL70 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCB1_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -; mRNA.
DR PIR; PH0863; PH0863.
DR HSP; P01607; IBBW.
DR SMR; Q9UL70; 1-108.
DR InterPro; IPR007110; IG-Like.
DR SMART; SMO0406; IGV: 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 83.7%; Score 41; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 1.2;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 24 RASQSISSYLA 34

RESULT 10
KV1W HUMAN STANDARD; PRT; 129 AA.
AC KV1W;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCB1_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
MEDLINE=85014148; PubMed=6091049;
Klobeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.

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DR PIR; A01883; KIHUWK.
DR HSSP; P01607; IBWW.
DR SMR; P04431; 23-129.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG kappa chain V-I region Walker.
FT REGION 23 45 Framework-1.
FT REGION 46 56 Complementarity-determining-1.
FT REGION 57 71 Framework-2.
FT REGION 72 78 Complementarity-determining-2.
FT REGION 79 110 Framework-3.
FT REGION 111 119 Complementarity-determining-3.
FT REGION 120 129 Framework-4.
FT DISULFID 45 110 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 83.7%; Score 41; DB 1; Length 129;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 46 RASQISNYL 55

RESULT 11
Q723Y4 HUMAN
ID Q723Y4 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.

TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC005332; AA05332.1; -; mRNA.
DR HSSP; P01834; IHEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 83.7%; Score 41; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 2.9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 46 RASQDISNYLA 56

RESULT 12
KVID_HUMAN
ID KVID_HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
protein.";
RL Eur. J. Biochem. 49:377-391(1974).
CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
marker.
CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01864; KIHUAR.
DR HSSP; P80362; IWTL.
DR SMR; P01596; 1-107.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW Immunoglobulin V region.
FT CARBOHYD 28 28 N-linked (GlcNAc... ).
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11704 MW; E1BF0DF9844C3346 CRC64;

Query Match 81.6%; Score 40; DB 1; Length 107;

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Best Local Similarity 72.7%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 24 RASQSVSSYLA 34

RESULT 13
Q9UL83 HUMAN
ID Q9UL83 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.W.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation.";
RL Euk. J. Immunol. 23:391-397(1993).
DR EMBL; AF035031; AAD56267.1; -; mRNA.
DR PIR; B30609; B30609.
DR PIR; C30609; C30609.
DR PIR; D30609; D30609.
DR PIR; S34098; S34098.
DR PIR; S34099; S34099.
DR HSSP; P01625; ILVE.
DR SMR; Q9UL83; 1-108.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 81.6%; Score 40; DB 2; Length 108;
Best Local Similarity 90.9%; Pred. No. 2;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 24 RASQSVSSYLA 34

RESULT 14
KV3K HUMAN
ID KV3K HUMAN STANDARD; PRT; 128 AA.
AC P03311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
```

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC -----
DR EMBL; Z00021; CAA77316.1; -; Genomic_DNA.
DR PIR; A01899; K3HU41.
DR HSSP; P01625; ISEQ.
DR SMR; P06311; 21-128.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128
FT REGION 21 43
FT REGION 44 54
FT REGION 55 69
FT REGION 70 76
FT REGION 77 108
FT REGION 109 117
FT REGION 118 128
FT DISULFID 43 108
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 81.6%; Score 40; DB 1; Length 128;
Best Local Similarity 90.9%; Pred. No. 2.4;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
Db 44 RASQSVSSYLA 54

RESULT 15
KV1N HUMAN
ID KV1N HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
```



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CC removed.
CC -----
CC PIR: A01872; K1HUOU.
CC HSP; P01607; 1BWV.
CC GO: GO:0005576; C:extracellular region; NAS.
CC GO: GO:0003823; F:antigen binding; NAS.
CC GO: GO:0006955; P:immune response; NAS.
CC InterPro: IPR007110; IG-like.
CC SMART: SM00406; IG_v.
CC PROSITE; PS00835; IG-Like; 1.
CC Direct protein sequencing; Immunoglobulin domain;
CC Immunoglobulin V region.
CC REGION 1 23
CC REGION 24 34
CC REGION 35 49
CC REGION 50 56
CC REGION 57 88
CC REGION 89 97
CC REGION 98 107
CC DISULFID 23 88
CC NON_TER 108 108
CC SEQUENCE 108 AA; 11779 MW; 8283D4A24105827E CRC64;

Query Match 79.6%; Score 39; DB 1; Length 108;
Best Local Similarity 70.0%; Pred. No. 3.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 24 RASZTISSYL 33

RESULT 16
Q9UL79 HUMAN PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobbeck H.G., Zachau H.G.;
RT "Ongoing v kappa-J kappa recombination after formation of a productive
RT v kappa-J kappa coding joint."
RL Eur. J. Immunol. 22:1561-1565(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are

```

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RT distributed over a large portion of the V kappa locus and do not show
RT somatic mutation."
RL Eur. J. Immunol. 23:391-397(1993).
DR EMBL; AF035035; AAD56271.1; -; mRNA.
DR PIR; S23638; S23638.
DR PIR; S30521; S30521.
DR PIR; S34090; S34090.
DR HSP; P01607; 1BWV.
DR SMR; Q9UL79; 1-108.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IG_v.
DR PROSITE; PS00835; IG-Like; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 79.8%; Score 39; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 3.3;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 11
Db 24 RMSQGISSYL 34

RESULT 17
Q6GNX8 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GNX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1601042;
RA Huber C., Klobbeck H.G., Zachau H.G.;
RT "Ongoing v kappa-J kappa recombination after formation of a productive
RT v kappa-J kappa coding joint."
RL Eur. J. Immunol. 22:1561-1565(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are

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DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; CI-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559BFC9 CRC64;

Query Match 79.6%; Score 39; DB 2; Length 236;
 Best Local Similarity 72.7%; Pred. No. 7.9;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYLA 11
 ||||| :|||
 Db 46 RASQGISWLA 56

RESULT 18

KV3C HUMAN
 ID KV3C HUMAN STANDARD; PRT; 100 AA.

AC P01621;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Ig kappa chain V-III region NG9 precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

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 CC PIR; A01894; K3HUNG.
 DR HSSP; P01621; 1EQ.
 DR SMR; P01621; 6-99.
 DR Ensemble; ENSG00000169769; Homo sapiens.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-LIKE.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL <1 4
 FT CHAIN 5 100 Ig kappa chain V-III region NG9.
 FT DISULFID 27 93 By similarity.
 FT NON_TER 1 1
 FT NON_TER 100 100
 SQ SEQUENCE 100 AA; 10729 MW; 5D9AF363CC52632F CRC64;

Query Match 78.6%; Score 38.5; DB 1; Length 100;
 Best Local Similarity 91.7%; Pred. No. 3.9;
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSV-SSYLA 11

Db 28 RASQSVSSYLA 39
 ||||| |||||

RESULT 19

KV3B HUMAN
 ID KV3B HUMAN STANDARD; PRT; 109 AA.

AC P01620;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Ig kappa chain V-III region SIE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC PIR; A01892; K3HUSI.
 DR HSSP; P01625; 1LVE.
 DR SMR; P01620; 1-109.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-LIKE.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DISULFID 23 89 By similarity.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 78.6%; Score 38.5; DB 1; Length 109;
 Best Local Similarity 91.7%; Pred. No. 4.3;
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSVS-SYLA 11
 ||||| |||||

Db 24 RASQSVSNSYLA 35

RESULT 20

Q9UL86 HUMAN
 ID Q9UL86 HUMAN PRELIMINARY; PRT; 109 AA.

AC Q9UL86;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC PIR; A01892; K3HUSI.
 DR HSSP; P01625; 1LVE.
 DR SMR; P01620; 1-109.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-LIKE.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region.
 FT DISULFID 23 89 By similarity.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 78.6%; Score 38.5; DB 1; Length 109;
 Best Local Similarity 91.7%; Pred. No. 4.3;
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSVS-SYLA 11
 ||||| |||||

Db 24 RASQSVSNSYLA 35

Query Match 78.6%; Score 38.5; DB 1; Length 109;
 Best Local Similarity 91.7%; Pred. No. 4.3;
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSV-SSYLA 11

```

RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR ENBL; AF035028; AAD56264.1; -; mRNA.
DR PIR; B30607; B30607.
DR PIR; B30601; I30601.
DR HSP; P01625; 1EK3.
DR SMR; Q9UL86; 1-109.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 78.6%; Score 38.5; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 4.3;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 RASQSV-SSYLA 11
Db ||||| |||||
24 RASQSVSSSYLA 35

RESULT 21
Q9UL78 HUMAN
ID Q9UL78 HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1373487;
RA Zebedes S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
RA DeGraw J., Pyati J., LaPolla R., Burton D.R., Ierner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
RT antigen.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "v kappa gene segments rearranged in chronic lymphocytic leukemia are
RT distributed over a large portion of the v kappa locus and do not show
RT somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1552291;
RA Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
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RT "Evidence for somatic selection of natural autoantibodies.";
RL J. Exp. Med. 175:983-991(1992).
DR ENBL; AF035036; AAD56272.1; -; mRNA.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.
DR PIR; H44151; H44151.
DR PIR; I30601; I30601.
DR PIR; PH0963; PH0963.
DR PIR; PH0964; PH0964.
DR PIR; PH0965; PH0965.
DR PIR; S33988; S33988.
DR PIR; S34096; S34096.
DR HSP; P01625; 1EK3.
DR SMR; Q9UL78; 1-109.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 78.6%; Score 38.5; DB 2; Length 109;
Best Local Similarity 91.7%; Pred. No. 4.3;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 RASQSV-SSYLA 11
Db ||||| |||||
24 RASQSVSSSYLA 35

RESULT 22
KV3L HUMAN
ID KV3L HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC -----
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CC removed.
CC -----
DR PIR: P10022; K3HUHA.
DR HSSP: P01625; 1EQ.
DR SMR: P18135; 21-129.
DR Ensembl: ENSG00000169769; Homo sapiens.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT REGION 21 43
FT REGION 44 55
FT REGION 56 70
FT REGION 71 77
FT REGION 78 109
FT REGION 110 118
FT REGION 119 129
FT DISULFID 43 109
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match 78.6%; Score 38.5; DB 1; Length 129;
Best Local Similarity 91.7%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSV-SSYLA 11
Db 44 RASQSVSSSYLA 55

RESULT 23
KV3M HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- Disease: The protein is one of the surface immunoglobulin M
autoantibodies expressed in patients with chronic lymphocytic
leukemia.
CC -----
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CC use as long as its content is in no way modified and this statement is not
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CC -----
DR PIR: P10021; K3HUHI.
DR HSSP: P01625; 1EQ.
DR SMR: P18136; 21-129.
DR Ensembl: ENSG00000169769; Homo sapiens.
DR GO: GO:0005576; C:extracellular region; NAS.

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DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT REGION 21 43
FT REGION 44 55
FT REGION 56 70
FT REGION 71 77
FT REGION 78 109
FT REGION 110 118
FT REGION 119 129
FT DISULFID 43 109
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2B874D6 CRC64;

Query Match 78.6%; Score 38.5; DB 1; Length 129;
Best Local Similarity 91.7%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSV-SSYLA 11
Db 44 RASQSVSSSYLA 55

RESULT 24
KV10 RABIT
ID KV10_RABIT STANDARD; PRT; 117 AA.
AC P01691;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V region 12F2 precursor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83273646; PubMed=6410392;
RA Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
RT "cDNA clone encoding a complete rabbit immunoglobulin kappa light
chain of b4 allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
CC -1- MISCELLANEOUS: This clone was derived from the rabbit-mouse
hybridoma 12F2; the chain produced is a monoclonal antibody
against streptococcal group C vaccine.
CC -----
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CC -----
DR EMBL: K01358; AAB59259.1; ALT_TERM; mRNA.
DR PIR: A01954; K4RBF2.
DR HSSP: P01607; 1BWW.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Hybridoma; Immunoglobulin domain; Immunoglobulin V region;
Monoclonal antibody; Signal.
FT SIGNAL <1 6
FT CHAIN 7 117
FT REGION 7 29
FT REGION 30 40
FT REGION 41 55

```

Query Match 76.5%; Score 37.5; DB 1; Length 109;

Best Local Similarity 83.3%; Pred. No. 7;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 RASQSVS-SYLA 11
|||||:|
Db 24 RASQSIINSYLA 35

RESULT 27

KVIF HUMAN
ID KVIF HUMAN STANDARD; PRT; 108 AA.
AC P01598;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=71064023; PubMed=5489770;
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RL acid sequence of the light chain."
RL Biochemistry 9:3155-3161(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds."
RL Biochemistry 9:3188-3196(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.

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PIR; A90562; KIHUEU.
DR HSSP; P01607; 1BWW.
DR SMR; P01598; 1-107.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 9;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RASQSVS-SYLA 11
|||||:|
Db 24 RASQSIINSYLA 35

RESULT 28

KVIV HUMAN
ID KVIV HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwulet F.B., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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PIR; A01878; KIHUBN.
DR HSSP; P80362; 1WTL.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 9;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RASQSVS-SYLA 11
|||||:|

Db 24 RASQSIINTWLA 34
|||||:|

RESULT 28

KVIV HUMAN
ID KVIV HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwulet F.B., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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use as long as its content is in no way modified and this statement is not
removed.

PIR; A01878; KIHUBN.
DR HSSP; P80362; 1WTL.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IG_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 108;
Best Local Similarity 72.7%; Pred. No. 9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RASQSVS-SYLA 11
|||||:|

Db 24 RASQSVTYNYVA 34
|||||:|

RESULT 29

KVSK MOUSE
ID KVSK MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;


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FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11999 MW; 4C98599C08EBA09A CRC64;

Query Match
Best Local Similarity 75.5%; Score 37; DB 1; Length 108;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 24 RASQDISNYL 33
|||||:|:|

RESULT 32
KV3H HUMAN
ID KV3H HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M12740; AAAS8992.1; -; Genomic_DNA.
DR HSSP; P01625; 1LVE.
DR SMR; P04207; 21-129.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region CLL.
FT REGION 21 43 Framework-1.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Framework-2.
FT REGION 70 76 Complementarity-determining-2.
FT REGION 77 108 Framework-3.
FT REGION 109 118 Complementarity-determining-3.
FT REGION 119 129 JKL segment.
FT DISULFID 43 108 By similarity.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match
Best Local Similarity 75.5%; Score 37; DB 1; Length 129;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Best Local Similarity 81.8%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 11
Db 44 RASQSVSNLA 54
|||||:|:|

RESULT 33
Q7NDD9 GLOVI
ID Q7NDD9 GLOVI PRELIMINARY; PRT; 916 AA.
AC Q7NDD9;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Glr4296 protein.
GN OrderedLocusNames=glr4296;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Teuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpō S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
DR EMBL; BA000045; BAC92237.1; -; Genomic_DNA.
DR HSSP; P06129; 1UJW.
DR GO; GO:0019867; C:outer membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000531; TonB_receptor.
DR Pfam; PF00593; TonB_dep_Rc; 1.
KW Complete proteome; Membrane; Outer membrane; TonB box.
SQ SEQUENCE 916 AA; 100215 MW; 0798A1FD997489A3 CRC64;

Query Match
Best Local Similarity 75.5%; Score 37; DB 2; Length 916;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SQSVSSYL 11
Db 508 SQSVNSYL 516
|||||:|:|

RESULT 34
KVSD MOUSE
ID KVSD MOUSE STANDARD; PRT; 108 AA.
AC P01636;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region MOPC 149.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX STRAIN=BAUS/c;
RX MEDLINE=82057806; PubMed=6795447; DOI=10.1016/0161-5890(80)90176-5;
RA Appella E., Alvarez V.L.;
RT "Amino acid sequence of the variable region of M149 mouse myeloma
RT light chain: comparison with the nucleotide sequence of K2 and K3
RT clones.";
RL Mol. Immunol. 17:1507-1513(1980).
```


CC -1- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -----
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CC removed.
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DR PIR; A01919; KIMS49.
DR PDB; 1ARI; X-ray; C=..
DR Ensembl; ENSMUSG0000062574; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23
FT REGION 24 34
FT REGION 35 49
FT REGION 50 56
FT REGION 57 88
FT REGION 89 97
FT REGION 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12030 MW; 0B5244D2B410D84C CRC64;

Query Match 73.5%; Score 36; DB 1; Length 108;
Best Local Similarity 63.6%; Pred. No. 15;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSYLA 11
|||:: ||||
Db 24 RASENIYSYLA 34

RESULT 35
O30750 PASMU
ID O30750 PASMU PRELIMINARY; PRT; 114 AA.
AC O30750;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=0131 Izatnager P25;
RX MEDLINE=97093285; PubMed=8938847; DOI=10.1016/S0034-5288(96)90063-6;
RA Townsend K.M., Dawkins H.J., Zeng B.J., Watson M.W.,
RP Papadimitriou J.M.;
RT "Cloning of a unique sequence specific to isolates of type B:2
RT Pasteurella multocida.";
RL Res. Vet. Sci. 61:199-205(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=0131 Izatnager P25;
RX MEDLINE=98201943; PubMed=9542944;
RA Townsend K.M., Frost A.J., Lee C.W., Papadimitriou J.M.,
RA Dawkins H.J.S.;
RT "Development of PCR assays for species- and type-specific
RT identification of Pasteurella multocida isolates.";
RL J. Clin. Microbiol. 36:1096-1100(1998).
DR EMBL; AF016260; AAB69129.1; -; Genomic_DNA.
DR InterPro; IPR009752; DUF1320.
DR Pfam; PF07030; DUF1320; 1.
KW Hypothetical protein.
FT NON TER 1 1
SQ SEQUENCE 114 AA; 12860 MW; 364F3776E3DB6340 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 114;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQSVSYLA 11
|||:: ||||
Db 16 ASQTIDSYLA 25

RESULT 36
Q7VPF1 HAEDU
ID Q7VPF1 HAEDU PRELIMINARY; PRT; 139 AA.
AC Q7VPF1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mu-like prophage protein GP36.
GN OrderedLocusNames=HD0134;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017151; AAP95130.1; -; Genomic_DNA.
DR InterPro; IPR009752; DUF1320.
DR Pfam; PF07030; DUF1320; 1.
KW Complete proteome.
SQ SEQUENCE 139 AA; 15474 MW; DCF5A10336133DC CRC64;

Query Match 73.5%; Score 36; DB 2; Length 139;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQSVSYLA 11
|||:: ||||
Db 41 ASQTIDSYLA 50

RESULT 37
Q4PNG6_9BACT
ID Q4PNG6_9BACT PRELIMINARY; PRT; 211 AA.
AC Q4PNG6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Putative metallo-beta-lactamase superfamily protein.
OS Uncultured marine bacterium 66A03.
OC Bacteria; environmental samples.
OX NCBI_TaxID=331677;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16008504;
RA Sabehi G., Loy A., Jung K.H., Partha R., Spudich J.L., Isaacson T.,
RA Hirschberg J., Wagner M., Beja O.;
RT "New Insights into Metabolic Properties of Marine Bacteria Encoding
RT Proteorhodopsins.";
RL PLoS Biol. 3:E273-E273(2005).
DR EMBL; DQ065755; AAY68333.1; -; Genomic_DNA.
DR InterPro; IPR005503; FliL.
DR Pfam; PF03748; FliL; 1.
SQ SEQUENCE 211 AA; 23681 MW; 27C7A1E355F1C9BE CRC64;

Query Match 73.5%; Score 36; DB 2; Length 211;
Best Local Similarity 72.7%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
||:|||||
DB 122 RANLAVSSYLA 132

RESULT 38

Q6GMW0 HUMAN
ID Q6GMW0 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKVI-5 protein.
GN Name=IGKVI-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smallos D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -, mRNA.
DR SMR; Q6GMW0; 21-233.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003306; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 235;
Best Local Similarity 72.7%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
|||||:
DB 44 RASQSISSYLA 54

RESULT 39

Q6GMX9 HUMAN
ID Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smallos D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -, mRNA.
DR SMR; Q6GMX9; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003306; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25924 MW; FD2093DC560CF7 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 236;
Best Local Similarity 72.7%; Pred. No. 36;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RASQSVSSYLA 11
|||||:
DB 46 RASQNVSRWLA 56

RESULT 40

Q65Z11 MOUSE
ID Q65Z11 MOUSE PRELIMINARY; PRT; 262 AA.
AC Q65Z11;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-HIV-1 reverse transcriptase single-chain variable.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=96211469; PubMed=8648670;
RA Shaheen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;
RT "Targeting human immunodeficiency virus type 1 reverse transcriptase
RT by intracellular expression of single-chain variable fragments to
RT inhibit early stages of the viral life cycle.";
RL J. Virol. 70:3392-3400(1996).
DR EMBL; U48716; AB64342.1; -; mRNA.
DR SMR; Q65211; 2-132.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Immunoglobulin domain; RNA-directed DNA polymerase.
SQ SEQUENCE 262 AA; 27842 MW; 7DF20138E53865E4 CRC64;

Query Match 73.5%; Score 36; DB 2; Length 262;
Best Local Similarity 70.0%; Pred No. 40;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RASQSVSSYL 10
Db 25 RASQSIDFL 34
|||||:|

Search completed: December 14, 2005, 07:30:49
Job time : 61.3621 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:11:28 : Search time 39.8276 Seconds
(without alignments)
77.224 Million cell updates/sec

Title: US-10-720-323-5

Perfect score: 34

Sequence: 1 DASNRAT 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004as.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	4	AAB85369
2	34	100.0	7	4	AAB66417 Human Fab
3	34	100.0	7	5	ABP62391 Human Imm
4	34	100.0	7	5	AAU76331 Human ant
5	34	100.0	7	6	ABP96285 Anti-HTNF
6	34	100.0	7	6	AAE38098 Human COU
7	34	100.0	7	6	AAE38074 Human 2H9
8	34	100.0	7	7	ADD69239 Human lig
9	34	100.0	7	7	ADD69233 Human lig
10	34	100.0	7	7	ADD69236 Human lig
11	34	100.0	7	8	ADM41607 Interleuk
12	34	100.0	7	8	ADS88068 Human CD2
13	34	100.0	7	8	ADS88074 Human CD2
14	34	100.0	7	8	ADS88080 Human CD2
15	34	100.0	7	8	ADS19300 Light cha
16	34	100.0	7	8	ADS52433 Fab targe
17	34	100.0	7	8	ADS52385 Fab targe
18	34	100.0	7	9	ADM07071 Anti-Psaa
19	34	100.0	7	9	ADM07087 Anti-Psaa
20	34	100.0	7	9	ADM77463 Human pla
21	34	100.0	7	9	ADY26808 Human ant
22	34	100.0	7	9	ADY26814 Human ant
23	34	100.0	7	9	ADY93861 Anti-SARS
24	34	100.0	7	9	Aea53720 Novel hum

25	34	100.0	7	9	AEA53713
26	34	100.0	7	9	AEA45053
27	34	100.0	7	9	AEB01040 Human IP1
28	34	100.0	7	9	AEB01035 Human IP1
29	34	100.0	7	9	AEB01042 Human IP1
30	34	100.0	7	9	AEB28710 Human CDR
31	34	100.0	7	9	AEB28758 Human CDR
32	34	100.0	8	7	ADD89875 Human ant
33	34	100.0	8	8	ADS64650 Human ant
34	34	100.0	88	8	ADU04212 Human Imm
35	34	100.0	94	7	ADD69248 Human lig
36	34	100.0	95	6	ABO27154 Human ger
37	34	100.0	95	6	ABO27153 Human ger
38	34	100.0	95	7	ADF10195 Antibody
39	34	100.0	95	7	ADF10093 VEGF anti
40	34	100.0	95	7	ADF10196 Antibody
41	34	100.0	95	7	ADF09989 Antibody
42	34	100.0	95	7	ADF09988 Antibody
43	34	100.0	95	7	ADF10094 VEGF anti
44	34	100.0	95	7	ADJ80273 V kappa ge
45	34	100.0	95	7	ADJ80274 V kappa ge
46	34	100.0	95	8	ADO07342 Human ant
47	34	100.0	95	8	ADO07343 Human ant
48	34	100.0	95	8	ADU86536 Immunoglo
49	34	100.0	95	8	ADU86537 Immunoglo
50	34	100.0	95	9	ADY75448 Human ger
51	34	100.0	95	9	ADY75447 Human ger
52	34	100.0	95	9	AEA53928 Novel hum
53	34	100.0	95	9	AEB13648 Human var
54	34	100.0	95	9	AEB13649 Human var
55	34	100.0	96	9	AEA53874 Novel hum
56	34	100.0	101	9	AEB01068 Human lig
57	34	100.0	102	9	ADY33953 Anti-Tie
58	34	100.0	102	9	ADY33949 Anti-Tie
59	34	100.0	102	9	ADY33961 Anti-Tie
60	34	100.0	104	2	AAW31723 Alpha lig
61	34	100.0	104	9	ADZ42036 Ig L chai
62	34	100.0	104	9	ADZ42035 Ig L chai
63	34	100.0	105	7	ABR61567 HIV-1 neu
64	34	100.0	106	8	AD122136 Anti-plat
65	34	100.0	106	9	ADM07075 Anti-Psaa
66	34	100.0	107	4	AAB80988 Human ant
67	34	100.0	107	4	AAB85350 Antibody
68	34	100.0	107	4	AAB66414 Human Fab
69	34	100.0	107	6	ABR54915 Light cha
70	34	100.0	107	6	ABR54917 Light cha
71	34	100.0	107	6	ABR54916 Light cha
72	34	100.0	107	6	AAE38061 Human 2H9
73	34	100.0	107	6	ABR55830 Kappa cha
74	34	100.0	107	8	AD122135 Anti-plat
75	34	100.0	107	8	ADO07301 Human pro
76	34	100.0	107	9	ADY34076 Anti-Tie
77	34	100.0	107	9	ADY26776 Anti-NGF
78	34	100.0	107	9	ADY26774 Anti-NGF
79	34	100.0	107	9	ADY74802 Human Ig
80	34	100.0	107	9	ADY93871 Anti-SARS
81	34	100.0	107	9	ADY93864 Anti-SARS
82	34	100.0	107	9	AEA45102 Apolipop
83	34	100.0	107	9	AEB19292 IgG kappa
84	34	100.0	107	9	AEB19293 IgG kappa
85	34	100.0	107	9	AEB19291 IgG kappa
86	34	100.0	107	9	AEB47724 Anti-PCPV
87	34	100.0	108	4	AAAB72884 Human ant
88	34	100.0	108	4	AAAB62780 Human HIV
89	34	100.0	108	5	AAAM51165 Anti-tumo
90	34	100.0	108	5	AAAM51173 Human Vg/
91	34	100.0	108	5	AAU76334 Human ant
92	34	100.0	108	6	ADA89224 Human ant
93	34	100.0	108	7	ADD69212 Human ant
94	34	100.0	108	7	ADD69214 Human ant
95	34	100.0	108	7	ADD69213 Human ant
96	34	100.0	108	7	ADJ73533 Erythropro
97	34	100.0	108	7	ADJ73534 Erythropro

98 34 100.0 108 8 ADI22138 Adi22138 Anti-plat
99 34 100.0 108 8 ADS19298 Adsi19298 Light cha
100 34 100.0 108 9 ADW07091 Adw07091 Anti-Psaa

ALIGNMENTS

RESULT 1
AAB85369
ID AAB85369 standard; peptide; 7 AA.
XX
AC AAB85369;
XX
DT 17-SEP-2001 (first entry)
XX
DE Antibody AAL 160 light chain variable domain CDR2 region.
XX
KW Interleukin lbeta; IL-lbета; antibody AAL 160; immunosuppressive;
KW cerebroprotective; antiinflammatory; antiallergic; antiasthmatic;
KW osteopathic; vasotropic; antiarthritic; dermatological; antithyroid;
KW neuroprotective; vulnery; immunomodulator; cytostatic; anti-HIV.
XX
OS Homo sapiens.
XX
PN WO200153353-A2.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-EP000591.
XX
PR 21-JAN-2000; 2000GB-00001448.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Gram H, Di Padova FE;
XX
WPI; 2001-451903/48.
XX
PT New anti-IL-lbета antibody molecule, comprising at least 1 one
PT immunoglobulin heavy chain variable domain (VH) which comprises
PT hypervariable regions CDR1, CDR2 and CDR3, for treating autoimmune and
PT inflammatory diseases.
XX
PS Claim 3; Page 28; 36pp; English.
XX
CC The invention provides an interleukin lbeta (IL-lbета) binding molecule,
CC in particular a human antibody to human IL-lbета. The IL-lbета binding
CC molecules of the invention are used to treat IL-1 mediated diseases or
CC disorders e.g. septicemia, septic or endotoxic shock, allergies, asthma,
CC bone loss, ischemia, stroke, rheumatoid arthritis, autoimmune diseases
CC (e.g. hemolytic anemia, systemic lupus erythematosus, myasthenia gravis,
CC Crohn's disease, inflammatory bowel syndrome, Graves disease, multiple
CC sclerosis) and inflammatory disorders (e.g. bronchitis and pulmonary
CC emphysema), adult respiratory distress syndrome, meningitis, pneumonia,
CC severe burns, cachexia, cancer, IL-1-dependent tumors and acquired
CC immunodeficiency syndrome (AIDS)-related cachexia. The IL-lbета binding
CC molecules may also be used to prevent graft-versus-host disease in
CC transplant patients. The present sequence represents a complementarity
CC determining region (CDR) of the light chain variable domain of antibody
CC AAL 160, an IL-lbета binding molecule
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 2
AAB66417
ID AAB66417 standard; peptide; 7 AA.
XX
AC AAB66417;
XX
DT 04-APR-2001 (first entry)
XX
DE Human Fab clone LD9 VL CDR2.
XX
KW Human; VH; heavy chain variable region; VL; light chain variable region;
KW cytostatic; antiarthritic; antipsoriatic; antidiabetic; antirheumatic;
KW opthalmological; vasotropic; gynaecological; gene therapy;
KW epithelial glycoprotein-2; EGP-2; cancer; leukaemia; haemangioma;
KW acoustic neuroma; rheumatoid arthritis; psoriasis; angiogenesis;
KW telangiectasia; diabetes; vasculogenesis; reproductive disorder; LD9;
KW complementarity determining region 2; CDR2.
XX
OS Homo sapiens.
XX
PN WO200069914-A2.
XX
PD 23-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-GB001910.
XX
PR 18-MAY-1999; 99GB-00011569.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Hoogenboom HRJM, Reurs A, Beiboer SHWB;
XX
WPI; 2001-016213/02.
XX
DR N-PSDB; AAF29508.
XX
PT Novel human antibody that recognizes the epithelial glycoprotein-2
PT antigen useful for diagnosis, prevention and/or treatment of cancer-
PT related diseases.
XX
PS Disclosure; Fig 9; 86pp; English.

XX
CC The present sequence is given in a specification relating to a novel
CC human antibody that is capable of recognising the Epithelial Glycoprotein
CC -2 (EGP-2) antigen. The antibody is useful for prevention and/or
CC treatment of conditions associated with cancer. Such conditions include
CC solid tumours, blood born tumours such as leukaemia, tumour metastasis,
CC benign tumours, for e.g. haemangiomas, acoustic neuromas, rheumatoid
CC arthritis, psoriasis, ocular angiogenic diseases, diabetic retinopathy,
CC myocardial angiogenesis, telangiectasia, wound granulation, angiogenesis,
CC diabetic neovascularisation, vasculogenesis, ovulation, menstruation and
CC placentaion. The antibody is useful for in vivo imaging of cancer and
CC for adjuvant treatment of cancer. Vectors expressing the antibody are
CC useful for inducing an immunological response in a mammal in vivo. The
CC vector is selected from fowl pox virus (FPV), canary pox (ALVAC),
CC entomopox virus, vaccinia virus such as modified virus ankara (MVA) and
CC NVVAC or other non-replicating viral vector systems in order to provide a
CC dual immunotherapeutic approach
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 3
ABP62391
ID ABP62391 standard; peptide; 7 AA.

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XX AC ABP62391;
XX DT 10-OCT-2002 (first entry)
XX DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #68.
XX KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
XX KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
XX KW NS3 protein; viral infection.
XX OS Homo sapiens.
XX PN WO200259340-A1.
XX PD 01-AUG-2002.
XX PF 25-JAN-2002; 2002WO-US002303.
XX PR 26-JAN-2001; 2001US-0264451P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX WPI; 2002-599801/64.
XX PT New human immunopolypeptide with binding specificity for certain envelope
XX PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
XX PT diagnosing or treating patients having or suspected of having HCV
XX PT infection.
XX PS Claim 1; Fig 17; 308pp; English.
XX CC The present invention relates to human immunopolypeptides, produced by a
XX CC phage transfected cell library. The present sequence is one such
XX CC immunopolypeptide. The immunopolypeptides have binding specificity for
XX CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
XX CC virus (HCV). E2 glycoprotein is believed to be responsible for target
XX CC cell binding and contains neutralising epitopes, while NS3 is thought to
XX CC be involved in the replication of HCV. The immunopolypeptides are useful
XX CC for diagnosing and treating a patient having or suspected to be having
XX CC HCV infection
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 1 DASNRAT 7
RESULT 4
AAU76331
ID AAU76331 standard; peptide; 7 AA.
XX AC AAU76331;
XX DT 21-MAY-2002 (first entry)
XX DE Human anti-dual integrin antibody light chain variable region CDR2.
XX KW Human; antibody; dual integrin; CDR; light chain variable region; LC CDR;
XX KW medical device; immune related disease; rheumatoid arthritis;
XX KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
XX KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
XX KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
XX KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
XX KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
XX KW neurological disease; multiple sclerosis; Parkinson's disease;

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KW Alzheimer's disease; Creutzfeldt-Jakob disease.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 6..7 /note= "Encoded by GCC"
XX PN WO200212501-A2.
XX PD 14-FEB-2002.
XX PF 07-AUG-2001; 2001WO-US024784.
XX PR 07-AUG-2000; 2000US-0223363P.
XX PR 01-AUG-2001; 2001US-00920267.
XX PA (CENZ ) CENTOCOR INC.
XX PI Giles-Komar J, Heavner G, Snyder L, Trikha M;
XX WPI; 2002-217193/27.
XX DR N-PSDB; ABK10118.
XX PT Novel isolated mammalian anti-dual integrin antibody, useful for
XX PT diagnosing or treating dual integrin related condition such as rheumatoid
XX PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.
XX PS Claim 29; Page 133; 144pp; English.
XX CC The invention relates to an isolated mammalian anti-dual integrin
XX CC antibody having at least one of the human heavy chain or light chain
XX CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
XX CC included are the nucleic acids encoding the CDRs, a vector comprising the
XX CC nucleic acids, a host cell comprising the vector, an anti-idiotypic
XX CC antibody that binds to the anti-dual integrin, a medical device comprising
XX CC the antibody suitable for administration by parenteral, subcutaneous,
XX CC intramuscular, intravenous, intrarticular, intrabronchial,
XX CC intraabdominal, intracapsular, intracartilaginous, intracavitary,
XX CC intracerebellar, or other routes as given in specification. The antibody
XX CC is useful for diagnosing or treating a dual integrin related condition in
XX CC an animal for example, immune related disease such as rheumatoid
XX CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
XX CC sickle cell anaemia, diabetes, cardiovascular disease such as
XX CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
XX CC myocardial infarction, infectious disease in a cell such as bacterial,
XX CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
XX CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
XX CC lymphoma, multiple myeloma; neurological disease such as multiple
XX CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
XX CC Creutzfeldt-Jakob disease and many other diseases given in the
XX CC specification. The present sequence is an anti-dual integrin human light
XX CC chain CDR
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 1 DASNRAT 7
RESULT 5
ABP96285
ID ABP96285 standard; peptide; 7 AA.
XX AC ABP96285;
XX XX ABP96285;
XX DT 20-MAY-2003 (first entry)
XX

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Anti-hTNFSF13b human antibody light chain CDR2 SEQ ID NO:6.

DE XX Anti-hTNFSF13b human antibody; antibody; human; TNFSF13b; antiulcer;
 XX XX immunosuppressive; antiinflammatory; dermatological; antiarthritis;
 KW XX antiarthritis; antiasthmatic; antiallergic; antipsoriatic; antiparasitic;
 KW XX antinfertility; antithyroid; thyromimetic; haemostatic; cytostatic;
 KW XX tumour necrosis factor antagonist; TNF antagonist; rheumatoid arthritis;
 KW XX systemic lupus erythematosus; juvenile chronic arthritis; Lyme arthritis;
 KW XX Crohn's disease; ulcerative colitis; inflammatory bowel disease; asthma;
 KW XX allergic disease; psoriasis; immune disease; organ transplant rejection;
 KW XX graft-versus-host disease; sarcoidosis; infectious disease; cancer;
 KW XX parasitic disease; female infertility; autoimmune thrombocytopaenia;
 KW XX autoimmune thyroid disease; Hashimoto's disease; Sjogren's syndrome;
 KW XX complementarity determining region; CDR.
 XX XX Homo sapiens.
 OS XX Synthetic.
 XX XX WO2003016468-A2.
 XX XX 27-FEB-2003.
 XX XX 15-AUG-2002; 2002WO-US021842.
 XX XX 16-AUG-2001; 2001US-0312808P.
 XX XX (ELIL) LILLY & CO ELI.
 XX XX Gelfanova VP, Hale JE, Kikly KK, Witcher DR, Rathnachalam R;
 XX XX WPI; 2003-268308/26.
 DR XX N-PSDB; ABZ79999.
 XX XX New anti-hTNFSF13b human antibody, useful in manufacturing a medicament
 PT for inhibiting TNFSF13b activity in a subject suffering from a disorder
 PT in which TNFSF13b activity is detrimental, e.g. asthma, cancer or
 PT rheumatoid arthritis.
 XX XX Claim 1; Page 37; 52pp; English.
 PS XX The present invention describes an anti-hTNFSF13b human antibody (I). (I)
 CC has immunosuppressive, antiinflammatory, dermatological, antiulcer,
 CC antiarthritis, antiasthmatic, antiallergic, antipsoriatic,
 CC antiparasitic, antinfertility, antithyroid, thyromimetic, haemostatic
 CC and cytostatic activities, and can be used as a tumour necrosis factor
 CC (TNF) antagonist. The anti-hTNFSF13b human antibody or an antibody that
 CC neutralises TNFSF13b activity by binding an epitope of TNFSF13b is useful
 CC in manufacturing a medicament for administering to a subject suffering
 CC from a disorder in which TNFSF13b activity is detrimental, e.g. systemic
 CC lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis,
 CC Lyme arthritis, Crohn's disease, ulcerative colitis, inflammatory bowel
 CC disease, asthma, allergic diseases, psoriasis, acute or chronic immune
 CC disease associated with organ transplantation, organ transplant
 CC rejection, graft-versus-host disease, sarcoidosis, infectious diseases,
 CC parasitic diseases, female infertility, autoimmune thrombocytopaenia,
 CC autoimmune thyroid disease, Hashimoto's disease, Sjogren's syndrome, or
 CC cancer. The present sequence represents the complementarity determining
 CC region 2 (CDR2) of anti-hTNFSF13b light chain, which is given in the
 CC exemplification of the present invention
 XX XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7

RESULT 6
 , AAE38098

AAE38098 standard; peptide; 7 AA.
 AAE38098;
 06-NOV-2003 (first entry)
 Human COU-1 antibody VL CDR2 peptide #1.
 Human; cancer-associated epitope; cytokeratin K8; cytokeratin K18; VL;
 adenocarcinoma; therapy; cancer; antibody; light chain variable region;
 complementarity determining region; CDR.
 Homo sapiens.
 WO2003057168-A2.
 17-JUL-2003.
 03-JAN-2003; 2003WO-US000297.
 03-JAN-2002; 2002US-0345208P.
 (SCRI) SCRIPPS RES INST.
 Ditzel H, Jensenius JC;
 WPI; 2003-598315/56.
 Novel isolated cancer-associated epitope comprising two separate
 polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
 polypeptide, useful as component of vaccine for preventing or treating
 adenocarcinoma.
 Claim 15; Page 36; 155pp; English.
 The invention provides a cancer-associated epitope comprising two
 separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
 polypeptide. Vaccine composition of the invention is useful for treating
 or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
 adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
 adenocarcinoma or non-seminoma testis carcinoma. The invention is also
 useful for preparing a medicament for treating or preventing cancer in a
 mammal. The present sequence is human COU-1 cancer-associated epitope
 antibody VL (light chain variable region) CDR (complementarity
 determining region) peptide
 Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DASNRAT 7
 Db 1 DASNRAT 7
 RESULT 7
 AAE38074
 ID AAE38074 standard; peptide; 7 AA.
 AAE38074;
 06-NOV-2003 (first entry)
 Human 2H9 CD30 antibody VL CDR2 peptide.
 Human; antibody; CD30; tumour; autoimmune disease; rheumatoid arthritis;
 systemic lupus erythematosus; systemic sclerosis; Grave's disease; AICL;
 atopic dermatitis; Hashimoto's thyroiditis; chronic renal failure; AILD;
 acute infectious mononucleosis; angioimmunoblastic lymphadenopathy; HIV;
 Hodgkin's disease; Castleman's disease; Kaposi's sarcoma; lymphoma; ATL;
 adult T cell lymphoma; human immunodeficiency virus; carcinoma; therapy;

KW Wegner's granulomatosis; anaplastic large cell lymphoma; Omen's syndrome;
light chain variable domain; VL; complementarity determining region; CDR.

OS Homo sapiens.

PN WO2003059282-A2.

PD 24-JUL-2003.

PF 07-JAN-2003; 2003WO-US0000440.

PR 09-JAN-2002; 2002US-0347649P.

PR 19-AUG-2002; 2002US-0404427P.

PR 06-DEC-2002; 2002US-0431684P.

XX (MEDA-) MEDAREX INC.

PI Keiler T, Graziano R, Trembl J;

DR WPI; 2003-598476/56.

DR N-PSDB; AAD57386.

XX New human monoclonal antibody that binds to human CD30, useful for

treating or preventing tumor or autoimmune disease, e.g., rheumatoid

arthritis.

PS Claim 13; Page 119; 122pp; English.

XX The invention relates to human monoclonal antibody that binds to human
CD30. The antibody is useful for treating or preventing tumour or
autoimmune disease e.g. rheumatoid arthritis, systemic lupus
erythematosus, systemic sclerosis, atopic dermatitis, Grave's disease,
Hashimoto's thyroiditis, Wegner's granulomatosis, Omen's syndrome,
chronic renal failure, acute infectious mononucleosis, herpes or HIV
(human immunodeficiency virus) virus-associated diseases. The antibody is
also useful for treating Hodgkin's disease, anaplastic large cell
lymphoma (ALCL), adult T cell lymphoma (ATL), angioimmunoblastic
lymphadenopathy (AILD)-like T cell lymphoma, HIV associated body cavity
based lymphomas, embryonal carcinomas, undifferentiated carcinomas of the
rhino-pharynx (e.g. Schmincke's tumour), Castleman's disease, Kaposi's
Sarcoma and other T-cell or B-cell lymphomas. The present sequence is
human CD30 antibody VL (light chain variable domain) CDR (complementarity
determining region) peptide

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 1 DASNRAT 7

RESULT 8

ID ADD69239 standard; peptide; 7 AA.

XX AC ADD69239;

XX 15-JAN-2004 (first entry)

DE Human light chain variable region CDR2 peptide - SEQ ID 43.

XX monoclonal antibody; heavy chain variable region; light; framework;
complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
prostate specific membrane antigen; PSMA; cytostatic; tumour;
colon cancer; renal carcinoma; gene therapy; human.

OS Homo sapiens.

XX WO2003064606-A2.

PN

XX

PD 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002448.

XX 28-JAN-2002; 2002US-00059989.

XX (MEDA-) MEDAREX INC.

XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;

XX WPI; 2003-618360/58.

XX New isolated human monoclonal antibody comprising a human heavy chain and
a human light chain variable regions, both comprising FR1, CDR1, FR2,
CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
cancer.

PS Claim 2; SEQ ID NO 43; 136pp; English.

XX The invention relates to a novel isolated human monoclonal antibody
comprising a human heavy chain variable region and a human light chain
variable region both comprising FR (framework region)-1, CDR
(complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
sequences. The antibody is directed against the human prostate specific
membrane antigen (PSMA). The monoclonal antibody of the invention
demonstrates cytostatic activity and may be useful for treating or
preventing a disease characterised by the growth of tumour cells such as
cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
well as doing gene therapy procedures. The current sequence is that of
the human light chain variable region CDR2 peptide of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 1 DASNRAT 7

RESULT 9

ADD69233

ID ADD69233 standard; peptide; 7 AA.

XX AC ADD69233;

XX 15-JAN-2004 (first entry)

DE Human light chain variable region CDR2 peptide - SEQ ID 37.

XX monoclonal antibody; heavy chain variable region; light; framework;
complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
prostate specific membrane antigen; PSMA; cytostatic; tumour;
colon cancer; renal carcinoma; gene therapy; human.

OS Homo sapiens.

XX WO2003064606-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002448.

XX 28-JAN-2002; 2002US-00059989.

XX (MEDA-) MEDAREX INC.

XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;

XX WPI; 2003-618360/58.

DR

XX New isolated human monoclonal antibody comprising a human heavy chain and
 PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
 PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
 PT cancer.

XX Claim 2; SEQ ID NO 37; 136pp; English.

XX The invention relates to a novel isolated human monoclonal antibody
 CC comprising a human heavy chain variable region and a human light chain
 CC variable region both comprising FR (framework region)-1, CDR
 CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4
 CC sequences. The antibody is directed against the human prostate specific
 CC membrane antigen (PSMA). The monoclonal antibody of the invention or
 CC demonstrates cytostatic activity and may be useful for treating or
 CC preventing a disease characterised by the growth of tumour cells such as
 CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
 CC well as during gene therapy procedures. The current sequence is that of
 CC the human light chain variable region CDR2 peptide of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7

RESULT 10

ADD69236
 ID ADD69236 standard; peptide; 7 AA.

XX ADD69236;

XX 15-JAN-2004 (first entry)

XX Human light chain variable region CDR2 peptide - SEQ ID 40.

XX monoclonal antibody; heavy chain variable region; light; framework;
 KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
 KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
 KW colon cancer; renal carcinoma; gene therapy; human.

XX Homo sapiens.

OS WO2003064606-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002448.

XX 28-JAN-2002; 2002US-00059989.

XX (MEDA-) MEDAREX INC.

XX Deo YM, Graziano R, Hudson D, Holmes EH, Tino WT, Black A;

XX WPI; 2003-618360/58.

XX New isolated human monoclonal antibody comprising a human heavy chain and
 PT a human light chain variable regions, both comprising FR1, CDR1, FR2,
 PT CDR2, FR3, CDR3 and FR4 sequences, useful for treating or preventing
 PT cancer.

XX Claim 2; SEQ ID NO 40; 136pp; English.

XX The invention relates to a novel isolated human monoclonal antibody
 CC comprising a human heavy chain variable region and a human light chain
 CC variable region both comprising FR (framework region)-1, CDR
 CC (complementarity determining region)-1, FR2, CDR2, FR3, CDR3 and FR4

CC sequences. The antibody is directed against the human prostate specific
 CC membrane antigen (PSMA). The monoclonal antibody of the invention or
 CC demonstrates cytostatic activity and may be useful for treating or
 CC preventing a disease characterised by the growth of tumour cells such as
 CC cancer, particularly prostate cancer, colon cancer or renal carcinoma, as
 CC well as during gene therapy procedures. The current sequence is that of
 CC the human light chain variable region CDR2 peptide of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 7; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7

RESULT 11

ADM41607

ID ADM41607 standard; peptide; 7 AA.

XX ADM41607;

XX 03-JUN-2004 (first entry)

XX Interleukin-1 receptor type 1 antibody light chain variable region CDR2.

XX Human; monoclonal antibody; antibody; interleukin-1; receptor;
 KW antisthmatic; antiinflammatory; dermatological; antiallergic;
 KW prozoacide; antiinflammatory; antiaathritic; osteopathic; vasotropic;
 KW analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
 KW anticonvulsant; dermatological; antignout; antiparkinsonian; antidiabetic;
 KW cytostatic; complementarity determining region.

XX Homo sapiens.

XX WO2004022718-A2.

XX 18-MAR-2004.

XX 05-SEP-2003; 2003WO-US027978.

XX 06-SEP-2002; 2002US-0408719P.

XX (AMGE-) AMGEN INC.

XX Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
 PI Elliott G;

XX WPI; 2004-248462/23.

XX Isolated human antibody that specifically binds interleukin-1 receptor
 PT type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
 PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.

XX Claim 47; SEQ ID NO 72; 179pp; English.

XX The present sequence is that of complementarity determining region 2
 CC (CDR2) of the human anti-interleukin-1 receptor type 1 (IL-1R1)
 CC monoclonal antibody (Mab) 26F5 and 27F2 light chain variable region
 CC ADM41547. Anti-IL-1R1 antibodies of the invention may comprise this CDR.
 CC These antibodies inhibit IL-1 signalling by competing with IL-1beta and
 CC IL-1alpha binding to IL-1R. Monoclonal antibodies, as well as single
 CC chain antibodies single chain Fv antibodies, Fab antibodies, Fab'
 CC antibodies and (Fab')2 antibodies, are used in methods of treating IL-1
 CC mediated diseases or for detecting the amount of IL-1R1 in a sample. IL-1
 CC mediated diseases include acute pancreatitis, amyotrophic lateral
 CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma.
 CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
 CC Clostridium associated illnesses, coronary conditions, cancer including
 CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,

CC fibromyalgia, glomerulonephritis, graft versus host disease.
 CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
 CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,
 CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
 CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,
 CC septic shock, side effects of radiation therapy, temporal mandibular
 CC joint disease, sleep disturbance, uveitis, or an inflammatory condition
 CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic
 CC surgery, infection or other disease processes.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 |||||
 Db 1 DASNRAT 7

RESULT 12

ADS88068
 ID ADS88068 standard; peptide; 7 AA.

XX AC ADS88068;

XX DT 18-NOV-2004 (first entry)

XX DE Human CD20 antibody-related CDR peptide SeqID17.

XX KW human monoclonal antibody; CD20;
 KW human B-lymphocyte-restricted differentiation antigen; Bp35; cytostatic;
 KW antiproliferative; antiinflammatory; neuroprotective; ophthalmological;
 KW nephrotropic; antiasthmatic; antiarteriosclerotic; antianaemic;
 KW antirheumatic; antiarthritic; antithyroid; anti-HIV; gene therapy;
 KW cancer; psoriasis; inflammatory bowel disease; meningitis; uveitis;
 KW glomerulonephritis; asthma; atherosclerosis; multiple sclerosis;
 KW haemolytic anaemia; myasthenia gravis; rheumatoid arthritis;
 KW Graves' disease; HIV; CDR; complementarity determining region; human.

XX OS Homo sapiens.

XX PN WO2004035607-A2.

XX PD 29-APR-2004.

XX PF 17-OCT-2003; 2003WO-US033057.

XX PR 17-OCT-2002; 2002US-0419163P.

XX PR 02-APR-2003; 2003US-0460028P.

XX PA (GENM-) GENMAB AS.

XX PI Teeling J, Ruuls S, Glennie M, Van De Winkel JGJ, Parren P;
 PI Petersen J, Baadsgaard ODMS, Huang H;

XX DR WPI; 2004-348434/32.

XX PT New human monoclonal antibodies against CD20, useful for diagnosing,
 PT preventing or treating diseases involving cells expressing CD20, e.g.
 PT cancer, psoriasis, HIV, glomerulonephritis, asthma, atherosclerosis or
 PT anaemia.

XX PS Claim 30; SEQ ID NO 17; 201pp; English.

XX CC This invention relates to a novel isolated human monoclonal antibody
 CC which binds to human CD20 (human B-lymphocyte-restricted differentiation
 CC antigen or Bp35). The invention may be useful for the production of
 CC compositions with a cytostatic, antipsoriatic, antiinflammatory,
 CC neuroprotective, ophthalmological, nephrotropic, antiasthmatic,
 CC antiarteriosclerotic, antianaemic, antirheumatic, antiarthritic,
 CC antithyroid or anti-HIV activity. In addition the invention may be useful

CC for gene therapy. The invention is useful for diagnosing, preventing or
 CC treating diseases or disorders involving cells expressing CD20, such as
 CC cancer, psoriasis, inflammatory bowel disease, meningitis, uveitis,
 CC glomerulonephritis, asthma, atherosclerosis, multiple sclerosis,
 CC haemolytic anaemia, myasthenia gravis, rheumatoid arthritis, Graves'
 CC disease or HIV. The anti-idiotypic antibody is used for detecting the
 CC level of human monoclonal antibody against CD20 in a sample. The present
 CC sequence is that of a human complementarity determining peptide (CDR)
 XX peptide which was used in the exemplification of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 |||||
 Db 1 DASNRAT 7

RESULT 13

ADS88074
 ID ADS88074 standard; peptide; 7 AA.

XX AC ADS88074;

XX DT 18-NOV-2004 (first entry)

XX DE Human CD20 antibody-related CDR peptide SeqID23.

XX KW human monoclonal antibody; CD20;
 KW human B-lymphocyte-restricted differentiation antigen; Bp35; cytostatic;
 KW antiproliferative; antiinflammatory; neuroprotective; ophthalmological;
 KW nephrotropic; antiasthmatic; antiarteriosclerotic; antianaemic;
 KW antirheumatic; antiarthritic; antithyroid; anti-HIV; gene therapy;
 KW cancer; psoriasis; inflammatory bowel disease; meningitis; uveitis;
 KW glomerulonephritis; asthma; atherosclerosis; multiple sclerosis;
 KW haemolytic anaemia; myasthenia gravis; rheumatoid arthritis;
 KW Graves' disease; HIV; CDR; complementarity determining region; human.

XX OS Homo sapiens.

XX PN WO2004035607-A2.

XX PD 29-APR-2004.

XX PF 17-OCT-2003; 2003WO-US033057.

XX PR 17-OCT-2002; 2002US-0419163P.

XX PR 02-APR-2003; 2003US-0460028P.

XX PA (GENM-) GENMAB AS.

XX PI Teeling J, Ruuls S, Glennie M, Van De Winkel JGJ, Parren P;
 PI Petersen J, Baadsgaard ODMS, Huang H;

XX DR WPI; 2004-348434/32.

XX PT New human monoclonal antibodies against CD20, useful for diagnosing,
 PT preventing or treating diseases involving cells expressing CD20, e.g.
 PT cancer, psoriasis, HIV, glomerulonephritis, asthma, atherosclerosis or
 PT anaemia.

XX PS Claim 34; SEQ ID NO 23; 201pp; English.

XX CC This invention relates to a novel isolated human monoclonal antibody
 CC which binds to human CD20 (human B-lymphocyte-restricted differentiation
 CC antigen or Bp35). The invention may be useful for the production of
 CC compositions with a cytostatic, antipsoriatic, antiinflammatory,
 CC neuroprotective, ophthalmological, nephrotropic, antiasthmatic,
 CC antiarteriosclerotic, antianaemic, antirheumatic, antiarthritic,
 CC antithyroid or anti-HIV activity. In addition the invention may be useful

CC for gene therapy. The invention is useful for diagnosing, preventing or
 CC treating diseases or disorders involving cells expressing CD20, such as
 CC cancer, psoriasis, inflammatory bowel disease, meningitis, uveitis,
 CC glomerulonephritis, asthma, atherosclerosis, multiple sclerosis,
 CC haemolytic anaemia, myasthenia gravis, rheumatoid arthritis, Graves'
 CC disease or HIV. The anti-idiotypic antibody is used for detecting the
 CC level of human monoclonal antibody against CD20 in a sample. The present
 CC sequence is that of a human complementarity determining peptide (CDR)
 CC peptide which was used in the exemplification of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7
 |||||

RESULT 14

ADS88080
 ID ADS88080 standard; peptide; 7 AA.

XX

AC ADS88080;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human CD20 antibody-related CDR peptide SeqID29.

XX

KW human monoclonal antibody; CD20;

KW human B-lymphocyte-restricted differentiation antigen; Bp35; cytostatic;
 KW antiproliferative; antineoplastic; neuroprotective; ophthalmological;
 KW nephrotropic; antiaesthetic; antiarteriosclerotic; antianaemic;
 KW antirheumatic; antiarthritic; antithyroid; anti-HIV; gene therapy;
 KW cancer; psoriasis; inflammatory bowel disease; meningitis; uveitis;
 KW glomerulonephritis; asthma; atherosclerosis; multiple sclerosis;
 KW haemolytic anaemia; myasthenia gravis; rheumatoid arthritis;
 KW Graves' disease; HIV; CDR; complementarity determining region; human.

XX Homo sapiens.

XX WO2004035607-A2.

XX

PD 29-APR-2004.

XX

PF 17-OCT-2003; 2003WO-US033057.

XX

PR 17-OCT-2002; 2002US-0419163P.

XX

PR 02-APR-2003; 2003US-0460028P.

XX (GENM-) GENMAB AS.

XX

PI Teeling J, Ruuls S, Glennie M, Van De Winkel JGJ, Parren P;

XX

PI Petersen J, Baadsgaard ODMS, Huang H;

XX

DR WPI; 2004-348434/32.

XX

XX New human monoclonal antibodies against CD20, useful for diagnosing,

XX preventing or treating diseases involving cells expressing CD20, e.g.

XX cancer, psoriasis, HIV, glomerulonephritis, asthma, atherosclerosis or

XX anaemia.

XX Claim 37; SEQ ID NO 29; 201pp; English.

XX This invention relates to a novel isolated human monoclonal antibody

XX which binds to human CD20 (human B-lymphocyte-restricted differentiation

XX antigen or Bp35). The invention may be useful for the production of

XX compositions with a cytostatic, antiproliferative, antineoplastic,

XX neuroprotective, ophthalmological, antiproliferative, antineoplastic,

XX antiatherosclerotic, antianaemic, antirheumatic, antiarthritic,

XX antithyroid or anti-HIV activity. In addition the invention may be useful

CC for gene therapy. The invention is useful for diagnosing, preventing or
 CC treating diseases or disorders involving cells expressing CD20, such as
 CC cancer, psoriasis, inflammatory bowel disease, meningitis, uveitis,
 CC glomerulonephritis, asthma, atherosclerosis, multiple sclerosis,
 CC haemolytic anaemia, myasthenia gravis, rheumatoid arthritis, Graves'
 CC disease or HIV. The anti-idiotypic antibody is used for detecting the
 CC level of human monoclonal antibody against CD20 in a sample. The present
 CC sequence is that of a human complementarity determining peptide (CDR)
 CC peptide which was used in the exemplification of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7
 |||||

RESULT 15

ADS19300
 ID ADS19300 standard; peptide; 7 AA.

XX

AC ADS19300;

XX

DT 18-NOV-2004 (first entry)

XX

DE Light chain CDR2 peptide of human mAb 3G6 antibody SeqID 11.

XX

KW human; antibody; mAb 3G6; lymphocyte migration;

KW inflammatory bowel disease; Crohn's disease; gastroenteritis;
 KW pulmonary inflammatory disease; asthma; chronic bronchitis;
 KW graft rejection; psoriasis; eczema; urticaria; scleroderma;
 KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;
 KW auto-immune thyroiditis; Behcet's syndrome; viral infection; cancer;
 KW neoplastic disease; leukaemia; lymphoma; antineoplastic; antiasthmatic;
 KW immunosuppressive; antiproliferative; dermatological; neuroprotective;
 KW antidiabetic; nephrotropic; virucide; cytostatic; vasotropic;
 KW alphaE integrin; CD103; alphaE-beta7.

XX Homo sapiens.

XX US2003232387-A1.

XX

PD 18-DEC-2003.

XX

PF 14-JUN-2002; 2002US-00173551.

XX

PR 14-JUN-2002; 2002US-00173551.

XX (MILL-) MILLENNIUM PHARM INC.

XX

PI Lu C;

XX

DR WPI; 2004-178738/17.

XX

XX Novel antibody which binds activated alpha-E integrin, specifically to

XX activation-induced epitope on integrin alpha-E chain (CD103), useful for

XX treating inflammatory bowel diseases e.g., Crohn's disease,

XX gastroenteritis.

XX Claim 8; SEQ ID NO 11; 67pp; English.

XX This invention relates to novel antibody and antigen-binding fragments of

XX antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically,

XX it refers to the binding of activation induced epitopes present on

XX activated alphaE integrins, where these integrins are activated by

XX exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable

XX growth factors and/or mitogens. The present invention describes the

XX alphaE-beta7 integrin as a homing receptor that mediates lymphocyte

XX migration to mucosal epithelium. As such, compositions of this invention

are useful for treating a subject having an inflammatory bowel disease such as Crohn's disease or gastroenteritis or pulmonary inflammatory diseases such as asthma or chronic bronchitis. Furthermore, such compositions can be used for inhibiting graft rejection, psoriasis, eczema, urticaria, scleroderma, autoimmune diseases such as multiple sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's syndrome, viral infections, cancer and/or neoplastic diseases such as leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory, antiasthmatic, immunosuppressive, antipsoriatic, dermatological, neuroprotective, antidiabetic, nephrotropic, virucide, cytostatic and vasotropic activities. This peptide sequence is a human antibody heavy chain complementarity determining region (CDR) that binds the integrin alphaE chain of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
| | | | |
Db 1 DASNRAT 7

RESULT 16

ADSS2433
ID ADS52433 standard; peptide; 7 AA.

XX AC ADS52433;

DT 16-DEC-2004 (first entry)

DE Fab targeting HLA-A2/Tax11-19, T4B7, light chain CDR 2.

XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
XX T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
XX major histocompatibility complex; MHC class I; viral infection;
XX human T lymphotropic virus-1 infection; viral oncoprotein;
XX mycoplasma infection; bacterial infection; fungal infection;
XX protozoal infection; phage display; light chain; CDR;
XX complementarity determining region.

XX Homo sapiens.

XX US2004191260-A1.

XX 30-SEP-2004.

XX 26-MAR-2003; 2003US-00396578.

XX 26-MAR-2003; 2003US-00396578.

XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Reiter Y, Cohen C;

XX WPI; 2004-735863/72.

XX New composition comprising a multimeric form of an antibody or fragment which specifically binds an antigen-presenting portion of a complex, useful for treating pathogen-associated diseases e.g., HIV.

XX Claim 5; SEQ ID NO 84; 68pp; English.

XX The invention relates to a composition-of-matter comprising (a multimeric form of) an antibody or antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. Also included are an isolated polynucleotide comprising a nucleic acid sequence encoding an antibody fragment (the antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed

CC of a human antigen-presenting molecule and an antigen derived from a
CC pathogen), a nucleic acid construct comprising the isolated
CC polynucleotide above (and a promoter sequence for directing transcription
CC of the isolated polynucleotide in a host cell), a host cell comprising
CC the nucleic acid construct above, a host virus comprising the nucleic
CC acid construct above, a virus comprising a coat protein fused to the
CC antibody fragment, detecting an antigen-presenting portion of a complex
CC composed of a human antigen-presenting molecule and an antigen derived
CC from a pathogen, a method of diagnosing an infection by a pathogen in an
CC individual, a method of killing or damaging a target cell
CC expressing/displaying an antigen-presenting portion of a complex
CC (composed of a human antigen-presenting molecule and an antigen derived
CC from a pathogen) and a method of detecting in a biological sample an
CC antigen-presenting portion of a complex as described above. The target
CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
CC or a dendritic cell. The composition-of-matter further comprises a
CC detectable moiety attached to the antibody or antibody fragment. The
CC detectable moiety is a recognition sequence of a biotin protein ligase, a
CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
CC polypeptide tag. The biotin protein ligase is BirA, the fluorophore is
CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
CC Pseudomonas exotoxin A or its portion, which is a translocation domain
CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
CC is a major histocompatibility complex (MHC), preferably MHC class I
CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
CC The antigen derived from a pathogen is restricted by the antigen-
CC presenting molecule and is a polypeptide selected from a segment of a
CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
CC composition comprising as an active ingredient the composition-of-matter
CC is useful in a method for treating a disease associated with a pathogen
CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
CC protozoans. The composition-of-matter or the methods are useful for
CC diagnosing an infection by a pathogen in an individual and for killing or
CC damaging a target cell expressing or displaying an antigen-presenting
CC portion of a complex composed of a human antigen-presenting molecule and
CC an antigen derived from a pathogen. A phage displayed library of human
CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
CC were then sequenced and their CDR (complementarity determining region)
CC sequences compared. The present sequence is a CDR from the light chain of
CC an isolated Fab clone.

XX Sequence 7 AA;

Query Match 100.0%; Score 34; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
| | | | |
Db 1 DASNRAT 7

RESULT 17

ADSS2385

ID ADS52385 standard; peptide; 7 AA.

XX AC ADS52385;

XX 16-DEC-2004 (first entry)

XX Fab targeting HLA-A2/Tax11-19, T3D3, light chain CDR 2.

XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
XX T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
XX major histocompatibility complex; MHC class I; viral infection;
XX human T lymphotropic virus-1 infection; viral oncoprotein;
XX mycoplasma infection; bacterial infection; fungal infection;
XX protozoal infection; phage display; light chain; CDR;
XX complementarity determining region.

XX Homo sapiens.

XX specifically binding an antigen-presenting portion of a complex composed

XX US2004191260-A1.
XX 30-SEP-2004.
XX 26-MAR-2003; 2003US-00396578.
XX 26-MAR-2003; 2003US-00396578.
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX Reiter Y, Cohen C;
XX WPI; 2004-735863/72.
XX New composition comprising a multimeric form of an antibody or fragment
PT which specifically binds an antigen-presenting portion of a complex,
PT useful for treating pathogen-associated diseases e.g., HIV.
XX
XX Claim 5; SEQ ID NO 36; 68pp; English.
XX
XX The invention relates to a composition-of-matter comprising (a multimeric
CC form of) an antibody or antibody fragment including an antigen-binding
CC region capable of specifically binding an antigen-presenting portion of a
CC complex composed of a human antigen-presenting molecule and an antigen
CC derived from a pathogen. Also included are an isolated polynucleotide
CC comprising a nucleic acid sequence encoding an antibody fragment (the
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule and an antigen derived from a
CC pathogen), a nucleic acid construct comprising the isolated
CC polynucleotide above (and a promoter sequence for directing transcription
CC of the isolated polynucleotide in a host cell), a host cell comprising
CC the nucleic acid construct above, a host virus comprising the nucleic
CC acid construct above, a virus comprising a coat protein fused to the
CC antibody fragment, detecting an antigen-presenting portion of a complex
CC composed of a human antigen-presenting molecule and an antigen derived
CC from a pathogen, a method of diagnosing an infection by a pathogen in an
CC individual, a method of killing or damaging a target cell
CC expressing/displaying an antigen-presenting portion of a complex
CC (composed of) a human antigen-presenting molecule and an antigen derived
CC from a pathogen) and a method of detecting in a biological sample an
CC antigen-presenting portion of a complex as described above. The target
CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
CC or a dendritic cell. The composition-of-matter further comprises a
CC detectable moiety attached to the antibody or antibody fragment. The
CC detectable moiety is a recognition sequence of a biotin protein ligase, a
CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
CC polyhistidine tag. The biotin protein ligase is BirA, the fluorophore is
CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
CC Pseudomonas exotoxin A or its portion, which is a translocation domain
CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
CC is a major histocompatibility complex (MHC), preferably MHC class I
CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
CC The antigen derived from a pathogen is restricted by the antigen-
CC presenting molecule and is a polypeptide selected from a segment of a
CC viral oncoprotein or a segment of a tax protein. A pharmaceutical
CC composition comprising as an active ingredient the composition-of-matter
CC is useful in a method for treating a disease associated with a pathogen
CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
CC protozoans. The composition-of-matter or the methods are useful for
CC diagnosing an infection by a pathogen in an individual and for killing or
CC damaging a target cell expressing or displaying an antigen-presenting
CC portion of a complex composed of a human antigen-presenting molecule and
CC an antigen derived from a pathogen. A phage displayed library of human
CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
CC and tested for specific binding to HLA-A2/Tax 11-19. Individual clones
CC were then sequenced and their CDR (complementarity determining region)
CC sequences compared. The present sequence is a CDR from the light chain of
CC an isolated Fab clone.
XX
XX Sequence 7 AA;
XX
XX Query Match 100.0%; Score 34; DB 9; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DASNRAT 7
XX | | | | | | |
XX 1 DASNRAT 7
XX
XX RESULT 18
XX ID ADM07071 standard; peptide; 7 AA.
XX AC ADM07071;
XX XX 07-APR-2005 (first entry)
XX DE Anti-Psaa-antibody 1-15E5 VK CDR2.
XX XX
XX KW antibacterial; antiinflammatory; immunosuppressive; antibody engineering;
XX KW pharmaceutical; infection; pneumonia; meningitis; sepsis;
XX KW pneumococcal surface adhesin A; Psaa; light chain variable region;
XX KW complementarity determining region 2; CDR2; ds.
XX OS Homo sapiens.
XX PN WO2005003174-A1.
XX XX 13-JAN-2005.
XX PF 08-JUL-2004; 2004WO-DK000492.
XX XX 08-JUL-2003; 2003DK-00001044.
XX PR 11-JUL-2003; 2003US-0486647P.
XX XX (GENE-) GENESEO AS.
XX XX Sorensen AP, Benfield TL, Lundgren JD, Kempe TD;
XX WPI; 2005-101476/11.
XX DR N-PSDB; ADM07070.
XX XX
XX PT New binding member towards Streptococcus pneumoniae surface adhesin A
XX protein, useful for treating or preventing pneumonia, meningitis and/or
XX sepsis.
XX
XX Disclosure; SEQ ID NO 20; 137pp; English.
XX
XX The invention describes an isolated binding member comprising at least
XX one binding domain capable of specifically binding Streptococcus
XX pneumoniae surface adhesin A (Psaa) protein, the binding domain having a
XX dissociation constant Kd for Psaa which is less than 1 x10⁻⁶ M. Also
XX described are: an isolated nucleic acid molecule encoding at least a part
XX of the binding member described above; a vector comprising the nucleic
XX acid molecule of (1); a host cell comprising the nucleic acid molecule of
XX (1); a cell line engineered to express the binding member described above
XX ; detecting or diagnosing a disease or disorder associated with
XX Streptococcus in an individual; a kit comprising at least one binding
XX member described above, the antibody being labeled; and a pharmaceutical
XX composition comprising at least one binding member described above. The
XX binding member is useful for producing a pharmaceutical composition for
XX the treatment of Pneumococcus infection. The binding member, methods and
XX composition are useful for treating or preventing an individual suffering
XX from disorders or diseases associated with S. pneumoniae, e.g. pneumonia,
XX meningitis and/or sepsis. This sequence encodes anti-pneumococcal surface
XX adhesin A (Psaa)-antibody 1-15E5 kappa light chain variable region
XX complementarity determining region 2 (CDR2).
XX
XX Sequence 7 AA;
XX
XX Query Match 100.0%; Score 34; DB 9; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 |||||

Db 1 DASNRAT 7
 |||||

RESULT 19
 ADM07087
 ID ADM07087 standard; peptide; 7 AA.
 XX
 AC
 XX
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE
 XX
 DE Anti-PsAA-antibody 9A7 VK CDR2.
 XX
 XX antibacterial; antiinflammatory; immunosuppressive; antibody engineering;
 KW pharmaceutical; infection; pneumonia; meningitis; sepsis;
 KW pneumococcal surface adhesin A; PsAA; light chain variable region;
 KW complementarity determining region 2; CDR2; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2005003174-A1.
 XX
 PD 13-JAN-2005.
 XX
 XX 08-JUL-2004; 2004WO-DK000492.
 PF
 XX 08-JUL-2003; 2003DK-00001044.
 PR
 XX 11-JUL-2003; 2003US-0486647P.
 XX
 XX (GENE-) GENESTO AS.
 FA
 XX
 XX Sorensen AP, Benfield TL, Lundgren JD, Kempe TD;
 PI
 XX WPI; 2005-101476/11.
 DR
 XX N-FSDB; ADM07086.
 DR
 XX
 PT New binding member towards Streptococcus pneumoniae surface adhesin A
 PT protein, useful for treating or preventing pneumonia, meningitis and/or
 PT sepsis.
 PS
 XX Disclosure; SEQ ID NO 36; 137pp; English.
 XX
 CC The invention describes an isolated binding member comprising at least
 CC one binding domain capable of specifically binding Streptococcus
 CC pneumoniae surface adhesin A (Psaa) protein, the binding domain having a
 CC dissociation constant Kd for Psaa which is less than 1 x10⁻⁶ M. Also
 CC described are: an isolated nucleic acid molecule encoding at least a part
 CC of the binding member described above; a vector comprising the nucleic
 CC acid molecule of (1); a host cell comprising the nucleic acid molecule of
 CC (1); a cell line engineered to express the binding member described above
 CC (1); detecting or diagnosing a disease or disorder associated with
 CC Streptococcus in an individual; a kit comprising at least one binding
 CC member described above, the antibody being labeled; and a pharmaceutical
 CC composition comprising at least one binding member described above. The
 CC binding member is useful for producing a pharmaceutical composition for
 CC the treatment of Pneumococcus infection. The binding member methods and
 CC composition are useful for treating or preventing an individual suffering
 CC from disorders or diseases associated with S. pneumoniae, e.g. pneumonia,
 CC meningitis and/or sepsis. This sequence encodes anti-pneumococcal surface
 CC adhesin A (Psaa)-antibody 9A7 kappa light chain variable region
 CC complementarity determining region 2 (CDR2).
 XX
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 |||||

Db 1 DASNRAT 7
 |||||

RESULT 21
 ADY26808
 ID ADY26808 standard; protein; 7 AA.
 XX
 AC ADY26808;

Db 1 DASNRAT 7
 |||||

RESULT 20
 ADM77463
 ID ADM77463 standard; peptide; 7 AA.
 XX
 AC ADM77463;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Human platelet membrane glycoprotein VI associated CDR SEQ ID NO 134.
 XX
 DE
 XX
 DE Antiarteriosclerotic; Thrombolytic; Anticoagulant; Antidiabetic;
 KW Ophthalmological; Immunosuppressive; Vasotropic; antibody;
 KW platelet membrane glycoprotein VI; diabetic retinopathy;
 KW cardiovascular disease; ocular disease; graft versus host disease;
 KW immune disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO2005007800-A2.
 XX
 PD 27-JAN-2005.
 XX
 XX 20-JUL-2004; 2004WO-JP010596.
 PF
 XX 18-JUL-2003; 2003JP-00199192.
 PR
 XX (MOCH) MOCHIDA PHARM CO LTD.
 PA
 XX Takayama H, Shirakawa K, Yamakawa T, Kawahara T;
 PI
 XX WPI; 2005-152077/16.
 DR
 XX
 XX Novel human antibody or its active fragment capable of binding
 PT specifically with human platelet membrane glycoprotein VI and not
 PT inducing human platelet aggregation by itself, useful for treatment or
 PT prevention of thrombosis.
 XX
 XX Example 8; SEQ ID NO 134; 124pp; Japanese.
 PS
 XX The invention relates to a human antibody or its active fragment capable
 CC of binding specifically with human platelet membrane glycoprotein VI and
 CC not inducing human platelet aggregation by itself. The antibody is useful
 CC in treatment or prevention of thrombosis, embolism or arteriosclerosis.
 CC The antibody is useful in diagnosis of the disease by detecting or
 CC determining glycoprotein VI. The antibody is useful in the prevention
 CC and/or treatment of vascular endothelium failure, vascular endothelium
 CC hypertrophy, blood vessel restenosis, disseminated intravascular
 CC coagulation (DIC), diabetic retinopathy, graft-versus-host disease, etc.
 CC The antibody exhibits high specificity with respect to glycoprotein VI,
 CC and can be obtained easily. The present sequence represents the amino
 CC acid sequence of a human platelet membrane glycoprotein VI associated
 CC CDR.
 XX
 XX Sequence 7 AA;
 SQ

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 |||||

Db 1 DASNRAT 7
 |||||

RESULT 21
 ADY26808
 ID ADY26808 standard; protein; 7 AA.
 XX
 AC ADY26808;

XX	19-MAY-2005	(first entry)
XX	DT	
XX	DE	Human anti-NGF-antibody light chain CDR2 SEQ ID NO 123.
XX	KW	analgesic; gene therapy; antibody engineering; pharmaceutical; pain;
XX	KX	neurological disease; NGF; nerve growth factor; heavy chain; CDR2.
XX	OS	Homo sapiens.
XX	PN	WO2005019266-A2.
XX	PD	03-MAR-2005.
XX	PF	15-JUL-2004; 2004WO-US022876.
XX	PR	15-JUL-2003; 2003US-0487431P.
XX	PA	(AMGE-) AMGEN INC.
XX	PI	Wild KD, Treanor JJS, Huang H, Inoue H, Zhang TJ, Martin F;
XX	DR	WPI; 2005-202606/21.
XX	PT	New human anti-nerve growth factor (NGF) neutralizing antibodies useful
XX	PT	for manufacturing a medicament for treating painful disorders (e.g. acute
XX	PT	pain) or conditions associated with increased expression or sensitivity
XX	PT	to NGF.
XX	PS	Claim 38; SEQ ID NO 123; 190pp; English.
XX	CC	The invention describes an isolated human antibody that interacts with or
XX	CC	binds specifically to human nerve growth factor (NGF) and neutralize the
XX	CC	function of NGF. Also described are: methods of treating a condition
XX	CC	caused by increased expression of NGF or increased sensitivity to NGF in
XX	CC	a patient; methods for detecting NGF in a biological sample; an NGF
XX	CC	specific binding agent comprising any of the 59 amino acid sequences
XX	CC	comprising, for e.g. 123, 107 or 14 amino acids, as mentioned in the
XX	CC	specification, and where the binding agent can bind to NGF; a
XX	CC	pharmaceutical composition comprising a pharmaceutical carrier and a
XX	CC	therapeutic amount of the antibody or binding agent cited above; or a
XX	CC	medicament for treating a painful disorder or condition associated with
XX	CC	increased expression of NGF or increased sensitivity to NGF, the
XX	CC	medicament comprising a pharmaceutical amount of a monoclonal antibody or
XX	CC	its immunologically functional immunoglobulin fragment, or pharmaceutical
XX	CC	salts of the monoclonal antibody or the fragment, where the monoclonal
XX	CC	antibody is at least one of the monoclonal antibody cited above, and a
XX	CC	pharmaceutical carrier, diluent or excipient; a nucleic acid molecule or
XX	CC	polynucleotide that encodes the above antibody or binding agent; an
XX	CC	isolated cell line that produces the above antibody or binding agent; an
XX	CC	expression vector comprising the above polynucleotide; and a host cell
XX	CC	comprising the nucleic acid or expression vector. The composition
XX	CC	(including the antibody) and methods are useful for manufacturing a
XX	CC	medicament for treating a painful disorder (e.g. acute pain, dental pain,
XX	CC	or pain from trauma or cancer), or a condition associated with increased
XX	CC	expression of NGF or increased sensitivity to NGF. This is the amino acid
XX	CC	sequence of a human NGF antibody heavy chain complementarity determining
XX	CC	region 2 (CDR2).
XX	SQ	Sequence 7 AA;
	Query Match	100.0%; Score 34; DB 9; Length 7;
	Best Local Similarity	100.0%; Pred. No. 2e+06; 0; Gaps 0;
	Matches	7; Conservative 0; Mismatches 0; Indels 0;
Qy	1 DASNRAT 7	
Db	1 DASNRAT 7	
RESULT 22		
ADY26814		
ID	ADY26814 standard; protein; 7 AA.	

ADY93861

ID ADY93861 standard; peptide; 7 AA.

XX AC ADY93861;

XX DT 16-JUN-2005 (first entry)

XX DE Anti-SARS 201.2 antibody VK CDR2 SEQ ID NO.11.

XX KW glycoprotein; respiratory-gen.; virucide; sars coronavirus infection;
XX KW antibody; light chain variable region.

XX OS SARS coronavirus.

XX PN US2005069869-A1.

XX PD 31-MAR-2005.

XX PF 04-AUG-2004; 2004US-00911838.

XX PR 04-AUG-2003; 2003US-0492529P.

XX PR 09-OCT-2003; 2003US-0510251P.

XX PR 18-FEB-2004; 2004US-0545670P.

XX PR 26-APR-2004; 2004US-0565595P.

XX PA (AMBR/) AMBROSINO D.

XX PA (HERN/) HERNANDEZ H.

XX PA (GREE/) GREENOUGH T.

XX PA (LUZU/) LUZURIAGA K.

XX PA (SOMA/) SOMASUNDARAN M.

XX PA (BABC/) BABCOCK G J.

XX PA (THOM/) THOMAS W D.

XX PA (SULL/) SULLIVAN J.

XX PI Ambrosino D, Hernandez H, Greenough T, Luzuriaga K;

XX PI Somasundaran M, Babcock GJ, Thomas WD, Sullivan J;

XX DR WPI; 2005-252952/26.

XX PT New isolated nucleic acid encoding a SARS-CoV spike glycoprotein
XX PT polypeptide, and optimized for expression in a human host, useful for
XX PT diagnosing, preventing and/or treating SARS-CoV infection.

XX PS Claim 48; SEQ ID NO 11; 138pp; English.

XX CC The invention relates to an isolated nucleic acid comprising a sequence
XX CC encoding a SARS coronavirus (SARS-CoV) spike glycoprotein (S protein), or
XX CC its fragment, where the sequence has been optimized for expression in a
XX CC human host. Also described: (1) a nucleic acid expression vector
XX CC comprising the above nucleic acid; (2) an isolated cell comprising the
XX CC expression vector of (1); (3) a polypeptide encoded by the above nucleic
XX CC acid; (4) an isolated polypeptide comprising an extracellular portion of
XX CC the SARS-CoV S polypeptide located between amino acids 15-1190 of
XX CC ADY93852, or its fragment; (5) an isolated antibody, or its antigen
XX CC binding fragment, that specifically binds to the polypeptide of (3); (6)
XX CC an isolated antibody, or its antigen binding fragment, that specifically
XX CC binds to an antigen binding fragment of an anti-S protein antibody; (7) a
XX CC composition comprising a polypeptide of (4) or an antibody, or its
XX CC antigen binding fragment, and a pharmaceutical carrier; (8) making an S
XX CC protein, or its fragment, of SARS-CoV; (9) making an antibody, or its
XX CC antigen binding fragment, of SARS-CoV; (10) evaluating a biological sample for the presence of SARS-CoV;
XX CC (11) evaluating an antibody, or its antigen binding fragment, for
XX CC inhibition of infection by SARS-CoV; (12) treating a subject at risk for,
XX CC or exposed to SARS-CoV; (13) an immunoconjugate comprising the antibody
XX CC of (5) linked to a therapeutic agent; (14) an isolated nucleic acid
XX CC molecule encoding the antibody, its antigen-binding portion, variable
XX CC heavy chain or variable light chain of (5); (15) an expression vector
XX CC comprising the nucleic acid molecule of (14); (16) a host cell comprising
XX CC the expression vector of (15); (17) a transgenic mammal comprising human
XX CC immunoglobulin heavy and light chain transgenes, where the mouse
XX CC expresses the antibody of (5); (18) a hybridoma prepared from the mammal
XX CC of (17), where the hybridoma produces the antibody; and (19) preparing an

CC anti-S protein antibody. The methods and compositions of the present
CC invention are useful for the diagnosis, prevention and/or treatment of
CC SARS-CoV infection. The present sequence represents the CDR2 amino acid
CC sequence from the anti-SARS 201.2 antibody light chain variable region
CC from the present invention.

SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 1 DASNRAT 7

RESULT 24

AEA53720

ID AEA53720 standard; peptide; 7 AA.

XX AC AEA53720;

XX DT 11-AUG-2005 (first entry)

XX DE Novel human MMP26-binding antibody-related CDR2 peptide #517.

XX KW antibody engineering; cytostatic; antiinflammatory; osteopathic;
XX KW antiarthritic; gene therapy; cancer; breast tumor; prostate tumor;
XX KW lung tumor; inflammation; rheumatoid arthritis; restenosis;
XX KW graft versus host disease; multiple sclerosis; gingivitis;
XX KW osteoarthritis.

XX OS Unidentified.

XX PN WO2005051299-A2.

XX PD 09-JUN-2005.

XX PF 19-NOV-2004; 2004WO-US039052.

XX PR 19-NOV-2003; 2003US-0523745P.

XX PA (DYAX-) DYAX CORP.

XX PI Dransfield DT, Rookey K, Ladner RC;

XX DR WPI; 2005-417817/42.

XX PT New protein comprising heavy and light chain immunoglobulin variable
XX PT domain sequences, useful in preparing a composition for treating or
XX PT preventing neoplastic or inflammatory disorders.

XX PS Example; Page 129; 192pp; English.

XX CC This invention relates to novel proteins, comprising a heavy chain
XX CC immunoglobulin variable domain sequence and a light chain immunoglobulin
XX CC variable domain sequence, which bind to matrix metalloproteinase (MMP)-26
XX CC and comprise at least one human complementarity determining region or
XX CC framework region. The invention may be useful for the development of
XX CC compounds with a cytostatic, antiinflammatory, osteopathic or
XX CC antiarthritic activity whilst the disclosed sequences may prove useful
XX CC for gene therapy. The protein is useful in preparing a composition for
XX CC treating or preventing neoplastic disorders, for example breast,
XX CC prostate, or lung cancer or inflammatory disorders, for example
XX CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
XX CC multiple sclerosis or a disorder characterized by excessive or undesired
XX CC MMP-26 activity, for example periodontitis, rheumatoid arthritis or
XX CC osteoarthritis. The present sequence is that of a CDR peptide which was
XX CC used during the development of the novel MMP26-binding antibodies of the
XX CC invention.

SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
 |||||

DB 1 DASNRAT 7
 |||||

RESULT 25
 AEA53713
 ID AEA53713 standard; peptide; 7 AA.
 AC AEA53713;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Novel human MMP26-binding antibody-related CDR2 peptide #510.
 KW antibody engineering; cytostatic; antiinflammatory; osteopathic;
 KW antiarthritic; gene therapy; cancer; breast tumor; prostate tumor;
 KW lung tumor; inflammation; rheumatoid arthritis; restenosis;
 KW graft versus host disease; multiple sclerosis; gingivitis;
 KW osteoarthritis.
 XX
 OS Unidentified.
 XX
 XX WO2005051299-A2.
 XX
 XX 09-JUN-2005.
 XX
 PF 19-NOV-2004; 2004WO-US039052.
 XX
 XX 19-NOV-2003; 2003US-0523745P.
 XX
 XX (DYAX-) DYAX CORP.
 PA
 XX Dransfield DT, Rookey K, Ladner RC;
 PI
 XX WPI; 2005-417817/42.
 DR
 XX
 PT New protein comprising heavy and light chain immunoglobulin variable
 PT domain sequences, useful in preparing a composition for treating or
 PT preventing neoplastic or inflammatory disorders.
 XX
 XX Example; Page 129; 192pp; English.
 PS
 XX This invention relates to novel proteins, comprising a heavy chain
 CC immunoglobulin variable domain sequence and a light chain immunoglobulin
 CC variable domain sequence, which bind to matrix metalloproteinase (MMP)-26
 CC and comprise at least one human complementarity determining region or
 CC framework region. The invention may be useful for the development of
 CC compounds with a cytostatic, antiinflammatory, osteopathic or
 CC antiarthritic activity whilst the disclosed sequences may prove useful
 CC for gene therapy. The protein is useful in preparing a composition for
 CC treating or preventing neoplastic disorders, for example breast,
 CC prostate, or lung cancer or inflammatory disorders, for example
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
 CC multiple sclerosis or a disorder characterized by excessive or undesired
 CC MMP-26 activity, for example periodontitis, rheumatoid arthritis or
 CC osteoarthritis. The present sequence is that of a CDR peptide which was
 CC used during the development of the novel MMP26-binding antibodies of the
 CC invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
 |||||

DB 1 DASNRAT 7
 |||||

Db 1 DASNRAT 7

RESULT 26
 AEA45053
 ID AEA45053 standard; peptide; 7 AA.
 XX
 AC AEA45053;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Apolipoprotein E C-terminal domain related sequence, SEQ ID 251.
 KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
 KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
 KW Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
 KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
 KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
 KW motor neurone disease; chronic obstructive pulmonary disease.
 XX
 OS Homo sapiens.
 OS
 PN GB2408508-A.
 XX
 XX 01-JUN-2005.
 PD
 XX 26-NOV-2004; 2004GB-00026043.
 PF
 XX 28-NOV-2003; 2003US-0525174P.
 PR
 XX (ASTR) ASTRAZENECA AB.
 PA (DYAX-) DYAX CORP.
 XX
 XX Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
 PI Hufton S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
 PI
 XX WPI; 2005-408785/42.
 DR
 XX
 XX New human antibody or antibody fragment which binds to a sequence of the
 PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
 PT manufacturing a medicament for treating or preventing an amyloid disorder
 PT e.g. Alzheimers disease.
 XX
 XX Example 23; SEQ ID NO 251; 392pp; English.
 PS
 XX The present invention relates to a human antibody or antibody fragment,
 CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
 CC AEA44803) and also to human plaques. The antibody or its fragment is
 CC useful for manufacturing a medicament for treating or preventing an
 CC amyloid disorder such as Alzheimers disease, primary systemic
 CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
 CC familial amyloid polynuropathy I, familial amyloid polynuropathy III,
 CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
 CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
 CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
 CC amyloid, type II diabetes. Hereditary renal amyloidosis, Pituitary-gland
 CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
 CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
 CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
 CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
 CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
 CC chronic obstructive pulmonary disease. The present sequence was used to
 CC illustrate the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
 |||||

DB 1 DASNRAT 7
 |||||

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
 DB 1 DASNRAT 7

RESULT 27
 AEB01040
 ID AEB01040 standard; peptide; 7 AA.
 XX
 AC AEB01040;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Human IP10 antibody light chain variable region, CDR2, SEQ ID NO 68.
 XX
 KW antibody; IP-10; inflammation; immune disorder; dermatological disease;
 KW respiratory disease; neurological disease; degeneration; infection;
 KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;
 KW Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;
 KW Antidiabetic; Antipsoriatic; Antithyroid; Antiasthmatic;
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
 KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Virucide;
 KW Antibacterial.
 XX
 OS Homo sapiens.
 XX
 PN WO2005058815-A2.
 XX
 PD 30-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-US041506.
 XX
 PR 10-DEC-2003; 2003US-0529180P.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
 XX
 DR WPI; 2005-467095/47.
 XX
 PT Isolated human monoclonal antibody or an antigen-binding portion, which
 PT specifically binds to human interferon gamma inducible protein 10 (IP-
 PT 10), useful for treating viral or bacterial infection, or inflammatory or
 PT autoimmune diseases.
 XX
 PS Claim 16; SEQ ID NO 68; 179pp; English.
 XX
 CC The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human ITAC. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative
 CC glomerulonephritis, rapidly progressive glomerulonephritis), or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the amino acid sequence of a human IP10 monoclonal
 CC antibody light chain variable region, CDR2.
 XX
 SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
 DB 1 DASNRAT 7

RESULT 28
 AEB01035
 ID AEB01035 standard; peptide; 7 AA.
 XX
 AC AEB01035;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Human IP10 antibody light chain variable region, CDR2, SEQ ID NO 63.
 XX
 KW antibody; IP-10; inflammation; immune disorder; dermatological disease;
 KW respiratory disease; neurological disease; degeneration; infection;
 KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;
 KW Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;
 KW Antidiabetic; Antipsoriatic; Antithyroid; Antiasthmatic;
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
 KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Virucide;
 KW Antibacterial.
 XX
 OS Homo sapiens.
 XX
 PN WO2005058815-A2.
 XX
 PD 30-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-US041506.
 XX
 PR 10-DEC-2003; 2003US-0529180P.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
 XX
 DR WPI; 2005-467095/47.
 XX
 PT Isolated human monoclonal antibody or an antigen-binding portion, which
 PT specifically binds to human interferon gamma inducible protein 10 (IP-
 PT 10), useful for treating viral or bacterial infection, or inflammatory or
 PT autoimmune diseases.
 XX
 PS Claim 16; SEQ ID NO 63; 179pp; English.
 XX
 CC The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human ITAC. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative
 CC glomerulonephritis, rapidly progressive glomerulonephritis), or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the amino acid sequence of a human IP10 monoclonal
 CC antibody light chain variable region, CDR2.
 XX
 SQ Sequence 7 AA;

CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the amino acid sequence of a human IP10 monoclonal
 CC antibody light chain variable region, CDR2.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
 |||||
 Db 1 DASNRAT 7

RESULT 29
 AEB01042
 ID AEB01042 standard; peptide; 7 AA.

AC AEB01042;

DT 08-SEP-2005 (first entry)

XX Human IP10 antibody light chain variable region, CDR2, SEQ ID NO 70.

XX antibody; IP-10; inflammation; immune disorder; dermatological disease;
 KW respiratory disease; neurological disease; degeneration; infection;
 KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;
 KW Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;
 KW Antidiabetic; Antiproliferative; Antithyroid; Antiasthmatic;
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
 KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Virucide;
 KW Antibacterial.

XX Homo sapiens.

XX WO2005058815-A2.

XX 30-JUN-2005.

XX 10-DEC-2004; 2004WO-US041506.

XX 10-DEC-2003; 2003US-0529180P.

XX (MEDA-) MEDAREX INC.

XX Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
 XX WPI; 2005-467095/47.

XX Isolated human monoclonal antibody or an antigen-binding portion, which

PT specifically binds to human interferon gamma inducible protein 10 (IP-
 PT 10), useful for treating viral or bacterial infection, or inflammatory or
 PT autoimmune diseases.

XX Claim 16; SEQ ID NO 70; 179pp; English.

XX The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human ITAC. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,

CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative
 CC glomerulonephritis, rapidly progressive glomerulonephritis), or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the amino acid sequence of a human IP10 monoclonal
 CC antibody light chain variable region, CDR2.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
 |||||
 Db 1 DASNRAT 7

RESULT 30
 AEB28710

ID AEB28710 standard; peptide; 7 AA.

XX AEB28710;

AC 22-SEP-2005 (first entry)

DE Human CDR2 of T3D3 Fab specifically binding HLA-A2/Tax11-19, SEQ: 36.

XX Diagnosis; therapeutic; infection; antimicrobial; light chain; T3D3.

XX Homo sapiens.

XX US2005152912-A1.

XX 14-JUL-2005.

XX 09-MAR-2005; 2005US-00074803.

XX 26-MAR-2003; 2003US-00396578.

XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Reiter Y, Cohen C;

XX WPI; 2005-496781/50.

XX New composition-of-matter capable of specifically binding an antigen-
 PT presenting molecule and a pathogen-derived antigen complexes, useful for
 PT treating diseases associated with a pathogen.

XX Claim 5; SEQ ID NO 36; 65pp; English.

XX The present invention relates to a composition-of-matter which comprises
 CC an antibody or antibody fragment or a multimeric form of an antibody or
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule (APM) and an antigen derived from
 CC a pathogen. The invention is useful for the specific detection of the
 CC antigen-presenting portion of the complex and for diagnosing/treating
 CC various types of diseases associated with a pathogen infection by
 CC killing/damaging pathogen infected cells. The present sequence is a
 CC complementarity determining regions (CDR) of Fab light chain antibody
 CC specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex.
 CC Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-
 CC 1).

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7
 |||||

RESULT 31
 AEB28758
 ID AEB28758 standard; peptide; 7 AA.
 XX AC AEB28758;
 XX DT 22-SEP-2005 (first entry)
 XX DE Human CDR2 of T4B7 Fab specifically binding HLA-A2/Tax11-19, SEQ: 84.
 XX KW Diagnosis; therapeutic; infection; antimicrobial; light chain; T4B7.
 XX OS Homo sapiens.
 XX PN US2005152912-A1.
 XX PD 14-JUL-2005.
 XX PF 09-MAR-2005; 2005US-00074803.
 XX PR 26-MAR-2003; 2003US-00396578.
 XX PA (TECR) TECHNIQ RES & DEV FOUND LTD.
 XX PI Reiter Y, Cohen C;
 XX DR WPI; 2005-496781/50.
 XX PT New composition-of-matter capable of specifically binding an antigen-presenting molecule and a pathogen-derived antigen complexes, useful for treating diseases associated with a pathogen.
 XX PS Claim 5; SEQ ID NO 84; 65pp; English.
 XX CC The present invention relates to a composition-of-matter which comprises an antibody or antibody fragment or a multimeric form of an antibody or antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule (APM) and an antigen derived from a pathogen. The invention is useful for the specific detection of the antigen-presenting portion of the complex and for diagnosing/treating various types of diseases associated with a pathogen infection by killing/damaging pathogen infected cells. The present sequence is a complementarity determining regions (CDR) of Fab light chain antibody specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex. Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-1).

Query Match 100.0%; Score 34; DB 9; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7
 |||||

RESULT 32
 ADD89875
 ID ADD89875 standard; peptide; 8 AA.
 XX AC ADD89875;

XX 29-JAN-2004 (first entry)
 DT Human anti-tumour necrosis factor antibody light chain CDR2.
 DE Human; Tumour necrosis factor; TNF; antibody;
 KW complementarity determining region; cytostatic; anabolic;
 KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;
 KW neuroprotective.
 XX OS Homo sapiens.
 XX PN WO2003083061-A2.
 XX PD 09-OCT-2003.
 XX PF 24-MAR-2003; 2003WO-US009072.
 XX PR 26-MAR-2002; 2002US-0367903P.
 XX PA (CENZ) CENTOCOR INC.
 XX PI Giles-Komar J, Scallion BJ, Carton JM;
 XX DR WPI; 2003-804040/75.
 XX PT New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful for diagnosing or treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia, or bacterial infection.
 XX PS Claim 2; Page 85; 87pp; English.
 XX CC The present sequence is that of complementarity determining region 2 (CDR2) of the light chain variable region of claimed mammalian anti-tumour necrosis factor (TNF) antibodies of the invention. The CDR is derived from a human TNF reactive Igs monoclonal antibody generated by cloning variable and constant region DNA in vector pc4 and expression in CHO cells. The invention provides isolated human, primate, rodent, mammalian, chimeric, humanized and/or CDR-grafted anti-TNF antibodies, immunoglobulins, their cleavage products, other specified portions and variants, as well as anti-TNF antibody compositions, nucleic acids encoding these, vectors, host cells, methods for producing the antibodies using a host cell, transgenic animal or transgenic plant or plant cell, and therapeutic compositions, methods and devices. The antibody, nucleic acid, protein, composition and methods are useful for diagnosing or treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia, or an immune, cardiovascular, infectious, and/or neurological disease.

Query Match 100.0%; Score 34; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 1 DASNRAT 7
 |||||

RESULT 33
 ADS64650
 ID ADS64650 standard; peptide; 8 AA.
 XX AC ADS64650;
 XX DT 16-DEC-2004 (first entry)
 XX DE Human anti-TNF antibody light chain CDR1 peptide #2.
 XX KW Tumour necrosis factor; TNF; immunotherapy; TNF related diseases; obesity; immune related disease; rheumatoid arthritis;
 KW cardiovascular disease; stroke; malignant disease; leukaemia;
 KW neurological disease; multiple sclerosis; infection; hepatitis;

KW anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;
 KW neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;
 KW anti-TNF antibody; CDR; complementarity determining region; human;
 KW light chain.
 XX
 OS Homo sapiens.
 XX
 PN US2004185047-A1.
 XX
 XX 23-SEP-2004.
 XX
 XX 21-MAR-2003; 2003US-00394471.
 XX
 XX 21-MAR-2003; 2003US-00394471.
 XX
 XX (GILES/) GILES-KOMAR J.
 PA (SCALLON/) SCALLON B J.
 PA (CART/) CARTON J M.
 XX
 PI Giles-Komar J, Scallion BJ, Carton JM;
 XX
 XX WPI; 2004-676151/66.
 XX
 XX Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody
 PT capable of inhibiting binding of TNF alpha to TNF receptor, useful for
 PT treating TNF-related diseases such as obesity or rheumatoid arthritis.
 XX
 XX Claim 2; SEQ ID NO 13; 45pp; English.
 XX
 XX The present invention relates to a mammalian anti-tumour necrosis factor
 CC (TNF) antibody capable of inhibiting binding of TNF alpha to TNF
 CC receptor. The invention is useful for diagnosing or treating an anti-TNF
 CC related condition in a cell, tissue, organ or animal and in
 CC immunotherapy. The invention is also useful for treating TNF related
 CC diseases chosen from obesity, immune related disease such as rheumatoid
 CC arthritis, cardiovascular disease such as stroke, malignant disease such
 CC as leukaemia, neurological disease such as multiple sclerosis and
 CC bacterial or viral infections such as hepatitis. The present sequence is
 CC the human anti-TNF antibody light chain complementarity determining
 CC region 2 (CDR2) peptide.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 34; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DASNRAT 7
 Db 1 DASNRAT 7
 RESULT 34
 ADU04212
 ID ADU04212 standard; protein; 88 AA.
 XX
 XX ADU04212;
 AC
 XX 13-JAN-2005 (first entry)
 DT
 XX Human immunoglobulin kappa light chain protein 1.
 DE
 XX viral infection; virucide; autoimmune disease;
 KW lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin;
 KW antibody.
 XX
 OS Homo sapiens.
 XX
 XX WO2004090544-A2.
 PN
 XX 21-OCT-2004.
 PD
 XX 13-APR-2004; 2004WO-CA000544.
 PF

XX
 PR 09-APR-2003; 2003US-0461137P.
 PR 30-SEP-2003; 2003US-0506779P.
 XX
 PA (CABL-) CANADIAN BLOOD SERVICES.
 XX
 XX Hu Y, Brown E;
 PI
 XX WPI; 2004-766498/75.
 DR
 XX
 XX Characterizing a viral infection in a host, for developing treatment for
 PT severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining
 PT homology profile of a viral-based sequence element with an endogenous
 PT host element.
 XX
 XX Example 1; Fig 24; 166pp; English.
 PS
 XX The invention relates to a novel method for characterising a viral
 CC infection in a host. The method comprises identifying at least one viral-
 CC based sequence element in a biological sample obtained from the host,
 CC determining a homology profile of the viral-based sequence element with
 CC at least one endogenous host element and characterising the viral
 CC infection based on the homology profile, where the homology profile is
 CC indicative of a viral behaviour of the viral infection in the host. The
 CC method of the invention demonstrates virucide applications and may be
 CC useful for preparing a medicament for detecting and/or treating a viral
 CC infection or related condition, such as an autoimmune disease e.g. type
 CC II cryoglobulinaemia, or lymphoproliferative disorder. The viral
 CC infection may be due to HCV (Hepatitis C virus), HIV or a member of a
 CC Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae or
 CC Coronaviridae virus family. Treatment of the infection may utilise
 CC vaccine or gene therapy. The target compound of the invention may be
 CC useful for detecting the presence of a virus in a biological sample or
 CC for manufacturing a medicament for treating SARS coronavirus (SARS-CoV)
 CC and/or Human T-lymphotropic virus 1 (HTLV-I) infection. The methods are
 CC further useful for developing treatment regimes to target genotype-
 CC specific viral variants. The current sequence is that of a human
 CC immunoglobulin light chain kappa (IgVLk) protein of the invention.
 XX
 SQ Sequence 88 AA;
 Query Match 100.0%; Score 34; DB 8; Length 88;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DASNRAT 7
 Db 50 DASNRAT 56
 RESULT 35
 ADD69248
 ID ADD69248 standard; protein; 94 AA.
 XX
 XX ADD69248;
 AC
 XX 15-JAN-2004 (first entry)
 DT
 XX Human light chain L6 protein.
 DE
 XX monoclonal antibody; heavy chain variable region; light; framework;
 KW complementarity determining; CDR1; FR1; FR2; CDR2; FR3; CDR3; FR4;
 KW prostate specific membrane antigen; PSMA; cytostatic; tumour;
 KW colon cancer; renal carcinoma; gene therapy; human; L6.
 XX
 OS Homo sapiens.
 XX
 XX WO2003064606-A2.
 PN
 XX 07-AUG-2003.
 PD
 XX 28-JAN-2003; 2003WO-US002448.
 PF
 XX

CC determining region (CDR) from a non-human antibody and appropriate
 CC framework sequences (I) of human antibodies. (I) is selected by using
 CC canonical CDR structure types of non-human antibody in comparison to
 CC germline canonical CDR structure types of human antibodies as the basis
 CC for selection, for humanisation. The method is useful for making a
 CC humanised antibody or a converted antibody. The method is applicable for
 CC converting a subject antibody sequence of any subject species to a less
 CC immunogenic form suitable for use in an object species. The method is
 CC reliable for identifying suitable human framework sequences to support
 CC non-human CDR regions and to provide humanised antibodies that retain
 CC high antigen binding with low immunogenicity in humans, without the need
 CC for direct comparison of framework sequences, without the need for
 CC determining critically important amino acid residues in the framework,
 CC and without the need for multiple iteration and construction to obtain
 CC humanised antibodies with suitable therapeutic properties. The antibody
 CC has high affinity and low immunogenicity without need for comparing
 CC framework sequences between non-human and human antibodies. This sequence
 CC represents a human light chain variable region gene segment used in the
 CC creation of humanised antibodies
 XX
 SQ Sequence 95 AA;

Query Match 100.0%; Score 34; DB 6; Length 95;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 50 DASNRAT 56

RESULT 38
 ADF10195
 ID ADF10195 standard; protein; 95 AA.

XX ADF10195;
 XX 12-FEB-2004 (first entry)
 XX Antibody light chain variable region VLK_3-11.
 DE
 XX Antibody; stability; solubility; antigen binding affinity;
 KW variable region; human.
 KW Homo sapiens.
 XX OS
 XX WO2003074679-A2.
 XX 12-SEP-2003.

XX 03-MAR-2003; 2003WO-US006598.
 XX 01-MAR-2002; 2002US-0360843P.
 XX 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.
 XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
 XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies
 XX comprises analyzing the interactions of amino acids at variable
 XX positions.
 XX Example 16; Fig 40b; 135pp; English.
 XX The present invention relates to a method for optimizing at least one
 XX physico-chemical property of an antibody by a computational screening
 XX method. The method comprises: receiving a template antibody structure;
 XX selecting at least one variable position belonging to the antibody
 XX structure; selecting at least one amino acid to be considered at the
 XX variable position(s); analyzing the interaction of each selected amino

CC acid at each variable position with at least part of the remainder of the
 CC antibody, including the selected amino acids at other variable positions;
 CC and identifying a set of at least one antibody sequence with at least one
 CC optimized physico-chemical property. The method is useful for optimizing
 CC the physico-chemical properties of an antibody, especially the stability,
 CC solubility, or antigen binding affinity. The optimized antibody may be
 CC useful for treating a patient. The present sequence is an antibody
 CC variable region sequence used to illustrate the invention.
 XX
 SQ Sequence 95 AA;

Query Match 100.0%; Score 34; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 50 DASNRAT 56

RESULT 39
 ADF10093
 ID ADF10093 standard; protein; 95 AA.

XX ADF10093;
 XX 12-FEB-2004 (first entry)
 XX VEGF antibody light chain variable region VLK_3-11.
 DE
 XX Antibody; stability; solubility; antigen binding affinity;
 KW variable region; human; VEGF.
 KW Homo sapiens.
 XX OS
 XX WO2003074679-A2.
 XX 12-SEP-2003.

XX 03-MAR-2003; 2003WO-US006598.
 XX 01-MAR-2002; 2002US-0360843P.
 XX 29-MAY-2002; 2002US-0384197P.

XX (XENC-) XENCOR.
 XX Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
 XX WPI; 2003-722066/68.

XX Computer optimization of physicochemical properties of antibodies
 XX comprises analyzing the interactions of amino acids at variable
 XX positions.

XX Example 6; Fig 16b; 135pp; English.

XX The present invention relates to a method for optimizing at least one
 XX physico-chemical property of an antibody by a computational screening
 XX method. The method comprises: receiving a template antibody structure;
 XX selecting at least one variable position belonging to the antibody
 XX structure; selecting at least one amino acid to be considered at the
 XX variable position(s); analyzing the interaction of each selected amino
 XX acid at each variable position with at least part of the remainder of the
 XX antibody, including the selected amino acids at other variable positions;
 XX and identifying a set of at least one antibody sequence with at least one
 XX optimized physico-chemical property. The method is useful for optimizing
 XX the physico-chemical properties of an antibody, especially the stability,
 XX solubility, or antigen binding affinity. The optimized antibody may be
 XX useful for treating a patient. The present sequence is an antibody
 XX variable region sequence used to illustrate the invention.

XX Sequence 95 AA;
 SQ

Query Match 100.0%; Score 34; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 50 DASNRAT 56

RESULT 40

ADF10196
 ID ADF10196 standard; protein; 95 AA.

XX AC ADF10196;

XX DT 12-FEB-2004 (first entry)

XX DE Antibody light chain variable region VLK_3D-11.

XX KW Antibody; stability; solubility; antigen binding affinity;
 variable region; human.

XX OS Homo sapiens.

XX PN WO2003074679-A2.

XX PD 12-SEP-2003.

XX PF 03-MAR-2003; 2003WO-US006598.

XX PR 01-MAR-2002; 2002US-0360843P.

XX PR 29-MAY-2002; 2002US-0384197P.

XX PA (XENC-) XENCOR.

XX PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;

XX DR WPI; 2003-722066/68.

XX PT Computer optimization of physicochemical properties of antibodies
 comprises analyzing the interactions of amino acids at variable
 positions.

XX PS Example 16; Fig 40b; 135pp; English.

XX CC The present invention relates to a method for optimizing at least one
 physico-chemical property of an antibody by a computational screening
 method. The method comprises: receiving a template antibody structure;
 selecting at least one variable position belonging to the antibody
 structure; selecting at least one amino acid to be considered at the
 variable position(s); analyzing the interaction of each selected amino
 acid at each variable position with at least part of the remainder of the
 antibody, including the selected amino acids at other variable positions;
 and identifying a set of at least one antibody sequence with at least one
 optimized physico-chemical property. The method is useful for optimizing
 the physico-chemical properties of an antibody, especially the stability,
 solubility, or antigen binding affinity. The optimized antibody may be
 useful for treating a patient. The present sequence is an antibody
 variable region sequence used to illustrate the invention.

XX SQ Sequence 95 AA;

Query Match 100.0%; Score 34; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 Db 50 DASNRAT 56

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Title: US-10-720-323-5

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4: /cgm2_6/ptodata/1/iaa/PCTUS COMB pep:*
5: /cgm2_6/ptodata/1/iaa/RE COMB pep:*
6: /cgm2_6/ptodata/1/iaa/backfiles1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	95	2	US-10-194-975-86
2	34	100.0	95	2	Sequence 86, Appl
3	34	100.0	105	2	Sequence 87, Appl
4	34	100.0	107	2	Sequence 6, Appl
5	34	100.0	105	2	Sequence 9, Appl
6	34	100.0	115	1	US-08-844-215-9
7	34	100.0	115	1	US-08-053-131-179
8	34	100.0	115	1	US-08-053-131-181
9	34	100.0	115	1	US-08-096-762-179
10	34	100.0	115	1	US-08-096-762-181
11	34	100.0	115	2	US-09-042-353-42
12	34	100.0	115	2	US-09-042-353-44
13	34	100.0	115	2	US-08-758-417A-307
14	34	100.0	115	2	US-08-758-417A-309
15	34	100.0	224	2	US-09-456-090A-36
16	34	100.0	224	2	US-09-456-090A-46
17	34	100.0	224	2	US-09-456-090A-82
18	34	100.0	224	2	US-09-456-090A-88
19	34	100.0	224	2	US-09-456-090A-90
20	34	100.0	224	2	US-09-453-234-36
21	34	100.0	224	2	US-09-453-234-46
22	34	100.0	224	2	US-09-453-234-82
23	34	100.0	224	2	US-09-453-234-88
24	30	88.2	234	2	US-09-453-234-90
25	30	88.2	493	2	US-09-848-832-4
26	29	85.3	96	2	US-09-328-352-6753
27	29	85.3	106	2	US-10-194-975-83
					Sequence 14, Appl

28	85.3	224	2	US-09-456-090A-84	Sequence 84, Appl
29	85.3	224	2	US-09-453-234-84	Sequence 84, Appl
30	85.3	235	2	US-08-812-586-16	Sequence 16, Appl
31	85.3	235	2	US-09-535-832A-17	Sequence 17, Appl
32	85.3	239	2	US-08-812-586-29	Sequence 29, Appl
33	85.3	239	2	US-09-535-832A-30	Sequence 30, Appl
34	85.3	581	2	US-09-248-796A-15405	Sequence 15405, A
35	82.4	57	1	US-08-162-102C-38	Sequence 38, Appl
36	82.4	88	2	US-09-905-243-32	Sequence 32, Appl
37	82.4	107	1	US-08-276-852-87	Sequence 87, Appl
38	82.4	107	1	US-08-899-575-87	Sequence 87, Appl
39	82.4	107	1	US-08-899-575-87	Sequence 87, Appl
40	82.4	107	2	US-09-438-954-40	Sequence 40, Appl
41	82.4	107	2	US-08-844-215-12	Sequence 12, Appl
42	82.4	107	4	PCT-US95-08743-87	Sequence 87, Appl
43	82.4	108	1	US-08-276-852-99	Sequence 99, Appl
44	82.4	108	1	US-08-899-575-99	Sequence 99, Appl
45	82.4	108	1	US-08-899-575-99	Sequence 99, Appl
46	82.4	108	1	PCT-US95-08743-99	Sequence 99, Appl
47	82.4	109	1	US-08-276-852-147	Sequence 147, Appl
48	82.4	109	1	US-08-162-102C-23	Sequence 23, Appl
49	82.4	109	1	US-08-899-575-147	Sequence 147, Appl
50	82.4	109	1	US-08-899-575-147	Sequence 147, Appl
51	82.4	109	2	US-08-920-100B-23	Sequence 23, Appl
52	82.4	109	4	PCT-US93-08786-23	Sequence 23, Appl
53	82.4	109	4	PCT-US95-08743-147	Sequence 147, Appl
54	82.4	258	2	US-09-252-991A-24184	Sequence 24184, A
55	82.4	304	2	US-09-248-796A-15452	Sequence 15452, A
56	82.4	354	1	US-08-216-894-4	Sequence 4, Appl
57	82.4	354	2	US-09-115-746-4	Sequence 4, Appl
58	82.4	365	2	US-09-252-991A-30166	Sequence 30166, A
59	82.4	401	2	US-09-902-540-13647	Sequence 13647, A
60	82.4	484	2	US-09-902-540-10713	Sequence 10713, A
61	82.4	564	1	US-08-216-894-2	Sequence 2, Appl
62	82.4	564	2	US-09-115-746-2	Sequence 2, Appl
63	82.4	643	1	US-08-216-894-8	Sequence 8, Appl
64	82.4	643	2	US-09-115-746-8	Sequence 8, Appl
65	79.4	17	1	US-08-743-894B-29	Sequence 29, Appl
66	79.4	158	2	US-09-433-248A-4	Sequence 4, Appl
67	79.4	381	1	US-08-173-508-12	Sequence 12, Appl
68	79.4	381	1	US-08-265-310-12	Sequence 12, Appl
69	79.4	381	2	US-08-951-742-12	Sequence 12, Appl
70	79.4	566	1	US-08-415-823-4	Sequence 4, Appl
71	79.4	566	1	US-09-086-662-4	Sequence 4, Appl
72	79.4	1752	2	US-09-865-621A-2	Sequence 2, Appl
73	76.5	47	2	US-09-270-767-39990	Sequence 39990, A
74	76.5	47	2	US-09-270-767-55206	Sequence 55206, A
75	76.5	87	2	US-09-543-681A-5167	Sequence 5167, Ap
76	76.5	91	2	US-09-605-703B-2920	Sequence 2920, Ap
77	76.5	133	2	US-09-902-540-11050	Sequence 11050, A
78	76.5	165	2	US-09-252-991A-19000	Sequence 19000, A
79	76.5	178	2	US-09-780-717-38	Sequence 38, Appl
80	76.5	202	2	US-09-780-717-41	Sequence 41, Appl
81	76.5	211	2	US-09-270-767-36404	Sequence 36404, A
82	76.5	211	2	US-09-270-767-51621	Sequence 51621, A
83	76.5	221	2	US-09-107-433-2796	Sequence 2796, Ap
84	76.5	253	2	US-09-248-796A-17009	Sequence 17009, A
85	76.5	266	2	US-08-961-083A-14	Sequence 14, Appl
86	76.5	266	2	US-09-536-784-14	Sequence 14, Appl
87	76.5	266	2	US-09-765-271-14	Sequence 14, Appl
88	76.5	266	2	US-09-765-272A-14	Sequence 14, Appl
89	76.5	286	2	US-09-902-540-16395	Sequence 16395, A
90	76.5	289	2	US-09-270-767-38618	Sequence 38618, A
91	76.5	289	1	US-09-270-767-53835	Sequence 53835, A
92	76.5	289	1	US-08-137-175A-6	Sequence 6, Appl
93	76.5	289	2	US-08-479-017-6	Sequence 6, Appl
94	76.5	376	2	US-09-270-767-44173	Sequence 44173, A
95	76.5	515	2	US-09-270-767-43227	Sequence 43227, A
96	76.5	594	2	US-10-104-047-3281	Sequence 3281, Ap
97	76.5	647	2	US-09-540-236-2099	Sequence 2099, Ap
98	76.5	786	2	US-10-002-344A-221	Sequence 221, Appl
99	76.5	824	2	US-09-252-991A-18601	Sequence 18601, A
100	76.5	1014	2	US-09-252-991A-31338	Sequence 31338, A

ALIGNMENTS

RESULT 1

US-10-194-975-86
; Sequence 86, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-86

Query Match 100.0%; Score 34; DB 2; Length 95;

Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7

Db 50 DASNRAT 56

RESULT 2

US-10-194-975-87
; Sequence 87, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-87

Query Match 100.0%; Score 34; DB 2; Length 95;

Best Local Similarity 100.0%; Pred. No. 2.4; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7

Db 50 DASNRAT 56

RESULT 3

US-08-635-109-6
; Sequence 6, Application US/08635109
; Patent No. 6538114
; GENERAL INFORMATION:
; APPLICANT: Persson, Mats A. A.
; APPLICANT: Allander, Tobias E.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,109
FILING DATE: 19-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCracken, Thomas P
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 2300-6146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-635-109-6

Query Match 100.0%; Score 34; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7

Db 49 DASNRAT 55

RESULT 4

US-08-844-215-9
; Sequence 9, Application US/08844215
; Patent No. 6747136
; GENERAL INFORMATION:
; APPLICANT: PERSSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/635,109
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548

REFERENCE/DOCKET NUMBER: 80146.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-844-215-9

Query Match 100.0%; Score 34; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 2.7; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
Db 49 DASNRAT 55

RESULT 5
US-09-434-870-2
Sequence 2, Application US/09434870
Patent No. 6849425
GENERAL INFORMATION:
APPLICANT: Huse, William
APPLICANT: Watkins, Jeffrey
APPLICANT: Wu, Herren
TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
FILE REFERENCE: AME-08352
CURRENT APPLICATION NUMBER: US/09/434,870
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/159,689
PRIOR FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 107
TYPE: PRT
ORGANISM: Homo sapiens
US-09-434-870-2

Query Match 100.0%; Score 34; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 6
US-08-053-131-179
Sequence 179, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-053-131-179

Query Match 100.0%; Score 34; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 7
US-08-053-131-181
Sequence 181, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408

; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-053-131-181

Query Match 100.0%; Score 34; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 8

US-08-096-762-179
; Sequence 179, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 179:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-096-762-179

Query Match 100.0%; Score 34; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 9

US-08-096-762-181
; Sequence 181, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-096-762-181

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Query Match          100.0%; Score 34; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 10
US-09-042-353-42
; Sequence 42, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; PRIOR APPLICATION DATA:
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; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-042-353-42

Query Match          100.0%; Score 34; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 11
US-09-042-353-44
; Sequence 44, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-042-353-44

Query Match 100.0%; Score 34; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 12
US-08-758-417A-307
; Sequence 307, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 307:
US-08-758-417A-307

Query Match 100.0%; Score 34; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 13
US-08-758-417A-309
; Sequence 309, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/758,417A
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-Dec-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-0090300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 309:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 309:
US-08-758-417A-309

Query Match 100.0%; Score 34; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DASNRAT 76

RESULT 14
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 36

; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M1-1L
US-09-456-090A-36
Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 15
US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-456-090A-46

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 16
US-09-456-090A-82
; Sequence 82, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 17
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; TYPE: PRT
; LENGTH: 224
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 18
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; TYPE: PRT
; LENGTH: 224
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 19
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453.234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; TYPE: PRT
; LENGTH: 224
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-36

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 20
US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453.234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; TYPE: PRT
; LENGTH: 224
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 21
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
```


; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 22
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 23
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US

; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match 100.0%; Score 34; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 24
US-09-848-832-4
; Sequence 4, Application US/09848832
; Patent No. 6890532
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECIFIC NEUTRALIZING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; FILE REFERENCE: H0001.NP0002
; CURRENT APPLICATION NUMBER: US/09/848,832
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-848-832-4

Query Match 88.2%; Score 30; DB 2; Length 234;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 70 DTSNRAT 76

RESULT 25
US-09-328-352-6753
; Sequence 6753, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6753
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6753

Query Match 88.2%; Score 30; DB 2; Length 493;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;

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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DASNRAT 7
Db 24 DASNRAT 30
||||:|

RESULT 26
US-10-194-975-83
; Sequence 83, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-83

Query Match 85.3%; Score 29; DB 2; Length 96;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DASNRAT 7
Db 51 DASNRAT 57
||||:|

RESULT 27
US-08-844-215-14
; Sequence 14, Application US/08844215
; Patent No. 6747136
; GENERAL INFORMATION:
; APPLICANT: PERSSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,215
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/635,109
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 80146.002
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-844-215-14

Query Match 85.3%; Score 29; DB 2; Length 106;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DASNRAT 7
Db 50 DASNRAT 56
||||:|

RESULT 28
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84

Query Match 85.3%; Score 29; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DASNRAT 6
Db 50 DASNRAT 55
||||:|

RESULT 29
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84
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Query Match      85.3%; Score 29; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRA 6
Db      50 DASNRA 55

RESULT 30
US-08-812-586-16
; Sequence 16, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-812-586-16

Query Match      85.3%; Score 29; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      72 DASSRAT 78

RESULT 31
US-09-535-832A-17
; Sequence 17, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
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; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-535-832A-17

Query Match      85.3%; Score 29; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      72 DASSRAT 78

RESULT 32
US-08-812-586-29
; Sequence 29, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-812-586-29

Query Match      85.3%; Score 29; DB 2; Length 239;
Best Local Similarity 85.7%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      75 DASSRAT 81

RESULT 33
US-09-535-832A-30
; Sequence 30, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
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RESULT 37
US-08-276-852-87
; Sequence 87, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-276-852-87
Query Match 82.4%; Score 28; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ASNRAT 7
Db 50 ASNRAT 55
RESULT 38
US-08-276-852-87
; Sequence 87, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel

; STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-899-575-87
Query Match 82.4%; Score 28; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ASNRAT 7
Db 50 ASNRAT 55
RESULT 39
US-08-899-575-87
; Sequence 87, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/899,575
; FILING DATE: 24-JUL-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/276,852
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/954,148
; FILING DATE: 30-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-899-575-87

Query Match 82.4%; Score 28; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASNRAT 7
Db 50 ASNRAT 55

RESULT 40
US-09-438-954-40
; Sequence 40, Application US/09438954
; Patent No. 6458334
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of human antibody (X82934)
US-09-438-954-40

Query Match 82.4%; Score 28; DB 2; Length 107;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASRRAT 56

Search completed: December 14, 2005, 07:33:22
Job time : 11.2586 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:54 ; Search time 32.1034 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-720-323-5

Perfect score: 34

Sequence: 1 DASNRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	34	100.0	7	3	US-09-920-267C-5
2	34	100.0	7	4	US-10-173-551-11
3	34	100.0	7	4	US-10-338-366-34
4	34	100.0	7	4	US-10-658-789-72
5	34	100.0	7	4	US-10-687-799-17
6	34	100.0	7	4	US-10-687-799-23
7	34	100.0	7	4	US-10-687-799-29
8	34	100.0	7	4	US-10-720-323-5
9	34	100.0	7	4	US-10-396-578-36
10	34	100.0	7	4	US-10-396-578-84
11	34	100.0	7	5	US-10-883-020-17
12	34	100.0	7	5	US-10-911-838-11
13	34	100.0	7	5	US-10-484-790A-6
14	34	100.0	7	5	US-10-891-658-123
15	34	100.0	7	5	US-10-891-658-129
16	34	100.0	7	6	US-11-074-803-36
17	34	100.0	7	6	US-11-074-803-84
18	34	100.0	7	6	US-11-009-731-63
19	34	100.0	7	6	US-11-009-731-68
20	34	100.0	7	6	US-11-009-731-70
21	34	100.0	7	6	US-11-102-403-45
22	34	100.0	8	4	US-10-394-471B-13
23	34	100.0	95	4	US-10-194-975-86
24	34	100.0	95	4	US-10-194-975-87
25	34	100.0	95	4	US-10-308-817-33
26	34	100.0	95	4	US-10-308-817-34
27	34	100.0	95	4	US-10-453-698-33

28	34	100.0	95	4	US-10-453-698-34	Sequence 34, Appl
29	34	100.0	95	4	US-10-378-392-93	Sequence 93, Appl
30	34	100.0	95	4	US-10-378-392-94	Sequence 94, Appl
31	34	100.0	101	6	US-11-009-731-96	Sequence 96, Appl
32	34	100.0	102	5	US-10-916-840-26	Sequence 26, Appl
33	34	100.0	102	5	US-10-916-840-30	Sequence 30, Appl
34	34	100.0	102	5	US-10-916-840-38	Sequence 38, Appl
35	34	100.0	105	2	US-08-844-215-9	Sequence 9, Appl
36	34	100.0	105	4	US-10-409-938-19	Sequence 19, Appl
37	34	100.0	106	6	US-11-021-715-99	Sequence 99, Appl
38	34	100.0	107	3	US-09-791-153A-69	Sequence 69, Appl
39	34	100.0	107	3	US-09-791-153A-71	Sequence 71, Appl
40	34	100.0	107	3	US-09-982-464-2	Sequence 2, Appl
41	34	100.0	107	4	US-10-263-805-62	Sequence 62, Appl
42	34	100.0	107	4	US-10-181-324-4	Sequence 4, Appl
43	34	100.0	107	4	US-10-338-366-8	Sequence 8, Appl
44	34	100.0	107	4	US-10-251-085B-141	Sequence 141, App
45	34	100.0	107	4	US-10-251-085B-142	Sequence 142, App
46	34	100.0	107	4	US-10-251-085B-143	Sequence 143, App
47	34	100.0	107	4	US-10-697-399-2	Sequence 2, Appl
48	34	100.0	107	4	US-10-737-252-141	Sequence 141, App
49	34	100.0	107	4	US-10-737-252-142	Sequence 142, App
50	34	100.0	107	4	US-10-737-252-143	Sequence 143, App
51	34	100.0	107	5	US-10-697-400-2	Sequence 2, Appl
52	34	100.0	107	5	US-10-911-838-14	Sequence 14, Appl
53	34	100.0	107	5	US-10-911-838-21	Sequence 21, Appl
54	34	100.0	107	5	US-10-891-658-89	Sequence 89, Appl
55	34	100.0	107	5	US-10-891-658-91	Sequence 91, Appl
56	34	100.0	107	5	US-10-937-596-27	Sequence 27, Appl
57	34	100.0	107	5	US-10-916-840-157	Sequence 157, App
58	34	100.0	107	6	US-11-021-715-98	Sequence 98, Appl
59	34	100.0	107	6	US-11-102-403-1	Sequence 1, Appl
60	34	100.0	107	6	US-11-102-403-3	Sequence 3, Appl
61	34	100.0	107	6	US-11-102-403-17	Sequence 17, Appl
62	34	100.0	108	3	US-09-920-267C-8	Sequence 8, Appl
63	34	100.0	108	4	US-10-305-347A-8	Sequence 8, Appl
64	34	100.0	108	4	US-10-371-942-68	Sequence 68, Appl
65	34	100.0	108	4	US-10-173-551-9	Sequence 9, Appl
66	34	100.0	108	4	US-10-720-323-8	Sequence 8, Appl
67	34	100.0	108	5	US-10-886-838-4	Sequence 4, Appl
68	34	100.0	108	5	US-10-954-900A-8	Sequence 8, Appl
69	34	100.0	108	6	US-11-009-731-85	Sequence 85, Appl
70	34	100.0	108	6	US-11-009-731-90	Sequence 90, Appl
71	34	100.0	108	6	US-11-009-731-92	Sequence 92, Appl
72	34	100.0	108	6	US-11-021-715-101	Sequence 101, App
73	34	100.0	108	6	US-11-102-403-9	Sequence 9, Appl
74	34	100.0	108	6	US-11-102-403-11	Sequence 11, Appl
75	34	100.0	109	4	US-10-408-901-8	Sequence 8, Appl
76	34	100.0	109	4	US-10-408-901-16	Sequence 16, Appl
77	34	100.0	109	4	US-10-408-901-24	Sequence 24, Appl
78	34	100.0	109	4	US-10-408-901-28	Sequence 28, Appl
79	34	100.0	109	5	US-10-484-790A-2	Sequence 2, Appl
80	34	100.0	111	5	US-10-916-840-66	Sequence 66, Appl
81	34	100.0	113	4	US-10-374-600-21	Sequence 21, Appl
82	34	100.0	113	4	US-10-374-531-21	Sequence 21, Appl
83	34	100.0	125	4	US-10-693-629-54	Sequence 54, Appl
84	34	100.0	126	4	US-10-693-629-30	Sequence 30, Appl
85	34	100.0	127	4	US-10-687-799-4	Sequence 4, Appl
86	34	100.0	127	4	US-10-687-799-8	Sequence 8, Appl
87	34	100.0	127	4	US-10-687-799-12	Sequence 12, Appl
88	34	100.0	127	4	US-10-687-799-57	Sequence 57, Appl
89	34	100.0	128	4	US-10-656-769-12	Sequence 12, Appl
90	34	100.0	128	4	US-10-478-056-31	Sequence 31, Appl
91	34	100.0	129	4	US-10-693-629-34	Sequence 34, Appl
92	34	100.0	129	4	US-10-478-056-19	Sequence 19, Appl
93	34	100.0	129	4	US-10-478-056-23	Sequence 23, Appl
94	34	100.0	130	4	US-10-394-471B-16	Sequence 16, Appl
95	34	100.0	139	4	US-10-687-799-55	Sequence 55, Appl
96	34	100.0	214	5	US-10-484-790A-19	Sequence 19, Appl
97	34	100.0	215	4	US-10-408-901-32	Sequence 32, Appl
98	34	100.0	215	4	US-10-408-901-40	Sequence 40, Appl
99	34	100.0	215	4	US-10-408-901-48	Sequence 48, Appl
100	34	100.0	215	4	US-10-408-901-52	Sequence 52, Appl

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ALIGNMENTS

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD30
; FILE REFERENCE: MXI-180
; CURRENT APPLICATION NUMBER: US/10/338,366
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/347649
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/404427
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/431684
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-366-34

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
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Db      1 DASNRAT 7

RESULT 4
US-10-656-769-72
; Sequence 72, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-72

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
        |||||
Db      1 DASNRAT 7

RESULT 5
US-10-687-799-17
; Sequence 17, Application US/10687799
; Publication No. US20040167319A1
; GENERAL INFORMATION:
; APPLICANT: Teeling, Jessica
; APPLICANT: Ruuls, Sigrid
; APPLICANT: Glennie, Martin
; APPLICANT: van de Winkel, Jan
; APPLICANT: Parren, Paul
; APPLICANT: Petersen, Jorgen
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055

; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-5

Query Match      100.0%; Score 34; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
        |||||
Db      1 DASNRAT 7

RESULT 2
US-10-173-551-11
; Sequence 11, Application US/10173551
; Publication No. US2003023387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-11

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
        |||||
Db      1 DASNRAT 7

RESULT 3
US-10-338-366-34
; Sequence 34, Application US/10338366
; Publication No. US20040006215A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Graziano, Robert
; APPLICANT: Trembl, John
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; CURRENT APPLICATION NUMBER: US/10/687,799
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,163
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/460,028
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-799-17

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Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 DASNRAT 7
Db      1 DASNRAT 7

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RESULT 6

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US-10-687-799-23
; Sequence 23, Application US/10687799
; Publication No. US20040167319A1
; GENERAL INFORMATION:
; APPLICANT: Teeling, Jessica
; APPLICANT: Ruuls, Sigrid
; APPLICANT: Glennie, Martin
; APPLICANT: van de Winkel, Jan
; APPLICANT: Parren, Paul
; APPLICANT: Petersen, Jorgen
; APPLICANT: Baadsgaard, Ole
; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055
; CURRENT APPLICATION NUMBER: US/10/687,799
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,163
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/460,028
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-799-23

```

```

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DASNRAT 7
Db      1 DASNRAT 7

```

RESULT 7

```

US-10-687-799-29
; Sequence 29, Application US/10687799
; Publication No. US20040167319A1
; GENERAL INFORMATION:
; APPLICANT: Teeling, Jessica
; APPLICANT: Ruuls, Sigrid
; APPLICANT: Glennie, Martin
; APPLICANT: van de Winkel, Jan
; APPLICANT: Parren, Paul
; APPLICANT: Petersen, Jorgen
; APPLICANT: Baadsgaard, Ole

```

```

; APPLICANT: Huang, Haichun
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST CD20
; FILE REFERENCE: GMI-055
; CURRENT APPLICATION NUMBER: US/10/687,799
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,163
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/460,028
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-799-29

```

```

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DASNRAT 7
Db      1 DASNRAT 7

```

RESULT 8

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US-10-720-323-5
; Sequence 5, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-5

```

```

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DASNRAT 7
Db      1 DASNRAT 7

```

RESULT 9

```

US-10-396-578-36
; Sequence 36, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97

```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-36

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      1 DASNRAT 7

RESULT 10
US-10-396-578-84
; Sequence 84, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-84

Query Match      100.0%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      1 DASNRAT 7

RESULT 11
US-10-883-020-17
; Sequence 17, Application US/10883020
; Publication No. US20050048070A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Cancer-Associated Epitope
; FILE REFERENCE: 1361.017U51
; CURRENT APPLICATION NUMBER: US/10/883,020
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US03/00297
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
;
```

```
; ORGANISM: Homo sapiens
US-10-883-020-17

Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      1 DASNRAT 7

RESULT 12
US-10-911-838-11
; Sequence 11, Application US/10911838
; Publication No. US20050069869A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: LUZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: M11-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: SARS-Associated Coronavirus
US-10-911-838-11

Query Match      100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      1 DASNRAT 7

RESULT 13
US-10-484-790A-6
; Sequence 6, Application US/10484790A
; Publication No. US20050070694A1
; GENERAL INFORMATION:
; APPLICANT: Gelfanova, et al., Valentina
; TITLE OF INVENTION: Antagonistic Anti-HTNF3b Human Antibodies
; FILE REFERENCE: X-15239
; CURRENT APPLICATION NUMBER: US/10/484,790A
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-790A-6
```

```
Query Match          100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 14
US-10-891-658-123
; Sequence 123, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 123
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-123

Query Match          100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 15
US-10-891-658-129
; Sequence 129, Application US/10891658
; Publication No. US20050074821A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth, Wild
; APPLICANT: Treanor, James
; APPLICANT: Huang, Haichun
; APPLICANT: Inoue, Heather
; APPLICANT: Zhang, Tie J.
; APPLICANT: Martin, Frank
; TITLE OF INVENTION: Human anti-NGF Neutralizing Antibodies as Selective NGF Pathway
; FILE REFERENCE: 02-1240
; CURRENT APPLICATION NUMBER: US/10/891,658
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/487,431
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-10-891-658-129

Query Match          100.0%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 16
US-11-074-803-36
; Sequence 36, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-11-074-803-36

Query Match          100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 17
US-11-074-803-84
; Sequence 84, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-11-074-803-84

Query Match          100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 18
```

US-11-009-731-63
; Sequence 63, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-63

Query Match 100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 19
US-11-009-731-68
; Sequence 68, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-68

Query Match 100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 20
US-11-009-731-70
; Sequence 70, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-70

Query Match 100.0%; Score 34; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 1 DASNRAT 7

RESULT 21
US-11-102-403-45
; Sequence 45, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PARREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 45
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-45

Query Match 100.0%; Score 34; DB 6; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
| | | | |
Db 1 DASNRAT 7

RESULT 22

US-10-394-471B-13
; Sequence 13, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallion, Bernard J.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-13

Query Match 100.0%; Score 34; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
| | | | |
Db 1 DASNRAT 7

RESULT 23

US-10-194-975-86
; Sequence 86, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-86

Query Match 100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
| | | | |
Db 50 DASNRAT 56

RESULT 24

US-10-194-975-87
; Sequence 87, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies

; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-87

Query Match 100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
| | | | |
Db 50 DASNRAT 56

RESULT 25

US-10-308-817-33
; Sequence 33, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
US-10-308-817-33

Query Match 100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 DASNRAT 7
| | | | |
Db 50 DASNRAT 56

RESULT 26

US-10-308-817-34
; Sequence 34, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
US-10-308-817-34

Query Match 100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

```
Qy      1  DASNRAT 7
      |||||||
Db      50  DASNRAT 56

RESULT 27
US-10-453-698-33
; Sequence 33, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
US-10-453-698-33

Query Match      100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  DASNRAT 7
      |||||||
Db      50  DASNRAT 56

RESULT 28
US-10-453-698-34
; Sequence 34, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
US-10-453-698-34

Query Match      100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  DASNRAT 7
      |||||||
Db      50  DASNRAT 56

RESULT 29
US-10-379-392-93
; Sequence 93, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
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; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-93

Query Match      100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  DASNRAT 7
      |||||||
Db      50  DASNRAT 56

RESULT 30
US-10-379-392-94
; Sequence 94, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Basil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-94

Query Match      100.0%; Score 34; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  DASNRAT 7
      |||||||
Db      50  DASNRAT 56

RESULT 31
US-11-009-731-96
; Sequence 96, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirikant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
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; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-96

Query Match 100.0%; Score 34; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 32
US-10-916-840-26
; Sequence 26, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
; APPLICANT: Hufton, Simon E.
; APPLICANT: Pieters, Henk
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Rookey, Kristen
; TITLE OF INVENTION: T1E1-BINDING LIGANDS
; FILE REFERENCE: 10280-083001
; CURRENT APPLICATION NUMBER: US/10/916,840
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide

US-10-916-840-26

Query Match 100.0%; Score 34; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 51 DASNRAT 57

RESULT 33
US-10-916-840-30
; Sequence 30, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
; APPLICANT: Hufton, Simon E.
; APPLICANT: Pieters, Henk
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Rookey, Kristen
; TITLE OF INVENTION: T1E1-BINDING LIGANDS
; FILE REFERENCE: 10280-083001
; CURRENT APPLICATION NUMBER: US/10/916,840
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30

; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-916-840-30

Query Match 100.0%; Score 34; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 51 DASNRAT 57

RESULT 34
US-10-916-840-38
; Sequence 38, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
; APPLICANT: Hufton, Simon E.
; APPLICANT: Pieters, Henk
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Rookey, Kristen
; TITLE OF INVENTION: T1E1-BINDING LIGANDS
; FILE REFERENCE: 10280-083001
; CURRENT APPLICATION NUMBER: US/10/916,840
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide

Query Match 100.0%; Score 34; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 51 DASNRAT 57

RESULT 35
US-08-844-215-9
; Sequence 9, Application US/08844215
; Publication No. US20020016445A1
; GENERAL INFORMATION:
; APPLICANT: PERSSON, MATS AXEL
; APPLICANT: ALLANDER, TOBIAS ERIK
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,215
; FILING DATE: 17-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/635,109
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 80146.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-844-215-9

Query Match 100.0%; Score 34; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 49 DASNRAT 55

RESULT 36

US-10-409-938-19
; Sequence 19, Application US/10409938
; Publication No. US20030219733A1
; GENERAL INFORMATION:
; APPLICANT: Clark et al.
; TITLE OF INVENTION: ANTIBODY GENE TRANSFER AND RECOMBINANT AAV THEREFOR
; FILE REFERENCE: 28335/39282
; CURRENT APPLICATION NUMBER: US/10/409,938
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/371,501
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-409-938-19

Query Match 100.0%; Score 34; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 47 DASNRAT 53

RESULT 37

US-11-021-715-99
; Sequence 99, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304

; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-99

Query Match 100.0%; Score 34; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 38

US-09-791-153A-69
; Sequence 69, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-69

Query Match 100.0%; Score 34; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 39

US-09-791-153A-71
; Sequence 71, Application US/09791153A
; Publication No. US20030103978A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Hitz, Anna
; APPLICANT: Boyle, William
; APPLICANT: Sullivan, John
; TITLE OF INVENTION: SELECTIVE BINDING AGENTS OF OSTEOCALCIN BINDING PROTEIN
; FILE REFERENCE: A-633A
; CURRENT APPLICATION NUMBER: US/09/791,153A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/511,139
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 107


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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-153A-71

Query Match      100.0%; Score 34; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      |||||
Db      50 DASNRAT 56

RESULT 40
US-09-982-464-2
; Sequence 2, Application US/09982464
; Publication No. US2003012004A1
; GENERAL INFORMATION:
; APPLICANT: Huse, William
; APPLICANT: Watkins, Jeffrey
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-06352
; CURRENT APPLICATION NUMBER: US/09/982,464
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: 09/434,870
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/159,689
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-464-2

Query Match      100.0%; Score 34; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      |||||
Db      50 DASNRAT 56

Search completed: December 14, 2005, 07:37:54
Job time : 33.1034 secs
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THE UNIVERSITY OF CHICAGO

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:25:44 ; Search time 2.17241 Seconds
(without alignments)
21.698 Million cell updates/sec

Title: US-10-720-323-5

Perfect score: 34

Sequence: 1 DASNRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	7	US-11-093-274-13	Sequence 13, Appl
2	34	100.0	7	US-11-093-274-14	Sequence 14, Appl
3	34	100.0	7	US-11-093-274-15	Sequence 15, Appl
4	34	100.0	94	US-11-093-274-33	Sequence 33, Appl
5	34	100.0	95	US-11-054-669-86	Sequence 86, Appl
6	34	100.0	95	US-11-054-669-87	Sequence 87, Appl
7	34	100.0	95	US-11-084-554-131	Sequence 131, Appl
8	34	100.0	95	US-11-084-554-138	Sequence 138, Appl
9	34	100.0	107	US-11-040-159-17	Sequence 17, Appl
10	34	100.0	107	US-11-093-274-24	Sequence 24, Appl
11	34	100.0	108	US-11-093-274-22	Sequence 22, Appl
12	34	100.0	108	US-11-093-274-23	Sequence 23, Appl
13	34	100.0	128	US-10-721-763-31	Sequence 31, Appl
14	34	100.0	129	US-10-721-763-19	Sequence 19, Appl
15	34	100.0	129	US-10-721-763-23	Sequence 23, Appl
16	34	100.0	251	US-11-054-515-1049	Sequence 1049, Ap
17	29	85.3	96	US-11-054-669-83	Sequence 83, Appl
18	29	85.3	96	US-11-084-554-105	Sequence 105, App
19	26	76.5	7	US-11-096-706-200	Sequence 200, App
20	25	73.5	125	US-10-793-626-1454	Sequence 1454, Ap
21	25	73.5	254	US-11-054-515-905	Sequence 905, App
22	25	73.5	474	US-11-008-331-4	Sequence 4, Appli
23	25	73.5	557	US-10-793-626-1486	Sequence 1486, Ap
24	25	73.5	586	US-11-073-112-18	Sequence 18, Appl
25	25	73.5	856	US-10-467-657-8534	Sequence 8534, Ap

Sequence 62, Appl
Sequence 3744, Ap

99 22 64.7 109 7 US-11-127-677-62
100 22 64.7 116 6 US-10-467-657-3744

ALIGNMENTS

RESULT 1

US-11-093-274-13
; Sequence 13, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-13

Query Match 100.0%; Score 34; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
| | | | |
Db 1 DASNRAT 7

RESULT 2

US-11-093-274-14
; Sequence 14, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-14

Query Match 100.0%; Score 34; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
| | | | |
Db 1 DASNRAT 7

RESULT 3

US-11-093-274-15
; Sequence 15, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-15

Query Match 100.0%; Score 34; DB 7; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
| | | | |
Db 1 DASNRAT 7

RESULT 4

US-11-093-274-33
; Sequence 33, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-33

Query Match 100.0%; Score 34; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
| | | | |
Db 50 DASNRAT 56

RESULT 5

US-11-054-669-86
; Sequence 86, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES

```
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-86

Query Match      100.0%; Score 34; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 6
US-11-054-669-87
; Sequence 87, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-87

Query Match      100.0%; Score 34; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 7
US-11-084-554-131
; Sequence 131, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-131

Query Match      100.0%; Score 34; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 8
US-11-084-554-138
; Sequence 138, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: AGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-138

Query Match      100.0%; Score 34; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 50 DASNRAT 56

RESULT 9
US-11-040-159-17
; Sequence 17, Application US/11040159
; Publication No. US2005025552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehrs, Kenneth
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Hong
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey T.
; APPLICANT: KaloBios, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; FILE REFERENCE: Binding Determinants
; TITLE OF INVENTION: 021167-001730US
; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 17
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:V-region of
; OTHER INFORMATION: anti-PcrV antibody 1F1 VL
US-11-040-159-17

Query Match      100.0%; Score 34; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      50 DASNRAT 56

RESULT 10
US-11-093-274-24
; Sequence 24, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-24

Query Match      100.0%; Score 34; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      50 DASNRAT 56

RESULT 11
US-11-093-274-22
; Sequence 22, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-22

Query Match      100.0%; Score 34; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      50 DASNRAT 56

RESULT 12
US-11-093-274-23
; Sequence 23, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-23

Query Match      100.0%; Score 34; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      50 DASNRAT 56

RESULT 13
US-10-721-763-31
; Sequence 31, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-31

Query Match      100.0%; Score 34; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
```

Db 70 DASNRAT 76
|||||
US-10-721-763-19
RESULT 14
US-10-721-763-19
; Sequence 19, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19
Query Match 100.0%; Score 34; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 70 DASNRAT 76
|||||
US-10-721-763-23
RESULT 15
US-10-721-763-23
; Sequence 23, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-23
Query Match 100.0%; Score 34; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 70 DASNRAT 76
|||||
US-11-054-515-1049
RESULT 16
US-11-054-515-1049
; Sequence 1049, Application US/11054515

; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1049
Query Match 100.0%; Score 34; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 192 DASNRAT 198
|||||
US-11-054-669-83
RESULT 17
US-11-054-669-83
; Sequence 83, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-83
Query Match 85.3%; Score 29; DB 7; Length 96;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 51 DASNRAT 57
|||||

RESULT 18

US-11-084-554-105
; Sequence 105, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korvetz, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ARGENIX.100A
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/11/084,554
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-105

Query Match 85.3%; Score 29; DB 7; Length 96;
Best Local Similarity 85.7%; Pred. No. 2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
| | | | |
DB 51 DASGRAT 57

RESULT 19

US-11-096-706-200
; Sequence 200, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-08220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-200

Query Match 76.5%; Score 26; DB 7; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.9e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DASNRAT 7
| | | | |
DB 1 DSSNRAT 7

RESULT 20

US-10-793-626-1454

; Sequence 1454, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1454
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1454

Query Match 73.5%; Score 25; DB 6; Length 125;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNR 5
| | | | |
DB 37 DASNR 41

RESULT 21

US-11-054-515-905
; Sequence 905, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 905
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-905

Query Match 73.5%; Score 25; DB 7; Length 254;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DASNRAT 7


```

Db      195 DVSSRAT 201
|:|:|:|
|:|:|:|

RESULT 22
US-11-008-331-4
; Sequence 4, Application US/11008331
; Publication No. US20050244925A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms
; FILE REFERENCE: GC386-PCT
; CURRENT APPLICATION NUMBER: US/11/008,331
; CURRENT FILING DATE: 2004-12-08
; PRIOR APPLICATION NUMBER: EP9719637.2
; PRIOR FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Schizocaccharomyces pombe
US-11-008-331-4

Query Match      73.5%; Score 25; DB 7; Length 474;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
|:|:|:|
|:|:|:|

Db      290 DASRRST 296

RESULT 23
US-10-793-626-1486
; Sequence 1486, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUJ480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1486
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1486

Query Match      73.5%; Score 25; DB 6; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNR 5
|:|:|:|
|:|:|:|

Db      37 DASNR 41

RESULT 24
US-11-073-112-18
; Sequence 18, Application US/11073112
; Publication No. US20050260627A1
; GENERAL INFORMATION:
; APPLICANT: Hincz et al.
; TITLE OF INVENTION: Mannosidases and Methods for using the Same
; FILE REFERENCE: 62447-02

; CURRENT APPLICATION NUMBER: US/11/073,112
; CURRENT FILING DATE: 2005-03-03
; PRIOR APPLICATION NUMBER: PCT/US00/27210
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/157,341
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-11-073-112-18

Query Match      73.5%; Score 25; DB 7; Length 586;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASNRAT 7
|:|:|:|
|:|:|:|

Db      31 AANRAT 36

RESULT 25
US-10-467-657-8534
; Sequence 8534, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8534
; LENGTH: 856
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8534

Query Match      73.5%; Score 25; DB 6; Length 856;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ASNRAT 7
|:|:|:|
|:|:|:|

Db      649 ASNRST 654

RESULT 26
US-11-075-185-5
; Sequence 5, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290

```

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; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 3655
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-11-075-185-5

Query Match      73.5%; Score 25; DB 7; Length 3655;
Best Local Similarity 71.4%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      ||: ||||
Db      3199 DAAGRAT 3205

RESULT 27
US-10-995-561-773
; Sequence 773, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 773
; LENGTH: 3803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-773

Query Match      73.5%; Score 25; DB 6; Length 3803;
Best Local Similarity 71.4%; Pred. No. 8.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      ||: ||||
Db      1598 DIQNRAT 1604

RESULT 28
US-10-995-561-771
; Sequence 771, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 771
; LENGTH: 3960
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-771

Query Match      73.5%; Score 25; DB 6; Length 3960;
Best Local Similarity 71.4%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      ||: ||||
Db      1598 DIQNRAT 1604

RESULT 29
US-10-995-561-556
; Sequence 556, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 556
; LENGTH: 4655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-556

Query Match      73.5%; Score 25; DB 6; Length 4655;
Best Local Similarity 71.4%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      ||: ||||
Db      3437 DGSNRQT 3443

RESULT 30
US-10-995-561-777
; Sequence 777, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 777
; LENGTH: 5335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-777

Query Match      73.5%; Score 25; DB 6; Length 5335;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      ||: ||||
Db      1506 DIQNRAT 1512

RESULT 31
US-10-995-561-774
; Sequence 774, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
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; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 5406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-774

Query Match      73.5%; Score 25; DB 6; Length 5406;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      | |||
Db      1598 DIQNRAT 1604

RESULT 32
US-10-995-561-779
; Sequence 779, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 779
; LENGTH: 5415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-779

Query Match      73.5%; Score 25; DB 6; Length 5415;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      | |||
Db      1598 DIQNRAT 1604

RESULT 33
US-10-995-561-775
; Sequence 775, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 775
; LENGTH: 5464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-775

Query Match      73.5%; Score 25; DB 6; Length 5464;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      | |||
Db      1598 DIQNRAT 1604

; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 5935
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-776

Query Match      73.5%; Score 25; DB 6; Length 5935;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      | |||
Db      2100 DIQNRAT 2106

RESULT 34
US-10-995-561-776
; Sequence 776, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 776
; LENGTH: 5935
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-776

Query Match      73.5%; Score 25; DB 6; Length 5935;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      | |||
Db      2100 DIQNRAT 2106

RESULT 35
US-11-096-706-202
; Sequence 202, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 202
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein binding
; OTHER INFORMATION: domain)
US-11-096-706-202

Query Match      70.6%; Score 24; DB 7; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.9e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      | |||
Db      1 DRSNRKT 7

RESULT 36
US-10-467-657-5076
; Sequence 5076, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
```

; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5076
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5076

Query Match 70.6%; Score 24; DB 6; Length 36;
Best Local Similarity 71.4%; Pred. No. 9.5;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|||
Db 19 DADNAAT 25

RESULT 37
US-10-793-626-1622
; Sequence 1622, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1622
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1622

Query Match 70.6%; Score 24; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SNRAT 7
|||||
Db 41 SNRAT 45

RESULT 38
US-10-467-657-5034
; Sequence 5034, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5034
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5034

Query Match 70.6%; Score 24; DB 6; Length 227;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASNRAT 7
|||||
Db 181 AKNRAT 186

RESULT 39
US-11-082-389-210
; Sequence 210, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 210
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-210

Query Match 70.6%; Score 24; DB 7; Length 260;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|||||
Db 114 DADERAT 120

RESULT 40
US-11-082-389-212

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; Sequence 212, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 212
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-212

Query Match 70.6%; Score 24; DB 7; Length 260;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 114 DADRRAT 120

Search completed: December 14, 2005, 07:38:16
Job time : 2.17241 secs
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11-10-1914

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:38 ; Search time 7.60345 Seconds
(without alignments)
88.581 Million cell updates/sec

Title: US-10-720-323-5

Perfect score: 34

Sequence: 1 DASNRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 80.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	100.0	78	S34102	Ig kappa chain V r
2	34	100.0	86	S16824	Ig kappa chain V r
3	34	100.0	86	S16837	Ig kappa chain V r
4	34	100.0	86	S16830	Ig kappa chain V r
5	34	100.0	86	S16833	Ig kappa chain V-I
6	34	100.0	86	S16829	Ig kappa chain V r
7	34	100.0	86	S16826	Ig kappa chain V r
8	34	100.0	92	S37506	Ig kappa chain V r
9	34	100.0	92	S37522	Ig kappa chain V r
10	34	100.0	92	S37516	Ig kappa chain V r
11	34	100.0	108	G44151	Ig kappa chain V r
12	34	100.0	111	S23628	Ig kappa chain V r
13	34	100.0	111	PN0537	Ig kappa chain V r
14	34	100.0	115	K3HUVG	Ig kappa chain pre
15	34	100.0	115	S11697	Ig kappa chain pre
16	34	100.0	125	S40344	Ig kappa chain V-J
17	34	100.0	128	A56701	Ig kappa chain V r
18	34	100.0	129	S29627	Ig kappa chain V r
19	34	100.0	130	S40360	Ig kappa chain - h
20	34	100.0	144	PL0106	Ig kappa chain pre
21	31	91.2	241	RRNZ	phosphoprotein P -
22	31	91.2	241	RRNZPP	phosphoprotein P -
23	31	91.2	1375	T37672	probable DNA repai
24	30	88.2	284	S38381	tropomyosin - Cali
25	30	88.2	284	A33085	tropomyosin - bloo
26	29	85.3	86	S16836	Ig kappa chain V r
27	29	85.3	91	S37521	Ig kappa chain V r
28	29	85.3	107	S57444	Ig kappa chain V-J
29	29	85.3	116	B25521	Ig kappa chain pre

30	29	85.3	133	2	D87593	hypothetical prote
31	29	85.3	211	2	F95851	probable nitrateni
32	29	85.3	215	2	A23746	Ig kappa chain V-I
33	29	85.3	215	2	JE0242	Ig kappa chain NIG
34	29	85.3	224	2	B83859	hypothetical prote
35	29	85.3	315	2	G95415	probable LysR-fam
36	29	85.3	1336	2	T18288	ABC transport prot
37	28	82.4	81	2	G82561	hypothetical prote
38	28	82.4	92	2	S37504	Ig kappa chain V r
39	28	82.4	92	2	S37512	Ig kappa chain V r
40	28	82.4	108	2	E30609	Ig kappa chain V-I
41	28	82.4	114	2	S54905	Ig kappa chain V r
42	28	82.4	128	2	S40379	Ig kappa chain V-J
43	28	82.4	128	2	S40345	Ig kappa chain V-J
44	28	82.4	131	2	S40346	Ig kappa chain V-J
45	28	82.4	215	2	JE0243	Ig kappa chain NIG
46	28	82.4	217	2	S50926	VT11 protein - yea
47	28	82.4	241	1	RRNZ18	phosphoprotein P -
48	28	82.4	483	2	D72559	hypothetical prote
49	28	82.4	667	2	T46094	hypothetical prote
50	28	82.4	815	2	H96494	protein F7f22.2 li
51	28	82.4	1128	2	T30296	R27-2 protein - Tr
52	28	82.4	2314	2	T28698	hypothetical prote
53	27	79.4	502	2	C86263	hypothetical prote
54	27	79.4	566	1	HYBSU	bacillolysin (EC 3
55	27	79.4	760	2	D71445	hypothetical prote
56	27	79.4	797	2	D70581	probable cation-tr
57	27	79.4	848	2	T38089	HSP 70 family prot
58	27	79.4	940	2	B87250	(protein-pil) urid
59	27	79.4	1021	2	I40805	collagenase - Clos
60	26	76.5	129	2	C71251	ribosomal protein
61	26	76.5	156	2	G82952	ATP synthase B cha
62	26	76.5	243	2	H90015	hypothetical prote
63	26	76.5	251	2	S62202	hypothetical prote
64	26	76.5	251	2	A91067	transposase of ins
65	26	76.5	251	2	A85911	IS30 transposase [
66	26	76.5	293	2	G70896	hypothetical prote
67	26	76.5	326	2	T15194	hypothetical prote
68	26	76.5	342	2	T46909	hypothetical prote
69	26	76.5	343	2	G90959	transposase of ins
70	26	76.5	366	1	MXXRST	sigma NS protein -
71	26	76.5	372	2	S67770	probable membrane
72	26	76.5	373	2	H83891	spore germination
73	26	76.5	375	2	T03325	gene i18 protein -
74	26	76.5	383	1	F65241	transposase - Esch
75	26	76.5	396	2	A85808	hypothetical prote
76	26	76.5	403	2	B70659	hypothetical prote
77	26	76.5	443	2	B86180	protein TIG11.3 li
78	26	76.5	446	2	S75708	hypothetical prote
79	26	76.5	448	2	A80301	conserved hypothet
80	26	76.5	482	2	D85913	succinate-semialde
81	26	76.5	482	2	B91069	succinate-semialde
82	26	76.5	482	2	F65045	succinate-semialde
83	26	76.5	484	2	S61006	RI01 protein - yea
84	26	76.5	524	2	S35341	ketin - fruit fly
85	26	76.5	589	2	A32567	stress-induced pro
86	26	76.5	603	2	AG2070	hypothetical prote
87	26	76.5	633	2	S75525	sensory transducti
88	26	76.5	636	2	H87789	protein G34G6.1 li
89	26	76.5	645	2	A82655	conserved hypothet
90	26	76.5	672	2	A97437	hypothetical 71.3K
91	26	76.5	704	2	H82381	toxin secretion AT
92	26	76.5	785	2	A82123	chemotaxis protein
93	26	76.5	884	2	A31928	glucose transport
94	26	76.5	941	2	AF2415	two-component hybr
95	26	76.5	943	2	E84429	probable receptor-
96	26	76.5	1020	2	B82427	sensor protein for
97	26	76.5	1066	2	T45283	growth polarity ma
98	26	76.5	1066	2	T41099	staurosporine targ
99	26	76.5	1147	2	T35781	hypothetical prote
100	26	76.5	1185	2	T39734	pyruvate carboxyla

ALIGNMENTS

RESULT 1
S34102
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34102
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-78 <WAG>
A:Cross-references: UNIPARC:UPI0000176B23; EMBL:X54828
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 34; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.57; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 DASNRAT 7
|||||
Db 41 DASNRAT 47

RESULT 2
S16824
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16824
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16824
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176DAB; EMBL:X54822
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 DASNRAT 7
|||||
Db 41 DASNRAT 47

RESULT 3
S16837
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16837
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16837
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176DA6; EMBL:X54835

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 DASNRAT 7
|||||
Db 41 DASNRAT 47

RESULT 4
S16830
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16830
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16830
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176DA9; EMBL:X54828
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 DASNRAT 7
|||||
Db 41 DASNRAT 47

RESULT 5
S16833
Ig kappa chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16833; S16838
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16833
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54831
A:Experimental source: clone bkv17
A:Accession: S16838
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLM>
A:Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54836
A:Experimental source: clone slkv14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0

Qy 1 DASNRAT 7
|||||

Db 41 DASNRAT 47

RESULT 6

S16829
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16829
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid factor
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16829
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176DAC; EMBL:X54827
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 41 DASNRAT 47

RESULT 7

S16826
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16826; S34101
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid factor
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16826
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000115B92; EMBL:X54824; NID:G33653; PIDN:CAA38593.1; PIDN:CAA38593.1; PIDN:CAA38593.1; PIDN:CAA38593.1
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in a distinct pattern
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <WAG>
A:Cross-references: UNIPARC:UPI0000115B92; EMBL:X67185
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 34; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 41 DASNRAT 47

RESULT 8

S37506
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37506

R:Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37506

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: UNIPARC:UPI0000116576; EMBL:Z26606; NID:G405653; PIDN:CAA81359.1; PIDN:CAA81359.1; PIDN:CAA81359.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 34; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.67;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 33 DASNRAT 39

RESULT 9

S37522
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37522

R:Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37522

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: UNIPARC:UPI0000116586; EMBL:Z26622; NID:G405686; PIDN:CAA81375.1; PIDN:CAA81375.1; PIDN:CAA81375.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 34; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.67;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 33 DASNRAT 39

RESULT 10

S37516
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37516

R:Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A:Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood

A:Reference number: S37501

A:Accession: S37516

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-92 <KLE>

A:Cross-references: UNIPARC:UPI0000116588; EMBL:Z26624; NID:G405674; PIDN:CAA81377.1; PIDN:CAA81377.1; PIDN:CAA81377.1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 34; DB 2; Length 92;

Best Local Similarity 100.0%; Pred. No. 0.67;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 33 DASNRAT 39

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Db      33 DASNRAT 39

RESULT 11
G44151
Ig kappa chain V region (JM-10) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C;Accession: G44151
R;Zabedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pva
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A;Reference number: A44151; MUID:92228746; PMID:1373487
A;Accession: G44151
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-108 <ZEB>
A;Cross-references: UNIPARC:UPI00001139AC; GB:M88317; NID:G183968; PIDN:AAA35975.1; PID:
A;Note: nucleotide translation not given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      |||||
Db      49 DASNRAT 55

RESULT 12
S23828
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23628
R;Olsee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23628
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <OLE>
A;Cross-references: UNIPARC:UPI0000115F96; EMBL:X59705; NID:G34022; PIDN:CAA42226.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      |||||
Db      50 DASNRAT 56

RESULT 13
PN0537
Ig kappa chain V region (clone LUNm03) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 21-Jan-2000
C;Accession: PN0537
R;Avila, M.A.; Vazquez, J.; Danielsson, L.; de Cossio, M.E.F.; Borrebaeck, C.A.K.
Gene 127, 273-274, 1993
A;Title: Sequence determination of variable region genes of two human monoclonal antibod
A;Reference number: PN0535; MUID:93273246; PMID:8500770
A;Accession: PN0537
A;Molecule type: DNA
A;Residues: 1-111 <AVI>
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A;Cross-references: UNIPARC:UPI0000118293; GB:M97805
A;Note: the authors translated the codon TAT for residue 50 as Ile
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      |||||
Db      51 DASNRAT 57

RESULT 14
K3HUVG
Ig kappa chain precursor V-III region (Vg) - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01900
R;Pech, M.; Zachau, H.G.
Nucleic Acids Res. 12, 9229-9236, 1984
A;Title: Immunoglobulin genes of different subgroups are interdigitated within the V-K 1
A;Reference number: A93549; MUID:85087932; PMID:6440122
A;Accession: A01900
A;Molecule type: DNA
A;Residues: 1-115 <PEC>
A;Cross-references: UNIPROT:P04433; UNIPARC:UPI0000116D05; GB:X01668; GB:K02768; NID:G33
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:I36266
A;Map position: 2p12-2p11
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V-III region (Vg) #status predicted <VAT>
F;21-43/Region: framework 1
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;55-69/Region: framework 2
F;70-76/Region: complementarity-determining 2
F;77-108/Region: framework 3
F;109-115/Region: complementarity-determining 3
F;43-108/Disulfide bonds: #status predicted

Query Match      100.0%; Score 34; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
      |||||
Db      70 DASNRAT 76

RESULT 15
S11697
Ig kappa chain precursor V-III region - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S11697
R;Pech, M.; Smola, H.; Pohlentz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A;Title: A large section of the gene locus encoding human immunoglobulin variable region
A;Reference number: S11697; MUID:85264787; PMID:3927006
A;Accession: S11697
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <PEC>
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A;Cross-references: UNIPARC:UPI0000115841; EMBL:X17264; NID:G37898; PIDN:CAA35168.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
C;Genetics: 17/1
A;Introns: 17/1
C;Species: Homo sapiens (man)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      70 DASNRAT 76

RESULT 16
S40344
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40344
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40344
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI000011615E; EMBL:X72454; NID:G441376; PIDN:CAA51122.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      70 DASNRAT 76

RESULT 17
A56701
Ig kappa chain V region precursor (HuA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C;Accession: A56701
R;Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A;Title: Human and mouse monoclonal antibodies to blood group A substance, which are nea
A;Reference number: A56701; MUID:95279371; PMID:7759488
A;Accession: A56701
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <NIC>
A;Cross-references: UNIPARC:UPI0000113B26; GB:L41174; NID:G762823; PIDN:AAA64877.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      70 DASNRAT 76

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RESULT 18
S29627
Ig kappa chain V region (60.3 hybridoma) - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34110; S29627
R;Walls, M.A.; Hsiao, K.; Harris, L.J.
Nucleic Acids Res. 21, 2921-2929, 1993
A;Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains wit
A;Reference number: S34110; MUID:93324379; PMID:8332501
A;Accession: S34110
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-129 <WA2>
A;Cross-references: UNIPARC:UPI000011649A; EMBL:Z17330; NID:G38511; PIDN:CAA78978.1; PIC
A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma cells
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      70 DASNRAT 76

RESULT 19
S40360
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40360
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40360
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-130 <KLE>
A;Cross-references: UNIPARC:UPI000011616E; EMBL:X72470; NID:G441408; PIDN:CAA51138.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-111/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 34; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DASNRAT 7
Db      71 DASNRAT 77

RESULT 20
PL0106
Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
R;Siiberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secr
A;Reference number: PL0106; MUID:89235583; PMID:2541221
A;Accession: PL0106
A;Molecule type: mRNA
A;Residues: 1-144 <SLI>

```

A;Cross-references: UNIPARC:UPI00001767A2
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-115/Domain: V region <VRE>
 F;36-110/Domain: immunoglobulin homology <IMM>
 F;44-54/Region: complementarity-determining 1
 F;70-76/Region: complementarity-determining 2
 F;109-115/Region: complementarity-determining 3
 F;116-127/Domain: J region <JRG>
 F;128-144/Domain: C region (fragment) <CRE>

Query Match 100.0%; Score 34; DB 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 ||:||||
 Db 70 DASNRAT 76

RESULT 21

RRNZ
 phosphoprotein P - human respiratory syncytial virus (strain A2)
 C;Species: human respiratory syncytial virus
 C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
 C;Accession: A04037
 R;Satake, N.; Elango, N.; Venkatesan, S.
 J. Virol. 52, 991-994, 1984
 A;Title: Sequence analysis of the respiratory syncytial virus phosphoprotein gene.
 A;Reference number: A04037; PMID:85033973; PMID:6548527
 A;Accession: A04037
 A;Molecule type: mRNA
 A;Residues: 1-241 <SAT>
 A;Cross-references: UNIPROT:P03421; UNIPARC:UPI0000134B5D; GB:M11486; GB:X02719; NID:g33
 C;Genetics:
 A;Gene: P
 C;Superfamily: respiratory syncytial virus phosphoprotein P
 C;Keywords: phosphoprotein

Query Match 91.2%; Score 31; DB 1; Length 241;
 Best Local Similarity 85.7%; Pred. No. 9.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 ||:||||
 Db 12 DANNRAT 18

RESULT 22

RRNZPP
 phosphoprotein P - human respiratory syncytial virus (strain Long)
 C;Species: human respiratory syncytial virus
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C;Accession: S07428
 R;Lopez, J.A.; Villanueva, N.; Melero, J.A.; Portela, A.
 Virus Res. 10, 243-262, 1988
 A;Title: Nucleotide sequence of the fusion and phosphoprotein genes of human respiratory
 A;Reference number: S07428; PMID:88323192; PMID:3414184
 A;Accession: S07428
 A;Molecule type: mRNA
 A;Residues: 1-241 <LOP>
 A;Cross-references: UNIPROT:P12579; UNIPARC:UPI0000134B5E; EMBL:M22644; NID:g3333949; PID
 C;Genetics:
 A;Gene: P
 C;Superfamily: respiratory syncytial virus phosphoprotein P
 C;Keywords: phosphoprotein

Query Match 91.2%; Score 31; DB 1; Length 241;
 Best Local Similarity 85.7%; Pred. No. 9.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 12 DANNRAT 18
 ||:||||

RESULT 23

T37672
 probable DNA repair protein - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: T37672
 R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
 submitted to the EMBL Data Library, October 1999
 A;Reference number: Z21736
 A;Accession: T37672
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1375 <MCD>
 A;Cross-references: UNIPROT:Q9UTL9; UNIPARC:UPI0000069886; EMBL:AL132675; PIDN:CAB59685.1

A;Experimental source: strain 972h-; cosmid c144
 C;Genetics:
 A;Gene: SPDB:SPAC144.05
 A;Map position: 1
 A;Introns: 1108/1; 1196/3; 1263/2; 1277/1
 F;1088-1135/Domain: RING finger homology <RRN>

Query Match 91.2%; Score 31; DB 2; Length 1375;
 Best Local Similarity 85.7%; Pred. No. 62;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 ||:||||
 Db 916 DASNRAT 922

RESULT 24

S38381
 tropomyosin - California red abalone
 C;Species: Haliotis rufescens (California red abalone)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S38381
 R;Degan, B.M.; Degan, S.M.; Morse, D.E.
 submitted to the EMBL Data Library, September 1993
 A;Description: Transient tropomyosin gene expression during larval and metamorphic muscle
 A;Reference number: S38381
 A;Accession: S38381
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-284 <DEG>
 A;Cross-references: UNIPROT:Q25145; UNIPARC:UPI0000079F95; EMBL:X75218; NID:g407416; PID
 C;Superfamily: tropomyosin

Query Match 88.2%; Score 30; DB 2; Length 284;
 Best Local Similarity 85.7%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
 ||:||||
 Db 234 DASNRAT 240

RESULT 25

A33085
 tropomyosin - bloodfluke planorb
 C;Species: Biomphalaria glabrata (bloodfluke planorb)
 C;Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Jul-2004
 C;Accession: A33085
 R;Dissous, C.; Torpier, G.; Duvaux-Miret, O.; Capron, A.
 submitted to the Protein Sequence Database, June 1990
 A;Reference number: A33085
 A;Accession: A33085
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-284 <DIS>

A;Cross-references: UNIPROT:P42636; UNIPARC:UPI0000137247
C;Superfamily: tropomyosin

Query Match 88.2%; Score 30; DB 2; Length 284;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|||
Db 234 DASNRAT 240

RESULT 26

S16836
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16836
R;Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid factor
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16836
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>

A;Cross-references: UNIPARC:UPI0000176061; EMBL:X54834
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 86;
Best Local Similarity 85.7%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|||
Db 41 DASNRAT 47

RESULT 27

S37521
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37521
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37521
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <KLE>

A;Cross-references: UNIPARC:UPI0000116587; EMBL:Z26623; NID:G405684; PIDN:CAA81376.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 85.3%; Score 29; DB 2; Length 91;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|||
Db 33 DASNRAT 39

RESULT 28

S57444
Ig kappa chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C;Accession: S57444

R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IGM antibodies cloned from motor neuropathic
A;Reference number: S57408
A;Accession: S57444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <PAT>

A;Cross-references: UNIPARC:UPI00001137AE; EMBL:X87898; NID:G871275; PIDN:CAA61149.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 6
|||
Db 50 DASNRAT 55

RESULT 29

B25521
Ig kappa chain precursor V region (305) - human
C;Species: Homo sapiens (man)
C;Date: 21-May-1988 #sequence_revision 21-May-1990 #text_change 21-Jan-2000
C;Accession: B25521
R;Chen, P.P.; Albrandt, K.; Orida, N.K.; Radoux, V.; Chen, E.Y.; Schrantz, R.; Liu, F.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 8318-8322, 1986
A;Title: Genetic basis for the cross-reactive idiotypes on the light chains of human IgM
A;Reference number: A94135; MUID:87041448; PMID:3095834
A;Accession: B25521
A;Molecule type: DNA
A;Residues: 1-116 <CHE>

A;Cross-references: UNIPARC:UPI0000113857; GB:M14507; NID:G186027; PIDN:AAAS8993.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-111/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 116;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|||
Db 71 DASNRAT 77

RESULT 30

D87593
hypothetical protein CC2780 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87593
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <STO>

A;Cross-references: UNIPROT:Q9A4Q0; UNIPARC:UPI000000C783C; GB:AE005673; NID:G13424378; P
C;Genetics:
A;Gene: CC2780

Query Match 85.3%; Score 29; DB 2; Length 133;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7

Db 90 DASHRAT 96
||||:||||

RESULT 31

F95851
A;Title: probable nitrate/nitrite response regulator protein [imported] - Sinorhizobium meliloti (C) Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95851
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <LEO>
A;Cross-references: UNIPROT:Q92X84; UNIPARC:UPI00000CB3DC; GB:AL591985; PIDN:CAC48478.1;
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
C;Genetics:
A;Contents: annotation
A;Gene: SMB20078
A;Genome: plasmid
C;Superfamily: response regulator with HTH DNA-binding domain, NarL type; response regul

Query Match 85.3%; Score 29; DB 2; Length 211;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|:|||||
Db 191 DISNRAT 197

RESULT 32

A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
A;Cross-references: UNIPARC:UPI0000176985
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 215;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|:|||||
Db 51 DASRAT 57

RESULT 33

JB0242

Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
A;Cross-references: UNIPARC:UPI0000176983
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 29; DB 2; Length 215;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
|:|||||
Db 51 DASRAT 57

RESULT 34

E83859
hypothetical protein BH1677 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: E83859
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E83859
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <STO>
A;Cross-references: UNIPROT:Q9KC96; UNIPARC:UPI00000C3C6F; GB:AP001512; GB:BA0000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1677
C;Superfamily: conserved hypothetical protein TM1511

Query Match 85.3%; Score 29; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRA 6
|:|||||
Db 166 DASNRA 171

RESULT 35

G95415
probable LysR-family transcription regulator [imported] - Sinorhizobium meliloti (strain
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95415
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95415
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <KUR>
A;Cross-references: UNIPROT:Q92XL3; UNIPARC:UPI00000CB363; GB:AE006469; PIDN:AAK65889.1;
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaull, P.; Vandenbol, M.; Vorholter, F.U.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
C:Genetics: annotation
A:Gene: Sma2287
A:Genome: plasmid
C:Superfamily: regulatory protein ampR

Query Match 85.3%; Score 29; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRA 6
Db 132 DASNRA 137

RESULT 36
T18288
ABC transport protein - slime mold (*Dictyostelium discoideum*) (fragment)
C:Species: *Dictyostelium discoideum*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18288
R:Loomis, W.F.
submitted to the EMBL Data Library, August 1996
A:Reference number: 218857
A:Accession: T18288
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1336 <LOC>
A:Cross-references: UNIPROT:Q94479; UNIPARC:UPI000017B173; EMBL:U66526; NID:g1513297; P1
C:Genetics:
A:Gene: abca

Query Match 85.3%; Score 29; DB 2; Length 1336;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRA 6
Db 372 DASNRA 377

RESULT 37
G82561
hypothetical protein XF2399 [imported] - *Xylella fastidiosa* (strain 9a5c)
C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: G82561
R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82561
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <SIM>
A:Cross-references: UNIPROT:Q9PAU6; UNIPARC:UPI00000C2A2A; GB:AE004049; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Pacincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjowski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2399

Query Match 82.4%; Score 28; DB 2; Length 81;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 23 DASNRAT 29

RESULT 38
S37504
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37504
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37504
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116578; EMBL:Z26508; NID:g405649; PIDN:CAA81361.1; P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 82.4%; Score 28; DB 2; Length 92;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 33 DASNRAT 39

RESULT 39
S37512
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37512
R:Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37512
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: UNIPARC:UPI0000116570; EMBL:Z26599; NID:g405666; PIDN:CAA81353.1; P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 82.4%; Score 28; DB 2; Length 92;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 33 DASNRAT 39

RESULT 40
E30609
Ig kappa chain V-III region (Jh) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
C;Accession: E30609
R;Goni, F.K.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo, J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: E30609
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-108 <GON>
A;Cross-references: UNIPARC:UPI0000176B0E
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;16-91/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 28; DB 2; Length 108;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 51 DASTRAT 57

Search completed: December 14, 2005, 07:31:53
Job time : 9.60345 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:28 ; Search time 37.7759 Seconds
(without alignments)
130.737 Million cell updates/sec

Title: US-10-720-323-5

Perfect score: 34

Sequence: 1 DASNRAT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	115	1 KV3I_HUMAN	P04433 homo sapien
2	34	100.0	244	2 Q981P7_RHIL0	Q981P7 rhizobium 1
3	31	91.2	106	2 Q416P1_GIBZE	Q416P1 gibberella
4	31	91.2	200	2 Q77CH1_BPP1	Q77CH1 bacterioph
5	31	91.2	203	2 Q21969_BPP1	Q21969 bacterioph
6	31	91.2	239	2 Q8KJ91_RHIL0	Q8KJ91 rhizobium 1
7	31	91.2	241	1 RRPp_HRSV	P14156 human respi
8	31	91.2	241	1 RRPp_HRSVA	P03421 human respi
9	31	91.2	241	1 RRPp_HRSVL	P12579 human respi
10	31	91.2	241	2 O09633_HRSV	O09633 human respi
11	31	91.2	241	2 O09717_9MNO	O09717 respiratory
12	31	91.2	241	2 P90196_HRSV	P90196 human respi
13	31	91.2	241	2 Q8UYD5_HRSV	Q8UYD5 human respi
14	31	91.2	241	2 Q8V218_HRSV	Q8V218 human respi
15	31	91.2	241	2 Q8V219_HRSV	Q8V219 human respi
16	31	91.2	241	2 Q4KRW8_HRSV	Q4KRW8 human respi
17	31	91.2	279	2 Q5LXA7_SILPO	Q5LXA7 silicibacte
18	31	91.2	437	2 Q7XT71_ORYSA	Q7XT71 oryza sativ
19	31	91.2	758	2 Q6SGY7_9BACT	Q6SGY7 uncultured
20	31	91.2	1375	2 Q8UT19_SCHPO	Q8UT19 schizosacch
21	30	88.2	160	2 Q77246_CRAVI	Q77246 crassostrea
22	30	88.2	202	2 Q6C6B5_YARLI	Q6C6B5 varrowia li
23	30	88.2	231	2 Q92KL9_RHIME	Q92KL9 rhizobium m
24	30	88.2	233	2 Q95WY0_CRAGI	Q95WY0 crassostrea
25	30	88.2	284	1 TPM1_BIOGL	P42636 biophalari
26	30	88.2	284	1 TPM2_BIOGL	P43689 biophalari
27	30	88.2	284	1 TPM_HALDV	Q9GZ71 halotis di
28	30	88.2	284	1 TPM_HALRU	Q25145 halotis ru
29	30	88.2	284	1 TPM_MIMNO	Q9GZ69 mimachlamys
30	30	88.2	284	1 TPM_MYTED	Q25457 mytilus edu
31	30	88.2	284	1 TPM_MYTGA	P91958 mytilus gal

ALIGNMENTS

32	30	88.2	284	1	TPM_PERV1	Q9GZ70 perna virid
33	30	88.2	284	2	O09343_PATYE	O09343 patinopecte
34	30	88.2	284	2	Q7YZR3_9VEST	Q7YZR3 halotis as
35	30	88.2	284	2	Q7YZR4_9VEST	Q7YZR4 halotis as
36	30	88.2	284	2	Q9GUW8_PATYE	Q9GUW8 patinopecte
37	30	88.2	284	2	Q9GUW9_PATYE	Q9GUW9 patinopecte
38	30	88.2	284	2	Q9NDL0_PATYE	Q9NDL0 patinopecte
39	30	88.2	402	2	Q7UFB2_RHOBA	Q7UFB2 rhodoplirell
40	30	88.2	886	2	Q9FYK0_ARATH	Q9FYK0 arabidopsis
41	30	88.2	905	2	Q7N649_PHOLL	Q7N649 photorhabd
42	30	88.2	924	2	Q9FXJ6_ARATH	Q9FXJ6 arabidopsis
43	30	88.2	1180	2	Q41CF3_GIBZE	Q41CF3 gibberella
44	30	88.2	1954	2	Q4Q0H1_LEIMA	Q4Q0H1 leishmania
45	29	85.3	133	2	Q9A4Q0_CAUCR	Q9A4Q0 caulobacter
46	29	85.3	147	2	Q9ACX6_STRCO	Q9ACX6 streptomyce
47	29	85.3	211	2	Q92X84_RHIME	Q92X84 rhizobium m
48	29	85.3	218	2	Q5B8F9_EMENI	Q5B8F9 aspergillus
49	29	85.3	224	2	Q9KC96_BACHD	Q9KC96 bacillus ha
50	29	85.3	226	2	Q8EQD0_OCEIH	Q8EQD0 oceanobacil
51	29	85.3	265	2	Q5GYW8_XANOR	Q5GYW8 xanthomonas
52	29	85.3	265	2	Q4UUA3_XANCP	Q4UUA3 xanthomonas
53	29	85.3	265	2	Q8P9J1_XANCP	Q8P9J1 xanthomonas
54	29	85.3	271	2	Q6CW71_KLULA	Q6CW71 kluyveromyc
55	29	85.3	280	2	Q8DI07_SYNEL	Q8DI07 synecococc
56	29	85.3	287	2	Q5ZB31_ORYSA	Q5ZB31 oryza sativ
57	29	85.3	298	2	Q5YRI4_NOCFA	Q5YRI4 nocardia fa
58	29	85.3	308	2	Q571X7_LYCES	Q571X7 lycopersico
59	29	85.3	315	2	Q92XL3_RHIME	Q92XL3 rhizobium m
60	29	85.3	349	2	Q8GVH7_SOLTU	Q8GVH7 solanum tub
61	29	85.3	396	2	Q869S6_DICDI	Q869S6 dictyosteli
62	29	85.3	411	2	Q4VA73_XENTR	Q4VA73 xenopus tro
63	29	85.3	501	2	Q72T83_LEPIC	Q72T83 leptospira
64	29	85.3	501	2	Q8F257_LEPIN	Q8F257 leptospira
65	29	85.3	545	2	Q5B8F5_EMENI	Q5B8F5 aspergillus
66	29	85.3	564	2	Q9EN64_NPVST	Q9EN64 spodoptera
67	29	85.3	576	2	Q89QX9_BRAJA	Q89QX9 bradyrhizob
68	29	85.3	585	2	Q54MW7_DICDI	Q54MW7 dictyosteli
69	29	85.3	623	2	Q54MX2_DICDI	Q54MX2 dictyosteli
70	29	85.3	655	2	Q94479_DICDI	Q94479 dictyosteli
71	29	85.3	683	2	Q76951_ANOGA	Q76951 anopheles g
72	29	85.3	683	2	Q7QCV8_ANOGA	Q7QCV8 anopheles g
73	29	85.3	759	2	Q5BBU2_EMENI	Q5BBU2 aspergillus
74	29	85.3	795	2	Q99PH6_MOUSE	Q99PH6 mus musculu
75	29	85.3	802	2	Q4UXN1_XANCP	Q4UXN1 xanthomonas
76	29	85.3	802	2	Q8P6D4_XANCP	Q8P6D4 xanthomonas
77	29	85.3	803	2	Q8PHU1_XANAC	Q8PHU1 xanthomonas
78	29	85.3	804	2	Q99NC2_MOUSE	Q99NC2 mus musculu
79	29	85.3	831	2	Q99PH7_MOUSE	Q99PH7 mus musculu
80	29	85.3	872	2	Q5ACU0_CANAL	Q5ACU0 candida alb
81	29	85.3	877	2	Q8T5Z7_DICDI	Q8T5Z7 dictyosteli
82	29	85.3	906	2	Q99PM5_MOUSE	Q99PM5 mus musculu
83	29	85.3	955	2	Q9W3G3_DROME	Q9W3G3 drosophila
84	29	85.3	965	2	Q99PW2_MOUSE	Q99PW2 mus musculu
85	29	85.3	1119	2	Q84DC8_MYCGA	Q84DC8 mycoplasma
86	29	85.3	1179	2	Q7S9M2_NEUCR	Q7S9M2 neurospora
87	29	85.3	1179	2	Q52DE2_MAGGR	Q52DE2 magnaporthe
88	29	85.3	1296	2	Q55Q20_CRYNE	Q55Q20 cryptococcu
89	29	85.3	1296	2	Q5KF77_CRYNE	Q5KF77 cryptococcu
90	29	85.3	1344	2	Q670Z5_FUGRU	Q670Z5 fugu rubrip
91	29	85.3	1736	2	Q80TJ5_MOUSE	Q80TJ5 mus musculu
92	29	85.3	1806	2	Q62N48_BURMA	Q62N48 burkholderi
93	29	85.3	1817	2	Q7K5Q8_PLAVI	Q7K5Q8 plasmodium
94	29	85.3	1830	2	Q7K5Q7_PLAVI	Q7K5Q7 plasmodium
95	29	85.3	1866	2	Q8T5C8_PLAVI	Q8T5C8 plasmodium
96	29	85.3	1987	2	Q99PB3_MOUSE	Q99PB3 mus musculu
97	29	85.3	2031	2	Q83X56_BURPS	Q83X56 burkholderi
98	29	85.3	2087	2	Q6DIC6_MOUSE	Q6DIC6 mus musculu
99	28	82.4	81	2	Q9PAU6_XYLFA	Q9PAU6 xylella fas
100	28	82.4	115	2	Q52AJ5_MAGGR	Q52AJ5 magnaporthe

```

RESULT 1
KV31 HUMAN
ID KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within
the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X01668; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; A01900; K3HUVG.
DR HSSP; P01625; 1EEQ.
DR SMR; P04433; 21-115.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-III region VG.
FT REGION 21 43 Framework-1.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Framework-2.
FT REGION 70 76 Complementarity-determining-2.
FT REGION 77 108 Framework-3.
FT REGION 109 115 Complementarity-determining-3.
FT DISULFID 43 108 By similarity.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 100.0%; Score 34; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
DB 70 DASNRAT 76

RESULT 2
Q981P7_RHILO
ID Q981P7_RHILO PRELIMINARY; PRT; 244 AA.
AC Q981P7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 25, Last annotation update)
DE Phosphonates transport ATP-binding protein; PhnL.
GN OrderedLocustNames=mlr9286;
OS Rhizobium loti (Mesorhizobium loti).
OG Plasmid pMLa.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

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OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; BA000013; BAB54662.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR PRODOM; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Inner membrane; Membrane;
KW Nucleotide-binding; Plasmid; Transport.
SQ SEQUENCE 244 AA; 26169 MW; 37CC272D10FBB8DD CRC64;

Query Match 100.0%; Score 34; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DASNRAT 7
DB 184 DASNRAT 190

RESULT 3
Q416P1_GIBZE
ID Q416P1_GIBZE PRELIMINARY; PRT; 106 AA.
AC Q416P1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Predicted protein.
GN ORFNames=FG07117.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collamore A., Cook K., Cooke P., Corum B., DeArelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton J., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Menus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Ntalen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,

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GN Name=phnL;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R7A;
RX MEDLINE=21999272; PubMed=12003951;
RX DOI=10.1128/JB.184.11.3086-3095.2002;
RA Sullivan J.F., Trzebiatowski J.R., Cruickshank R.W., Gouzy J.,
RA Brown S.G., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U.,
RA Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.;
RT "Comparative sequence analysis of the symbiosis island of
RT Mesorhizobium loti strain R7A."
RL J. Bacteriol. 184:3086-3095(2002).
CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AL672114; CAD31337.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA_1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Inner membrane; Membrane; Nucleotide-binding; Transport.
SQ SEQUENCE 239 AA; 25509 MW; 72CFB0F1C1D03351 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 239;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 197 DANNRAT 203
|||||

RESULT 7
RRPP HRSV STANDARD; PRT; 241 AA.
AC P14156;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phosphoprotein (P protein).
GN Name=P;
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=85263554; PubMed=3839520;
RA Lambden P.R.;
RT "Nucleotide sequence of the respiratory syncytial virus phosphoprotein
RT gene."
RL J. Gen. Virol. 66:1607-1612(1985).
CC -1- FUNCTION: This protein is probably a component of the active
CC polymerase. It may function in template binding.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M29342; AAA47416.1; -; mRNA.
CC InterPro; IPR003487; Pneumo_phosprot; 1.
CC Pfam; PF02478; Pneumo_phosprot; 1.

RESULT 9
RRPP HRSVL STANDARD; PRT; 241 AA.
ID RRPP_HRSVL
AC P12579;
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KW Phosphorylation.
FT MOD_RES 116 Phosphoserine (By similarity).
FT MOD_RES 117 Phosphoserine (By similarity).
FT MOD_RES 119 Phosphoserine (By similarity).
FT MOD_RES 143 Phosphoserine (By similarity).
FT MOD_RES 156 Phosphoserine (By similarity).
FT MOD_RES 161 Phosphoserine (By similarity).
SQ SEQUENCE 241 AA; 27162 MW; 3EEC20A478E4D42C CRC64;

Query Match 91.2%; Score 31; DB 1; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18
|||||

RESULT 8
RRPP HRSVA STANDARD; PRT; 241 AA.
ID RRPP_HRSVA
AC P03421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phosphoprotein (P protein).
GN Name=P;
OS Human respiratory syncytial virus A (strain A2).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11259;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RX MEDLINE=85033973; PubMed=6548527;
RA Satake M., Elango N., Venkatesan S.;
RT "Sequence analysis of the respiratory syncytial virus phosphoprotein
RT gene."
RL J. Virol. 52:991-994(1984).
CC -1- FUNCTION: This protein is probably a component of the active
CC polymerase. It may function in template binding.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M11486; AAB59853.1; -; Genomic_RNA.
CC InterPro; IPR003487; Pneumo_phosprot; 1.
CC Pfam; PF02478; Pneumo_phosprot; 1.
KW Phosphorylation.
FT MOD_RES 116 Phosphoserine (By similarity).
FT MOD_RES 117 Phosphoserine (By similarity).
FT MOD_RES 119 Phosphoserine (By similarity).
FT MOD_RES 143 Phosphoserine (By similarity).
FT MOD_RES 156 Phosphoserine (By similarity).
FT MOD_RES 161 Phosphoserine (By similarity).
SQ SEQUENCE 241 AA; 27148 MW; 21A9E45CA2DFD50C CRC64;

Query Match 91.2%; Score 31; DB 1; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18
|||||

RESULT 9
RRPP HRSVL STANDARD; PRT; 241 AA.
ID RRPP_HRSVL
AC P12579;
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DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Phosphoprotein (P protein).
GN Name=P;
OS Human respiratory syncytial virus A (strain Long).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11260;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88323192; PubMed=3414184; DOI=10.1016/0168-1702(88)90020-2;
RA Lopez J.A., Villanueva N., Mero J.A., Portela A.;
RT "Nucleotide sequence of the fusion and phosphoprotein genes of human
RT respiratory syncytial (RS) virus Long strain: evidence of subtype
RT genetic heterogeneity.";
RL Virus Res. 10:249-262(1988).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=91259076; PubMed=2045795;
RA Navarro J., Lopez-Otin C., Villanueva N.;
RT "Location of phosphorylated residues in human respiratory syncytial
RT virus phosphoprotein.";
RL J. Gen. Virol. 72:1455-1459(1991).
CC -I- FUNCTION: This protein is probably a component of the active
CC polymerase. It may function in template binding.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M22644; AAA47415.1; -; Genomic_RNA.
DR PIR; S07428; RNN2PP.
DR InterPro; IPR003487; Pneumo_phosprot.
DR Pfam; PF02478; Pneumo_phosprot; 1.
KW Phosphorylation.
FT MOD_RES 116 116 Phosphoserine.
FT MOD_RES 117 117 Phosphoserine.
FT MOD_RES 119 119 Phosphoserine.
FT MOD_RES 143 143 Phosphoserine.
FT MOD_RES 156 156 Phosphoserine.
FT MOD_RES 161 161 Phosphoserine.
SQ SEQUENCE 241 AA; 27147 MW; DCB2DJ942973DD59 CRC64;
Query Match 91.2%; Score 31; DB 1; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 12 DANNRAT 18
RESULT 10
O09633 HRSV
ID O09633 HRSV PRELIMINARY; PRT; 241 AA.
AC O09633;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoprotein (P).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=S2;
RA Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A.,
RA Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J.,

RA Pringle C.R.;
RT "Identification of mutations contributing to the reduced virulence of
RT a modified strain of respiratory syncytial virus.";
RL Vaccine 14:1637-1646(1996).
DR EMBL; U39662; AAC57023.1; -; Genomic RNA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR InterPro; IPR003487; Pneumo_phosprot.
DR Pfam; PF02478; Pneumo_phosprot; 1.
SQ SEQUENCE 241 AA; 27148 MW; 3BEC211478E4D42C CRC64;
Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 12 DANNRAT 18
RESULT 11
O09717 9MONO
ID O09717 9MONO PRELIMINARY; PRT; 241 AA.
AC O09717;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoprotein (P).
OS Respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=S2 ts1C;
RA Tolley K.P., Marriott A.C., Simpson A., Plows D.J., Matthews D.A.,
RA Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J.,
RA Pringle C.R.;
RT "Identification of mutations contributing to the reduced virulence of
RT a modified strain of respiratory syncytial virus.";
RL Vaccine 14:1637-1646(1996).
DR EMBL; U39661; AAC57033.1; -; Genomic RNA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR InterPro; IPR003487; Pneumo_phosprot.
DR Pfam; PF02478; Pneumo_phosprot; 1.
SQ SEQUENCE 241 AA; 27134 MW; 3BED90A47955642C CRC64;
Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DASNRAT 7
Db 12 DANNRAT 18
RESULT 12
P90196 HRSV
ID P90196 HRSV PRELIMINARY; PRT; 241 AA.
AC P90196;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Phosphoprotein P.
GN Name=P;
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=A2;
RA Longhurst S.J., Evans J.E., Johnson J.L., Cane P.A., Easton A.J.,

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RA Firestone C.Y., Whitehead S.S., Collins P.L., Murphy B.R.,
RA Crowe J.E. Jr.;
RT "Nucleotide sequence analysis of the respiratory syncytial virus
RT subgroup A cold-passaged (cp) temperature sensitive (ts) cpts-248/404
RT live attenuated virus vaccine candidate.";
RL Virology 225:419-422(1996).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=A2; PubMed=9557743;
RC MEDLINE=98216821; PubMed=9557743;
RX Whitehead S.S., Juhasz K., Firestone C.Y., Collins P.L., Murphy B.R.;
RA "Recombinant respiratory syncytial virus (RSV) bearing a set of
RT mutations from cold-passaged RSV is attenuated in chimpanzees.";
RL J. Virol. 72:4467-4471(1998).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=A2;
RC MEDLINE=95266253; PubMed=7747420;
RX Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;
RA "A cold-passaged, attenuated strain of human respiratory syncytial
RT virus contains mutations in the F and L genes.";
RL Virology 208:478-484(1995).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=A2;
RC MEDLINE=97187925; PubMed=9035372;
RX Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,
RA Murphy B.R.;
RT "Acquisition of the ts phenotype by a chemically mutagenized cold-
RT passaged human respiratory syncytial virus vaccine candidate results
RT from the acquisition of a single mutation in the polymerase (L)
RT gene.";
RL Virus Genes 13:269-273(1996).
DR EMBL; U63644; AAC55965.1; -; Genomic RNA.
DR EMBL; AF035006; AAC14897.1; -; Genomic RNA.
DR EMBL; U50362; AAB86659.1; -; Genomic RNA.
DR EMBL; U50363; AAB86671.1; -; Genomic RNA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR InterPro; IPR003487; Pnuemo_phosprot.
DR Pfam; PF02478; Pnuemo_phosprot; 1.
SQ SEQUENCE 241 AA; 27134 MW; EZB15FFFFA2DFC78E CRC64;

Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18

RESULT 13
Q8UYD5 HRSV
ID Q8UYD5 HRSV PRELIMINARY; PRT; 241 AA.
AC Q8UYD5
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Phosphoprotein P.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=changchun, and guangzhou;
RX MEDLINE=21364133; PubMed=11471029;
RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,
RA Wang L.T., Liu C.Q., Chang R.X.;
RT "Sequence analysis of phosphoprotein genes of respiratory syncytial
RT virus field strains isolated in China.";
RL Zhonghua Shi Yan He Lin Chuang Bing Du Xue Za Zhi 14:366-369(2000).
[2]

Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18

RESULT 14
Q8V218 HRSV
ID Q8V218 HRSV PRELIMINARY; PRT; 241 AA.
AC Q8V218
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoprotein P.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=hebei;
RX MEDLINE=21364133; PubMed=11471029;
RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,
RA Wang L.T., Liu C.Q., Chang R.X.;
RT "Sequence analysis of phosphoprotein genes of respiratory syncytial
RT virus field strains isolated in China.";
RL Zhonghua Shi Yan He Lin Chuang Bing Du Xue Za Zhi 14:366-369(2000).
[2]

Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18

RESULT 15
Q8V219 HRSV
ID Q8V219 HRSV PRELIMINARY; PRT; 241 AA.
AC Q8V219
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoprotein P.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=changchun, and guangzhou;
RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,
RA Wang L.T., Liu C.Q., Chang R.X.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453425; AAL50990.1; -; mRNA.
DR EMBL; AF453423; AAL50988.1; -; mRNA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR InterPro; IPR003487; Pnuemo_phosprot.
DR Pfam; PF02478; Pnuemo_phosprot; 1.
SQ SEQUENCE 241 AA; 27179 MW; 94404C0C6E060EF2 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18

RESULT 14
Q8V218 HRSV
ID Q8V218 HRSV PRELIMINARY; PRT; 241 AA.
AC Q8V218
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoprotein P.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=hebei;
RX MEDLINE=21364133; PubMed=11471029;
RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,
RA Wang L.T., Liu C.Q., Chang R.X.;
RT "Sequence analysis of phosphoprotein genes of respiratory syncytial
RT virus field strains isolated in China.";
RL Zhonghua Shi Yan He Lin Chuang Bing Du Xue Za Zhi 14:366-369(2000).
[2]

Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18

RESULT 15
Q8V219 HRSV
ID Q8V219 HRSV PRELIMINARY; PRT; 241 AA.
AC Q8V219
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphoprotein P.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;

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OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=beijing;
RX MEDLINE=21364133; PubMed=11471029;
RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,
RA Wang L.T., Liu C.Q., Chang R.X.;
RT "Sequence analysis of phosphoprotein genes of respiratory syncytial
RT virus field strains isolated in China.";
RL Zhonghua Shi Yan He Lin Chuang Bing Du Xue Za Zhi 14:366-369(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=beijing;
RA Zhao L.Q., Wang Z.L., Geng X.H., Qian Y., Deng J., Zhu R.N.,
RA Wang L.T., Liu C.Q., Chang R.X.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453422; AAL50987.1; -; mRNA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR InterPro; IPR003487; Pnuemo_phosprot.
DR Pfam; PF02478; Pnuemo_phosprot; 1.
SQ SEQUENCE 241 AA; 27246 MW; DFE092382C2F073 CRC64;

Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18

RESULT 16
Q4KRW8 HRSV
ID Q4KRW8 HRSV PRELIMINARY; PRT; 241 AA.
AC Q4KRW8
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Phosphoprotein.
GN Name=P;
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC VR-26;
RX PubMed=15994826; DOI=10.1128/JVI.79.14.9315-9319.2005;
RA Lo M.S., Brazas R.M., Holtzman M.J.;
RT "Respiratory Syncytial Virus Nonstructural Proteins NS1 and NS2
RT Mediate Inhibition of Stat2 Expression and Alpha/Beta Interferon
RT Responsiveness.";
RL J. Virol. 79:9315-9319(2005).
DR EMBL; AY911262; AAX23990.1; -; Genomic RNA.
SQ SEQUENCE 241 AA; 27159 MW; 65ABC9B6E1881E7B CRC64;

Query Match 91.2%; Score 31; DB 2; Length 241;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 12 DANNRAT 18

RESULT 17
Q5LXA7 SILPO
ID Q5LXA7 SILPO PRELIMINARY; PRT; 279 AA.
AC Q5LXA7
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

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DE EAL domain protein.
GN OrderedLocusNames=SP0327;
OS Silicibacter pomeroyi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Silicibacter.
OX NCBI_TaxID=89184;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSS-3 / ATCC 700808 / DSM 15171;
RX PubMed=15602564; DOI=10.1038/nature03170;
RA Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,
RA Kiene R.P., Henriksen J.R., King G.M., Belas R., Pai G., Eisen J.A.,
RA Brinkac L.M., Lewis M., Johri S., Weaver B., Miller T.R., Carlton J.,
RA Rahe E., Sheldon W.M., Ye W., Miller T.R., Carlton J., Eisen J.A.,
RA Paulsen I.T., Ren Q., Daugherty S.C., DeBoy R.T., Dodson R.J.,
RA Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J.,
RA Haft D.H., Selengut J., Ward N.;
RT "Genome sequence of Silicibacter pomeroyi reveals adaptations to the
RT marine environment.";
RL Nature 432:910-913(2004).
DR EMBL; CP000031; AAV93645.1; -; Genomic DNA.
DR InterPro; IPR000568; ATPsynt_Asub.
DR InterPro; IPR001633; EAL.
DR Pfam; PF00563; EAL; 1.
DR SMART; SM00052; DUF2; 1.
DR PROSITE; PS00449; ATPASE_A; UNKNOWN_1.
DR PROSITE; PS00883; EAL; 1.
DR Complete proteome.
KW SEQUENCE 279 AA; 30995 MW; BDF7F64C5D5F867B CRC64;

Query Match 91.2%; Score 31; DB 2; Length 279;
Best Local Similarity 85.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 212 DANNRAT 218

RESULT 18
Q7XT71 ORYSA
ID Q7XT71 ORYSA PRELIMINARY; PRT; 437 AA.
AC Q7XT71
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OSJNBa0029H02.23 protein.
GN Name=OSJNBa0029H02.23;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL606594; CAB01637.3; -; Genomic DNA.
DR GO; GO:0046872; P:metal ion binding; IEA.
DR GO; GO:0030001; P:metal ion transport; IEA.
SQ SEQUENCE 437 AA; 47490 MW; 01B26CFCD6559A70 CRC64;

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Query Match		91.2%; Score 31; DB 2; Length 437;
Best Local Similarity		85.7%; Pred. No. 1.1e+02;
Matches		6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 DASNRAT 7	
Db	407 DSSNRAT 413	
RESULT 19		
Q6SGY7_9BACT		
ID	Q6SGY7_9BACT PRELIMINARY;	PRT; 758 AA.
AC		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Aldehyde oxidoreductase, molybdopterin-binding subunit.	
GN	ORFNames=EBAC000-65D02.26;	
OS	uncultured bacterium 443.	
OC	Bacteria; environmental samples.	
OX	NCBI_TaxID=257393;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RA	DeLong E.F.;	
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RA	Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;	
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AY458640; AAR37832.1; -; Genomic DNA.	
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.	
DR	GO; GO:0006118; P:electron transport; IEA.	
DR	InterPro; IPR008274; Aldxan_dh_bind.	
DR	InterPro; IPR000674; Aldxan_dh_hamm.	
DR	Pfam; PF01315; Ald_Xan_dh_C; 1.	
DR	Pfam; PF02738; Ald_Xan_dh_C2; 2.	
SQ	SEQUENCE 758 AA; - 80708 MW; 1A3ECB0B9E0EABCD CRC64;	
Query Match		
Best Local Similarity 91.2%; Score 31; DB 2; Length 758;		
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 DASNRAT 7	
Db	54 DANNRAT 60	
RESULT 20		
Q9UTL9_SCHPO		
ID	Q9UTL9_SCHPO PRELIMINARY;	PRT; 1375 AA.
AC		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	SPAC144.05 protein.	
GN	ORFNames=SPAC144.05;	
OS	Schizosaccharomyces pombe (fission yeast).	
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;	
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;	
OC	Schizosaccharomycetes.	
OX	NCBI_TaxID=4896;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=972;	
RX	MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;	
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,	
RA	Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,	
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,	
RA	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,	
RA	Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,	
RA	Hollroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,	
RA	James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,	
RA	Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,	
RA	Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,	
RA	Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,	
RA	Skellon J., Simmonds M.N., Squares R., Squares S., Stevens K.,	
RA	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,	
RA	Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,	
RA	Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,	
RA	Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D.,	
RA	Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,	
RA	Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,	
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,	
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	
RA	Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Ihode G.,	
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,	
RA	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,	
RA	Curtti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	
RA	Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;	
RT	"The genome sequence of Schizosaccharomyces pombe.";	
RL	Nature 415:871-880(2002).	
DR	EMBL; AL132675; CAB59685.1; -; Genomic DNA.	
DR	PIR; T37672; T37672.	
DR	GeneDB Spombe; SPAC144.05; -.	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:0000151; C:ubiquitin ligase complex; IEA.	
DR	GO; GO:0005524; F:ATP binding; IEA.	
DR	GO; GO:0003677; F:DNA binding; IEA.	
DR	GO; GO:0004386; F:helicase activity; IEA.	
DR	GO; GO:0016787; F:hydrolase activity; IEA.	
DR	GO; GO:0046872; F:metal ion binding; IEA.	
DR	GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.	
DR	GO; GO:0008270; F:zinc ion binding; IEA.	
DR	GO; GO:0006281; P:DNA repair; IEA.	
DR	GO; GO:0016567; P:protein ubiquitination; IEA.	
DR	InterPro; IPR011545; DEAD/DEAH_N.	
DR	InterPro; IPR001650; Helicase_C.	
DR	InterPro; IPR000330; SNF2_N.	
DR	InterPro; IPR002035; VWF_A.	
DR	InterPro; IPR001841; Znf_RING.	
DR	Pfam; PF00271; Helicase_C; 1.	
DR	Pfam; PF00176; SNF2_N; 1.	
DR	Pfam; PF00097; zf-C3HC4; 1.	
DR	PRINTS; PR00453; VWFADOMAIN.	
DR	SMART; SM00487; DEXDC; 1.	
DR	SMART; SM00184; RING; 1.	
DR	PROSITE; PS00518; ZF_RING_1; 1.	
DR	PROSITE; PS00089; ZF_RING_2; 1.	
KW	Complete proteome.	
SQ	SEQUENCE 1375 AA; 159952 MW; 890E78F43EE91615 CRC64;	
Query Match		
Best Local Similarity 91.2%; Score 31; DB 2; Length 1375;		
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 DASNRAT 7	
Db	916 DASNRAT 922	
RESULT 21		
O77246_CRAVI		
ID	O77246_CRAVI PRELIMINARY;	PRT; 160 AA.
AC		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)	
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	
DE	Tropomyosin (fragment).	
GN	Name=tm-1;	
OS	Crassostrea virginica (Eastern oyster).	
OC	Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;	
OC	Ostreoida; Ostreidae; Crassostrea.	
OX	NCBI_TaxID=6565;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Mantle;	

Johnstone M.O., Wheeler A.P.;
 Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 EMBL: AF093290; AAC61869.1; -; mRNA.
 HSSP: P42639; 1C1G.
 InterPro: IPR000533; Tropomyosin.
 Pfam: PF00261; Tropomyosin; 1.
 PRINTS: PR00194; TROPOMYOSIN.
 PROSITE: PS00326; TROPOMYOSIN; 1.
 NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 160 AA; 18444 MW; BEBD08D2A818AAB CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 160;
 Best Local Similarity 85.7%; Pred. No. 62;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DASNRAT 7
 |||||
 Db 110 DASNRAT 116
 |||||
 RESULT 22
 Q6C6B5_YARLI PRELIMINARY; PRT; 202 AA.
 ID Q6C6B5_YARLI PRELIMINARY; PRT; 202 AA.
 AC Q6C6B5; AC
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similarity.
 GN OrderedLocNames=YALIOE108359;
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 NCBI_TaxID=4952;
 [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissbach J.,
 Wincker P., Souciet J.-L.,
 "Genome evolution in yeasts."
 Nature 430:35-44(2004).
 RL EMBL: CR382131; CAG79388.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 202 AA; 22681 MW; 651FF07D3C5397AB CRC64;
 Query Match 88.2%; Score 30; DB 2; Length 202;
 Best Local Similarity 85.7%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DASNRAT 7
 |||||
 Db 130 DGSNRAT 136
 |||||
 RESULT 23
 Q92KL9_RHIME PRELIMINARY; PRT; 231 AA.
 ID Q92KL9_RHIME PRELIMINARY; PRT; 231 AA.
 AC Q92KL9; AC
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

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ID TP11 BIOGL STANDARD; PRT; 284 AA.
AC P42636;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tropomyosin 1 (TMI) (Bg 39).
OS Biomphalaria glabrata (Bloodfluke planorb).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Biomphalaria.
OX NCBI_TaxID=6526;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91218806; PubMed=2090946; DOI=10.1016/0166-6851(90)90149-G;
RA Diasous C., Torpier G., Duvaux-Miret O., Capron A.;
RT "Structural homology of tropomyosins from the human trematode
RL Schistosoma mansoni and its intermediate host Biomphalaria glabrata.";
RL Mol. Biochem. Parasitol. 43:245-255(1990).
CC -1- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC -1- SIMILARITY: Belongs to the tropomyosin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M85199; AAA27817.1; -; mRNA.
CC PIR; A33085; A33085.
CC HSSP; P42639; IC1G.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin; 1.
CC PRINTS; PR00194; TROPOMYOSIN.
CC PROSITE; PS00326; TROPOMYOSIN; 1.
KW Coiled coil; Repeat.
FT COILED 1 284
SQ SEQUENCE 284 AA; 32716 MW; 13735417CE449AEB CRC64;

Query Match 88.2%; Score 30; DB 1; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DASNRAT 7
DB 234 DAENRAT 240
|||
TPM2 BIOGL STANDARD; PRT; 284 AA.
AC P42689;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tropomyosin 2 (TMI2).
OS Biomphalaria glabrata (Bloodfluke planorb).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Biomphalaria.
OX NCBI_TaxID=6526;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Brazilian;
RX MEDLINE=93294622; PubMed=7685709; DOI=10.1006/expr.1993.1044;
RA Weston D.S., Kemp W.M.;
RT "Schistosoma mansoni: comparison of cloned tropomyosin antigens shared
RT between adult parasites and Biomphalaria glabrata.";
RT Exp. Parasitol. 76:358-370(1993).

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CC -1- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC -1- SIMILARITY: Belongs to the tropomyosin family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M97554; AAA27816.1; -; mRNA.
CC HSSP; P42639; IC1G.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin; 1.
CC PRINTS; PR00194; TROPOMYOSIN.
CC PROSITE; PS00326; TROPOMYOSIN; 1.
KW Coiled coil; Repeat.
FT COILED 1 284
SQ SEQUENCE 284 AA; 32683 MW; 2E6103712D9B4C33 CRC64;

Query Match 88.2%; Score 30; DB 1; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DASNRAT 7
DB 234 DAENRAT 240
|||
TPM HALDV STANDARD; PRT; 284 AA.
AC Q9CZ71;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tropomyosin.
OS Haliotis diversicolor (Abalone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Veligastropoda; Haliotoidea; Haliotidae; Haliotis.
OX NCBI_TaxID=36095;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chu K.H., Wong S.H., Leung P.S.C.;
RT "Tropomyosin is the major mollusc allergen: RT-PCR, expression and IgE
RT reactivity.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC -1- SIMILARITY: Belongs to the tropomyosin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF216518; AAG08987.1; -; mRNA.
CC HSSP; P42639; IC1G.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin; 1.

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DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
KW Coiled coil; Repeat 284 By similarity.
FT COILED 1
SQ SEQUENCE 284 AA; 32823 MW; 3A4F5B3F0D3287F7 CRC64;

Query Match      88.2%; Score 30; DB 1; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DASNRAT 7
DB 234 DAENRAT 240

RESULT 28
TPM_HALRU
ID TPM_HALRU STANDARD; PRT; 284 AA.
AC Q25145;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tropomyosin.
OS Haliotis rufescens (California red abalone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Veligastropoda; Haliotidae; Haliotidae; Haliotis.
OX NCBI_TaxID=6454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Degan B.M., Degan S.M., Morse D.E.;
RT "Regulation of tropomyosin gene expression and metamorphic differs
RT among muscle systems examined at morphosis of the gastropod Haliotis
RT rufescens."
RL Dev. Genes Evol. 206:464-471(1997).
CC -!- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC -!- SIMILARITY: Belongs to the tropomyosin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR EMBL; X75218; CAA53028.1; -; mRNA.
DR PIR; S38381; S38381.
DR HSSP; P42639; ICIG.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN; 1.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
KW Coiled coil; Repeat.
FT COILED 1
SQ SEQUENCE 284 AA; 32773 MW; 7FCD287DAD26D627 CRC64;

Query Match      88.2%; Score 30; DB 1; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DASNRAT 7
DB 234 DAENRAT 240

RESULT 29
TPM_MIMNO
ID TPM_MIMNO STANDARD; PRT; 284 AA.
AC Q9GZ69;

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DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tropomyosin.
OS Minachlamys nobilis (Noble scallop) (Chlamys nobilis).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Mimachlamys.
OX NCBI_TaxID=106276;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chu K.H., Wong S.H., Leung P.S.C.;
RT "Tropomyosin is the major mollusc allergen: RT-PCR, expression and IGE
RT reactivity."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC -!- SIMILARITY: Belongs to the tropomyosin family.
CC -----
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CC -----
DR EMBL; AF216520; AAG08989.1; -; mRNA.
DR HSSP; P42639; ICIG.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN; 1.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
KW Coiled coil; Repeat.
FT COILED 1
SQ SEQUENCE 284 AA; 32667 MW; AADD83892359522C CRC64;

Query Match      88.2%; Score 30; DB 1; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DASNRAT 7
DB 234 DAENRAT 240

RESULT 30
TPM_MYTED
ID TPM_MYTED STANDARD; PRT; 284 AA.
AC Q25457;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tropomyosin.
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Anterior byssus retractor muscle;
RA Nyitray L., Yang W., Szent-Gyorgyi A.G.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC -!- SIMILARITY: Belongs to the tropomyosin family.
CC -----

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U40035; AAA82259.1; -; mRNA.
CC HSSP; P42639; 1C1G.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin; 1.
CC PRINTS; PR00194; TROPOMYOSIN.
CC PROSITE; PS00326; TROPOMYOSIN; 1.
CC COILED 1 284 By similarity.
CC SEQUENCE 284 AA; 32798 MW; 546800E7A03EFD62 CRC64;
CC -----
CC Query Match 88.2%; Score 30; DB 1; Length 284;
CC Best Local Similarity 85.7%; Pred. No. 1.2e+02;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 DASNRAT 7
CC DB 234 DAENRAT 240
CC -----
CC RESULT 31
CC ID - TPM MYTGA STANDARD; PRT; 284 AA.
CC AC P91558;
CC DT 30-MAY-2000 (Rel. 39, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
CC DE Tropomyosin.
CC OS Mytilus galloprovincialis (Mediterranean mussel).
CC OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
CC OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.
CC OX NCBI_TaxID=29158;
CC RN [1]
CC RP NUCLEOTIDE SEQUENCE.
CC RC TISSUE=Anterior byssus retractor muscle;
CC RA Iwasaki K., Kikuchi K., Funabara D., Watabe S.;
CC RT "cDNA cloning of tropomyosin from the anterior byssus retractor muscle
CC of mussel and its structural integrity from the deduced amino acid
CC sequence.";
CC RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC CC -!- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC CC -!- SUBUNIT: Homodimer (By similarity).
CC CC -!- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC CC -!- SIMILARITY: Belongs to the tropomyosin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB000907; BAA19209.1; -; mRNA.
CC HSSP; P42639; 1C1G.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin; 1.
CC PRINTS; PR00194; TROPOMYOSIN.
CC PROSITE; PS00326; TROPOMYOSIN; 1.
CC COILED 1 284 By similarity.
CC SEQUENCE 284 AA; 32770 MW; 5468021A8FEFD62 CRC64;
CC -----

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CC -----
CC Query Match 88.2%; Score 30; DB 1; Length 284;
CC Best Local Similarity 85.7%; Pred. No. 1.2e+02;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 DASNRAT 7
CC DB 234 DAENRAT 240
CC -----
CC RESULT 32
CC ID - TPM PERVI STANDARD; PRT; 284 AA.
CC AC Q9GZ70;
CC DT 29-MAR-2004 (Rel. 43, Created)
CC DT 29-MAR-2004 (Rel. 43, Last sequence update)
CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
CC DE Tropomyosin.
CC OS Perna viridis (Tropical green mussel).
CC OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
CC OC Mytiloidea; Mytilidae; Mytilinae; Perna.
CC OX NCBI_TaxID=73031;
CC RN [1]
CC RP NUCLEOTIDE SEQUENCE.
CC RA Chu K.H., Wong S.H., Leung P.S.C.;
CC RT "Tropomyosin is the major mollusc allergen: RT-PCR, expression and IGE
CC reactivity.";
CC RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC CC -!- FUNCTION: Tropomyosin, in association with the troponin complex,
CC plays a central role in the calcium dependent regulation of muscle
CC contraction.
CC CC -!- SUBUNIT: Homodimer (By similarity).
CC CC -!- DOMAIN: The molecule is in a coiled coil structure that is formed
CC by 2 polypeptide chains. The sequence exhibits a prominent seven-
CC residues periodicity.
CC CC -!- SIMILARITY: Belongs to the tropomyosin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF216519; AAC08988.1; -; mRNA.
CC HSSP; P42639; 1C1G.
CC InterPro; IPR002017; Spectrin.
CC InterPro; IPR000533; Tropomyosin.
CC Pfam; PF00261; Tropomyosin; 1.
CC PRINTS; PR00194; TROPOMYOSIN.
CC PROSITE; PS00326; TROPOMYOSIN; 1.
CC COILED 1 284 By similarity.
CC SEQUENCE 284 AA; 32749 MW; EE0B6FB4B2CB3D06 CRC64;
CC -----
CC Query Match 88.2%; Score 30; DB 1; Length 284;
CC Best Local Similarity 85.7%; Pred. No. 1.2e+02;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC -----
CC QY 1 DASNRAT 7
CC DB 234 DAENRAT 240
CC -----
CC RESULT 33
CC ID - O09343; PATYE PRELIMINARY; PRT; 284 AA.
CC AC O09343;
CC DT 01-JUL-1997 (TrEMBLrel. 04, Created)
CC DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
CC DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CC DE Tropomyosin.
CC OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
CC OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
CC OC Pectinoidea; Pectinidae; Mizuhopecten.

```

OX NCBI_TaxID=6573;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Nishita K., Inoue A., Ojima T.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004636; BAA20455.1; -; mRNA.
DR HSSP; P42639; 1CIG.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
SQ SEQUENCE 284 AA; 32598 MW; F4A3D2B090CACD10 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 234 DAENRAT 240
|||||

RESULT 34
Q7YZR3 9VEST
ID Q7YZR3 9VEST PRELIMINARY; PRT; 284 AA.
AC Q7YZR3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tropomyosin 2.
OS Haliotis asinina.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Vetigastropoda; Haliotidae; Haliotidae; Haliotis.
OX NCBI_TaxID=109174;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Counihan R.T., Degnan B.M., Preston N.P.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY320361; AAP85232.1; -; mRNA.
DR HSSP; P42639; 1CIG.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
SQ SEQUENCE 284 AA; 32901 MW; 425B71A5C2D02935 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 234 DAENRAT 240
|||||

RESULT 35
Q7YZR4 9VEST
ID Q7YZR4 9VEST PRELIMINARY; PRT; 284 AA.
AC Q7YZR4;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tropomyosin 1.
OS Haliotis asinina.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Vetigastropoda; Haliotidae; Haliotidae; Haliotis.
OX NCBI_TaxID=109174;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Counihan R.T., Degnan B.M., Preston N.P.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY320360; AAP85231.1; -; mRNA.

DR HSSP; P42639; 1CIG.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
SQ SEQUENCE 284 AA; 32850 MW; 79B0939180557F59 CRC64;

Query Match 88.2%; Score 30; DB 2; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 234 DAENRAT 240
|||||

RESULT 36
Q9GUW8 PATYE
ID Q9GUW8 PATYE PRELIMINARY; PRT; 284 AA.
AC Q9GUW8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tropomyosin.
GN Name=tropomyosin;
OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Mizuhopecten.
OX NCBI_TaxID=6573;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Hasegawa Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050985; BAB17858.1; -; mRNA.
DR HSSP; P42639; 1CIG.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PROSITE; PS00326; TROPOMYOSIN; 1.
SQ SEQUENCE 284 AA; 32708 MW; 6CC1E73AB13DDB9D CRC64;

Query Match 88.2%; Score 30; DB 2; Length 284;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DASNRAT 7
Db 234 DAENRAT 240
|||||

RESULT 37
Q9GUW9 PATYE
ID Q9GUW9 PATYE PRELIMINARY; PRT; 284 AA.
AC Q9GUW9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tropomyosin.
GN Name=tropomyosin;
OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Mizuhopecten.
OX NCBI_TaxID=6573;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Hasegawa Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB050984; BAB17857.1; -; mRNA.
DR HSSP; P42639; 1CIG.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF00261; Tropomyosin; 1.
DR PRINTS; PR00194; TROPOMYOSIN.

```
DR PROSITE; PS00326; TROPOMYOSIN; 1.  
SQ SEQUENCE 284 AA; 32655 MW; DFF351FBD354AC08 CRC64;  
  
Query Match 88.2%; Score 30; DB 2; Length 284;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 DASNRAT 7  
|||  
Db 234 DAENRAT 240  
  
RESULT 38  
Q9NDL0_PATYE PRELIMINARY; PRT; 284 AA.  
AC Q9NDL0;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Tropomyosin (Fragment).  
GN Name=tropomyosin;  
OS Patinopecten yessoensis (Ezo giant scallop) (Yesso scallop).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;  
OC Pectinoidea; Pectinidae; Mizuhopecten.  
OX NCBI_TaxID=6573;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Haegawa Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046202; BAB01765.1; -; mRNA.  
DR HSSP; P42639; 1CIG.  
DR InterPro; IPR000533; Tropomyosin.  
DR Pfam; PF00261; Tropomyosin.1.  
DR PRINTS; PR00194; TROPOMYOSIN.  
DR PROSITE; PS00326; TROPOMYOSIN; 1.  
FT NON TER 284 284  
SQ SEQUENCE 284 AA; 32742 MW; 9CC5BA8707E6B620 CRC64;  
  
Query Match 88.2%; Score 30; DB 2; Length 284;  
Best Local Similarity 85.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 DASNRAT 7  
|||  
Db 234 DAENRAT 240  
  
RESULT 39  
Q7UFB2_RHOBA PRELIMINARY; PRT; 402 AA.  
AC Q7UFB2;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocusNames=RL0221;  
OS Rhodopirellula baltica.  
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
OC Planctomycetacia; Pirellula.  
OX NCBI_TaxID=1117;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=I;  
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;  
RA Glueckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,  
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,  
RA Schlesner H., Amann R., Reinhardt R.;  
RT "Complete genome sequence of the marine planctomycete Pirellula sp.  
strain I.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).  
DR EMBL; BX294151; CAD78771.1; -; Genomic_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
```

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DR InterPro; IPR000157; TIR.  
SQ SEQUENCE 402 AA; 45797 MW; A259EFB64830F527 CRC64;  
  
Query Match 88.2%; Score 30; DB 2; Length 402;  
Best Local Similarity 85.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 DASNRAT 7  
|||  
Db 366 DASNRAT 372  
  
RESULT 40  
Q9FYKO_ARATH PRELIMINARY; PRT; 886 AA.  
ID Q9FYKO_ARATH PRELIMINARY;  
AC Q9FYKO;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE F21J9.31.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,  
RA Shinn P., Altafi H., Bei Q., Chin C., Chioi J., Choi E., Conn L.,  
RA Conn L., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,  
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,  
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
RA Ecker J.R.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chioi J., Choi E., Lam B.,  
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,  
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,  
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
RA Theologis A., Ecker J.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AC000103; AAF97970.1; -; Genomic_DNA.  
DR HSSP; P00523; 2PTK.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR007090; LRR_plant.  
DR InterPro; IPR000719; Prot_kinase.  
DR InterPro; IPR008271; Ser_thr_pkin_AS.  
DR Pfam; PF00560; LRR_1; 8.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PD00019; LEURICHRPT.  
DR PRODOM; PD000001; Prot_kinase; 1.  
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.  
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.  
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.  
KW ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding; Repeat;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 886 AA; 97406 MW; D3E232BD84F0E8FF CRC64;  
  
Query Match 88.2%; Score 30; DB 2; Length 886;  
Best Local Similarity 85.7%; Pred. No. 4.1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 DASNRAT 7
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Db |||||
 57 DASRVT 63

Search completed: December 14, 2005, 07:30:52
Job time : 40.7759 secs

11-11-11

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:11:28 ; Search time 45.5172 Seconds
(without alignments)
77.224 Million cell updates/sec

Title: US-10-720-323-6

Perfect score: 50

Sequence: 1 QQRSNWPP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	8	5	Aau76332 Human ant
2	50	100.0	9	9	Aeb12791 Antitibody
3	50	100.0	10	5	Aam51163 Antit-tumo
4	50	100.0	10	7	Add89876 Human ant
5	50	100.0	10	8	Adm41609 Interleuk
6	50	100.0	10	8	Adm19301 Light cha
7	50	100.0	10	8	Adm19311 Light cha
8	50	100.0	10	8	Adm19311 Light cha
9	50	100.0	10	9	Adw07089 Human ant
10	50	100.0	10	9	Aeb01051 Human IPI
11	50	100.0	10	9	Aeb01046 Human IPI
12	50	100.0	11	8	Adm52368 Fab targe
13	50	100.0	11	9	Aea46154 Apolipop
14	50	100.0	11	9	Aeb28693 Human CDR
15	50	100.0	102	9	Ady33961 Anti-Tie
16	50	100.0	106	9	Aeb12772 Antitibody
17	50	100.0	107	6	Abr54916 Light cha
18	50	100.0	107	9	Aeb19292 IgG kappa
19	50	100.0	108	4	Aab72884 Human ant
20	50	100.0	108	5	Aam51165 Antit-tumo
21	50	100.0	108	5	Aam51173 Human Vg/
22	50	100.0	108	5	Aau76334 Human ant
23	50	100.0	108	7	Adj73533 Erythrope
24	50	100.0	108	7	Adj73534 Erythrope

25	50	100.0	108	8	ADI22138	Adi22138	Anti-plat
26	50	100.0	108	8	ADS13298	Adsi13298	Light cha
27	50	100.0	108	8	ADS19308	Adsi19308	Light cha
28	50	100.0	108	9	Adw07091	Adw07091	Anti-Psaa
29	50	100.0	108	9	Adx01832	Adx01832	SARS coro
30	50	100.0	108	9	Aeb01057	Aeb01057	Human IPI
31	50	100.0	108	9	AEB01062	Aeb01062	Human IPI
32	50	100.0	109	6	ADA89232	Ada89232	Human ant
33	50	100.0	109	6	ADA89228	Ada89228	Human ant
34	50	100.0	109	7	ADF11411	Adf11411	16E1 anti
35	50	100.0	109	7	ADF11395	Adf11395	22B3 anti
36	50	100.0	110	9	ADx02205	Adx02205	SARS coro
37	50	100.0	110	9	ADx02049	Adx02049	SARS coro
38	50	100.0	128	7	ADJ73528	Adj73528	Erythrope
39	50	100.0	128	8	ADM41547	Adm41547	Anti-inte
40	50	100.0	129	5	RAM51174	Aam51174	Human mAb
41	50	100.0	129	5	RAM51175	Aam51175	Human mAb
42	50	100.0	130	7	ADD89877	Add89877	Human ant
43	50	100.0	130	8	ADS64664	Ads64664	Human ant
44	50	100.0	130	8	ADS64653	Ads64653	Human ant
45	50	100.0	214	8	ADH34591	Adh34591	023 light
46	50	100.0	215	7	ADF11435	Adf11435	16E1 anti
47	50	100.0	215	7	ADF11419	Adf11419	22B3 anti
48	50	100.0	224	4	AAB99371	Aab99371	Human int
49	50	100.0	224	4	AAB75004	Aab75004	Anti-IL8
50	50	100.0	235	8	ADM41573	Adm41573	Anti-inte
51	50	100.0	236	9	ADZ51040	Adz51040	Amino aci
52	50	100.0	247	8	ADH34575	Adh34575	scFv SC02
53	50	100.0	247	8	ADH34573	Adh34573	scFv SC02
54	50	100.0	248	9	ADx01838	Adx01838	SARS coro
55	50	100.0	251	9	ADx01956	Adx01956	SARS coro
56	50	100.0	252	9	ADx02034	Adx02034	SARS coro
57	46	92.0	156	4	AAG71323	Aag71323	Human gen
58	46	92.0	219	4	AAG71321	Aag71321	Human gen
59	46	92.0	236	4	AAG71272	Aag71272	Human gen
60	46	92.0	236	5	ABG63490	Abg63490	Human alb
61	46	92.0	236	8	ADL76755	Adl76755	Albumin f
62	44	90.0	148	4	ABG14555	Abg14555	Novel hum
63	44	88.0	108	9	ADM08864	Adm08864	IGF-IR an
64	44	88.0	108	9	ADM08866	Adm08866	IGF-IR an
65	44	88.0	109	7	ADF11403	Adf11403	2D8 anti-
66	44	88.0	109	7	ADF11415	Adf11415	9H7 anti-
67	44	88.0	215	7	ADF11439	Adf11439	9H7 anti-
68	44	88.0	215	7	ADF11427	Adf11427	2D8 anti-
69	43	86.0	9	6	ABP96286	Abp96286	Anti-hTNF
70	43	86.0	9	6	AAE38075	Aae38075	Human 2H9
71	43	86.0	9	8	ADH89430	Adh89430	Human tra
72	43	86.0	9	8	ADS88069	Ads88069	Human CD2
73	43	86.0	9	8	ADS88075	Ads88075	Human CD2
74	43	86.0	9	9	ADM07073	Adm07073	Anti-Psaa
75	43	86.0	9	9	ADM04789	Adm04789	PAPP-A im
76	43	86.0	9	9	ADY26815	Ady26815	Human ant
77	43	86.0	9	9	ADY93862	Ady93862	Anti-SARS
78	43	86.0	9	9	AEA53741	Aea53741	Novel hum
79	43	86.0	9	9	AEA53748	Aea53748	Novel hum
80	43	86.0	9	9	AEA46201	Aea46201	Apolipop
81	43	86.0	9	9	AEA45840	Aea45840	Apolipop
82	43	86.0	9	9	AEA24223	Aea24223	Anti-HAAR
83	43	86.0	9	9	AEA24231	Aea24231	Anti-HAAR
84	43	86.0	9	9	AEA24197	Aea24197	Anti-HAAR
85	43	86.0	9	9	AEA24228	Aea24228	Anti-HAAR
86	43	86.0	10	8	ADH17924	Adh17924	Human 1H3
87	43	86.0	10	9	AEA46076	Aea46076	Apolipop
88	43	86.0	95	6	ABO27153	Ab027153	Human ger
89	43	86.0	95	7	ADP10195	Adp10195	Antibody
90	43	86.0	95	7	ADP10093	Adp10093	VEGF anti
91	43	86.0	95	7	ADF09988	Adf09988	Antibody
92	43	86.0	95	7	ADJ80273	Adj80273	Vkappa ge
93	43	86.0	95	8	ADJO07342	Adj007342	Human ant
94	43	86.0	95	8	ADU86536	Adu86536	Immunoglo
95	43	86.0	95	9	ADY75447	Ady75447	Human ger
96	43	86.0	95	9	AEAS3928	Aea53928	Novel hum
97	43	86.0	95	9	AEB13648	Aeb13648	Human var

98 43 86.0 96 9 AEA53874 Aea53874 Novel hum
99 43 86.0 101 9 AEB01068 Aeb01068 Human lig
100 43 86.0 102 9 ADY33953 Ady33953 Anti-tie

ALIGNMENTS

RESULT 1
AAU76332
ID AAU76332 standard; peptide; 8 AA.
XX
AC AAU76332;
DT 21-MAY-2002 (first entry)
XX
DE Human anti-dual integrin antibody light chain variable region CDR3.
XX
KW Human; antibody; dual integrin; CDR; light chain variable region; LC CDR;
KW medical device; immune related disease; rheumatoid arthritis;
KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
KW neurological disease; multiple sclerosis; Parkinson's disease;
KW Alzheimer's disease; Creutzfeldt-Jakob disease.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 7. 8
FT /note= "Encoded by CCT"
XX
XX WO200212501-A2.
XX
XX 14-FEB-2002.
XX
XX 07-AUG-2001; 2001WO-US024784.
XX
XX 07-AUG-2000; 2000US-0223363P.
PR 01-AUG-2001; 2001US-00920267.
XX
XX (CENZ) CENTOCOR INC.
XX
XX Giles-Komar J, Heavner G, Snyder L, Trikha M;
XX WPI; 2002-217193/27.
XX
XX Novel isolated mammalian anti-dual integrin antibody, useful for
PT diagnosing or treating dual integrin related condition such as rheumatoid
PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.
XX
XX Claim 29; Page 134; 144pp; English.
XX
XX The invention relates to an isolated mammalian anti-dual integrin
CC antibody having at least one of the human heavy chain or light chain
CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
CC included are the nucleic acids encoding the CDRs, a vector comprising the
CC nucleic acids, a host cell comprising the vector, an anti-idiotype
CC antibody that binds to the anti-dual integrin, a medical device comprising
CC the antibody suitable for administration by parenteral, subcutaneous,
CC intramuscular, intravenous, intrarticular, intrabronchial,
CC intrabdominal, intracapsular, intracartilaginous, intracavitary,
CC intracerebellar, or other routes as given in specification. The antibody
CC is useful for diagnosing or treating a dual integrin related condition in
CC an animal for example, immune related disease such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, cardiovascular disease such as
CC atherosclerosis, atherosclerosis, restenosis, angina pectoris,
CC myocardial infarction, infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's

CC lymphoma, multiple myeloma; neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
CC Creutzfeldt-Jakob disease and many other diseases given in the
CC specification. The present sequence is an anti-dual integrin human light
CC chain CDR
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 50; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QQRSNWPP 8
Db 1 QQRSNWPP 8
RESULT 2
AEB12791
ID AEB12791 standard; peptide; 9 AA.
XX
AC AEB12791;
XX
DT 08-SEP-2005 (first entry)
XX
DE Antibody 80R light chain variable region CDR SEQ ID NO 39.
XX
KW virucide; respiratory-gen.; vaccine; monoclonal antibody;
KW antibody production; diagnosis; therapeutic;
KW Severe acute respiratory syndrome; sars coronavirus infection; antiviral;
KW respiratory disease; infection; single chain antibody; 80R;
KW light chain variable region.
XX
OS Homo sapiens.
XX
XX WO2005060520-A2.
XX
XX 07-JUL-2005.
XX
XX 24-NOV-2004; 2004WO-US039750.
PF
XX 25-NOV-2003; 2003US-0524840P.
PR
XX (DAND) DANA FARBER CANCER INST INC.
XX
XX Marasco W, Sui J;
XX WPI; 2005-488568/49.
XX
XX Novel monoclonal or scFv antibody capable of binding to epitope on region
PT of spike protein of severe acute respiratory syndrome coronavirus (SARS-
PT Cov) and neutralizing SARS-Cov, useful for treating SARS-Cov infection.
XX
XX Claim 63; SEQ ID NO 39; 93pp; English.
XX
XX The invention describes a monoclonal antibody (I) capable of neutralizing
CC SARS-Cov, binding to an epitope on a region of the spike protein of SARS-
CC Cov and neutralizing SARS-Cov, or an scFv antibody (II) capable of
CC neutralizing SARS-Cov, binding to an epitope on a region of the spike
CC protein of SARS-Cov and neutralizing SARS-Cov. Also described are:
CC vaccinating (M1) a patient against SARS-Cov; a composition (III)
CC comprising (I) and a carrier; a kit (IV) comprising (III) in one or more
CC containers; a passive vaccine (V) against SARS-Cov, comprising (III);
CC screening (M2) for compounds that modulate the interaction between SARS-
CC Cov and the SARS-Cov receptor ACE2; and enhancing (M3) the neutralization
CC activity of MAB or scFv 80R. (I) or (II) is useful for preventing a
CC disease or disorder caused by a coronavirus. (I) or (II) is useful for
CC treating a coronavirus-related disease or disorder. (I) is useful for
CC diagnosing a coronavirus-related disease or disorder. The coronavirus-
CC related disease or disorder is SARS. (I) is useful for detecting the
CC presence of a coronavirus in a sample, which involves contacting the
CC sample with (I), and detecting the presence or absence of an antibody-
CC antigen complex, thus detecting the presence of a coronavirus in a

CC sample. (I) is useful for identifying compounds useful to treat a SARS-Cov-related disease or disorder. The at least one SARS-Cov protein is provided as a SARS-Cov molecule. The at least one SARS-Cov protein is provided in a cell infected with the SARS-Cov (M1) is useful for vaccinating a patient against SARS-Cov. This is the amino acid sequence of anti-SARS-Cov spike protein of an N-terminal single chain (scFv)

CC antibody 80R light chain variable region CDR.

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSNWPP 8
| | | | | | | |
DB 1 QORSNWPP 8

RESULT 3

AAM51163
ID AAM51163 standard; peptide; 10 AA.

AC AAM51163;

DT 10-JUN-2002 (first entry)

DE Anti-tumour necrosis factor antibody light chain CDR3.

KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW complementarity determining region; antirheumatic; antiarthritic;
KW antiulcer; antischmatic; antiallergic; antiinflammatory; antisticking;
KW antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;
KW antianginal; cardiac; antibacterial; virucide; fungicide; antileptotic;
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy.

XX Homo sapiens.

OS WO200212502-A2.

PN 14-FEB-2002.

PD 07-AUG-2001; 2001WO-US024785.

PF 07-AUG-2000; 2000US-0223360P.

PR 29-SEP-2000; 2000US-0236826P.

PR 01-AUG-2001; 2001US-00920137.

XX (CENZ) CENTOCOR INC.

PA Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;

PI WPI; 2002-217194/27.

DR Novel isolated mammalian anti-tumor necrosis factor antibody, useful for

PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,

PT angina pectoris, myocardial infarction, leprosy.

PS Claim 21; Page 129; 131pp; English.

XX This sequence is that of complementarity determining region 3 (CDR3) of
CC the light chain of an anti-tumor necrosis factor (TNF) antibody. The
CC invention provides isolated human, primate, rodent, mammalian, chimeric,
CC humanised and/or CDR-grafted anti-TNF antibodies, immunoglobulins,
CC cleavage products and other specified portions and variants, as well as
CC anti-TNF antibody compositions, encoding or complementary nucleic acids,
CC vectors, host cells, compositions, formulations, devices, transgenic
CC animals, transgenic plants, and methods of making and using them. The
CC anti-TNF antibody comprises at least a portion of an immunoglobulin
CC molecule, especially the heavy chain and/or light chain variable regions
CC given in AAM51165-66, or either all of the CDRs of the heavy chain (see
CC AAM51158-60) or all of the CDRs of the light chain (see AAM51161-63). The

CC antibody may inhibit TNF-induced cell adhesion molecules, inhibit TNF
CC binding to receptor, or provide arthritic index improvement in a mouse
CC model. It is useful for diagnosing or treating a TNF related condition in
CC a cell, tissue, organ or animal (claimed) such as rheumatoid arthritis,
CC gastric ulcer, asthma, allergic rhinitis, Crohn's pathology, sickle cell
CC anaemia, diabetes, a cardiovascular disease such as arteriosclerosis,
CC atherosclerosis, restenosis, angina pectoris or myocardial infarction, an
CC infectious disease in a cell such as bacterial, viral, and fungal
CC infections, pneumonia, leprosy and malaria, a malignant disease such as
CC leukaemia, chronic myelocytic leukaemia, Burkitt's lymphoma and multiple
CC myeloma, or a neurological disease such as multiple sclerosis,
CC Parkinson's disease, spinal ataxia, Alzheimer's disease and Creutzfeldt-
CC Jakob disease

SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSNWPP 8
| | | | | | | |
DB 1 QORSNWPP 8

RESULT 4

ADD89876
ID ADD89876 standard; peptide; 10 AA.

XX AC ADD89876;

XX DT 29-JAN-2004 (first entry)

DE Human anti-tumour necrosis factor antibody light chain CDR3.

KW Human; Tumour necrosis factor; TNF; antibody;

KW complementarity determining region; cytostatic; anabolic;

KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;

KW neuroprotective.

OS Homo sapiens.

PN WO2003083061-A2.

PD 09-OCT-2003.

PR 24-MAR-2003; 2003WO-US009072.

PR 26-MAR-2002; 2002US-0367903P.

XX (CENZ) CENTOCOR INC.

PA Giles-Komar J, Scallion BJ, Carton JM;

PI WPI; 2003-804040/75.

DR New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful
PT for diagnosing or treating an anti-TNF related condition, e.g. cancer,
PT anorexia, cachexia, or bacterial infection.

PS Claim 2; Page 86; 87pp; English.

XX The present sequence is that of complementarity determining region 3
CC (CDR3) of the light chain variable region of claimed mammalian anti-
CC tumour necrosis factor (TNF) antibodies of the invention. The CDR is
CC derived from a human TNF reactive IgG monoclonal antibody generated by
CC cloning variable and constant region DNA in vector pc4 and expression in
CC CHO cells. The invention provides isolated human, primate, rodent,
CC mammalian, chimeric, humanized and/or CDR-grafted anti-TNF antibodies,
CC immunoglobulins, their cleavage products, other specified portions and
CC variants, as well as anti-TNF antibody compositions, nucleic acids
CC encoding these, vectors, host cells, methods for producing the antibodies
CC using a host cell, transgenic animal or transgenic plant or plant cell,

CC and therapeutic compositions, methods and devices. The antibody, nucleic acid, protein, composition and methods are useful for diagnosing or treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia, or an immune, cardiovascular, infectious, and/or neurological disease.

XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | | | | |
Db 1 QQRSNWPP 8

RESULT 5
ADM41609
ID ADM41609 standard; peptide; 10 AA.
XX
AC ADM41609;
DT
DT
DT
XX
DE Interleukin-1 receptor type 1 antibody light chain variable region CDR3.
XX
XX Human; monoclonal antibody; antibody; interleukin-1; receptor;
KW antiasthmatic; antiinflammatory; dermatological; antiallergic;
KW proteoglycan; antirheumatic; antiarthritic; osteopathic; vasotropic;
KW analgesic; antidiabetic; nephrotropic; antianemic; nootropic;
KW anticonvulsant; dermatological; antitumor; antiparkinsonian; antidiabetic;
KW cytosolic; complementarity determining region.
XX
OS Homo sapiens.
XX
XX WO2004022718-A2.
XX
XX 18-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027978.
XX
XX 06-SEP-2002; 2002US-0408719P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
PI Elliott G;
XX
XX WPI; 2004-248462/23.
XX
XX Isolated human antibody that specifically binds interleukin-1 receptor type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
XX Claim 46; SEQ ID NO 74; 179pp; English.

CC The present sequence is that of complementarity determining region 3 (CDR3) of the human anti-interleukin-1 receptor type 1 (IL-1R1) monoclonal antibody (MAB) 26F5 and 27F2 light chain variable region ADM41547. Anti-IL-1R1 antibodies of the invention may comprise this CDR. These antibodies inhibit IL-1 signalling by competing with IL-1beta and IL-1alpha binding to IL-1R. Monoclonal antibodies, as well as single chain antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies and (Fab')2 antibodies, are used in methods of treating IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample. IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral sclerosis, Alzheimer's disease, cachexia, anorexia, asthma, atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome, Clostridium associated illnesses, coronary conditions, cancer including leukaemia and tumour metastasis, diabetes, endometriosis, fever, fibromyalgia, glomerulonephritis, graft versus host disease, osteoarthritis, rheumatoid arthritis, inflammatory eye disease, ischaemia, Kawasaki's disease, learning impairment, lung diseases,

CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease, periodontal disease, pre-term labour, psoriasis, reperfusion injury, septic shock, side effects of radiation therapy, temporal mandibular joint disease, sleep disturbance, uveitis, or an inflammatory condition resulting from strain, sprain, cartilage damage, trauma, orthopaedic surgery, infection or other disease processes.

XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 50; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | | | | |
Db 1 QQRSNWPP 8

RESULT 6
ADS19301
ID ADS19301 standard; peptide; 10 AA.
XX
AC ADS19301;
DT
DT 18-NOV-2004 (first entry)
XX
XX Light chain CDR3 peptide of human mAb 3G6 antibody SeqID 12.
DE
DE human; antibody; mAb 3G6; lymphocyte migration;
KW inflammatory bowel disease; Crohn's disease; gastroenteritis;
KW pulmonary inflammatory disease; asthma; chronic bronchitis;
KW graft rejection; psoriasis; eczema; urticaria; scleroderma;
KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;
KW autoimmune thyroiditis; Behcet's syndrome; viral infection; cancer;
KW neoplastic disease; leukaemia; lymphoma; antineoplastic; antiaschmatic;
KW immunosuppressive; antipsoriatic; dermatological; neuroprotective;
KW antidiabetic; nephrotropic; virucide; cytostatic; vasotropic;
KW alphaE integrin; CD103; alphaE-beta7.
XX
XX Homo sapiens.
XX
XX US2003232387-A1.
XX
XX 18-DEC-2003.
XX
XX 14-JUN-2002; 2002US-00173551.
XX
XX 14-JUN-2002; 2002US-00173551.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lu C;
XX
XX WPI; 2004-178738/17.
XX
XX Novel antibody which binds activated alpha-E integrin, specifically to activation-induced epitope on integrin alpha-E chain (CD103), useful for treating inflammatory bowel diseases e.g., Crohn's disease, gastroenteritis.
XX
XX Claim 8; SEQ ID NO 12; 67pp; English.

CC This invention relates to novel antibody and antigen-binding fragments of antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically, it refers to the binding of activation induced epitopes presented on activated alphaE integrins, where these integrins are activated by exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable growth factors and/or mitogens. The present invention describes the alphaE-beta7 integrin as a homing receptor that mediates lymphocyte migration to mucosal epithelium. As such, compositions of this invention are useful for treating a subject having an inflammatory bowel disease such as Crohn's disease or gastroenteritis or pulmonary inflammatory diseases such as asthma and chronic bronchitis. Furthermore, such

CC compositions can be used for inhibiting graft rejection, psoriasis,
 CC eczema, urticaria, scleroderma, autoimmune diseases such as multiple
 CC sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's
 CC diseases and lymphomas. Accordingly, they exhibit antiinflammatory,
 CC leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory,
 CC antiasthmatic, immunosuppressive, antipsoriatic, dermatological,
 CC neuroprotective, antidiabetic, nephrotropic, virucide, cytostatic and
 CC vasotrophic activities. This peptide sequence is a human antibody heavy
 CC chain complementarity determining region (CDR) that binds the integrin
 CC alphaE chain of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 50; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 |||||
 Db 1 QQRSNWPP 8

RESULT 7
 ADS19311
 ID ADS19311 standard; peptide; 10 AA.

XX ADS19311;

XX 18-NOV-2004 (first entry)

DE Light chain CDR3 peptide of human mAb 5E4 antibody SeqID 22.

XX human; antibody; mAb 5E4; lymphocyte migration;
 KW inflammatory bowel disease; Crohn's disease; gastroenteritis;
 KW pulmonary inflammatory disease; asthma; chronic bronchitis;
 KW graft rejection; psoriasis; eczema; urticaria; scleroderma;
 KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;
 KW autoimmune thyroiditis; Behcet's syndrome; viral infection; cancer;
 KW neoplastic disease; leukaemia; lymphoma; antiinflammatory; antiasthmatic;
 KW immunosuppressive; antipsoriatic; dermatological; neuroprotective;
 KW antidiabetic; nephrotropic; virucide; cytostatic; vasotropic;
 KW alphaE integrin; CD103; alphaE-beta7.

XX Homo sapiens.

XX US2003232387-A1.

XX 18-DEC-2003.

XX 14-JUN-2002; 2002US-00173551.

XX 14-JUN-2002; 2002US-00173551.

XX (MILL-) MILLENNIUM PHARM INC.

XX Lu C;

XX WPI; 2004-178738/17.

XX Novel antibody which binds activated alpha-E integrin, specifically to
 PT activation-induced epitope on integrin alpha-E chain (CD103), useful for
 PT treating inflammatory bowel diseases e.g., Crohn's disease,
 PT gastroenteritis.

XX Claim 12; SEQ ID NO 22; 67pp; English.

XX This invention relates to novel antibody and antigen-binding fragments of
 CC antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically,
 CC it refers to the binding of activation induced epitopes present on
 CC activated alphaE integrins, where these integrins are activated by
 CC exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable
 CC growth factors and/or mitogens. The present invention describes the
 CC alphaE-beta7 integrin as a homing receptor that mediates lymphocyte

CC migration to mucosal epithelium. As such, compositions of this invention
 CC are useful for treating a subject having an inflammatory bowel disease
 CC such as Crohn's disease or gastroenteritis or pulmonary inflammatory
 CC diseases such as asthma and chronic bronchitis. Furthermore, such
 CC compositions can be used for inhibiting graft rejection, psoriasis,
 CC eczema, urticaria, scleroderma, autoimmune diseases such as multiple
 CC sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's
 CC syndrome, viral infections, cancer and/or neoplastic diseases such as
 CC leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory,
 CC antiasthmatic, immunosuppressive, antipsoriatic, dermatological,
 CC neuroprotective, antidiabetic, nephrotropic, virucide, cytostatic and
 CC vasotrophic activities. This peptide sequence is a human antibody heavy
 CC chain complementarity determining region (CDR) that binds the integrin
 CC alphaE chain of the invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 50; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 |||||
 Db 1 QQRSNWPP 8

RESULT 8
 ADS64651

ID ADS64651 standard; peptide; 10 AA.

XX ADS64651;

XX 16-DEC-2004 (first entry)

DE Human anti-TNF antibody light chain CDR1 peptide #2.

XX Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;
 KW obesity; immune related disease; rheumatoid arthritis;
 KW cardiovascular disease; stroke; malignant disease; leukaemia;
 KW neurological disease; multiple sclerosis; infection; hepatitis;
 KW anorectic; antiarthritic; cerebroprotective; vasotropic; cytostatic;
 KW neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;
 KW anti-TNF antibody; CDR; complementarity determining region; human;
 KW light chain.

XX Homo sapiens.

XX US2004185047-A1.

XX 23-SEP-2004.

XX 21-MAR-2003; 2003US-00394471.

XX 21-MAR-2003; 2003US-00394471.

XX (GILE/) GILES-KOMAR J.

XX (SCAL/) SCALLON B J.

XX (CART/) CARTON J M.

XX Giles-Komar J, Scallon BJ, Carton JM;

XX WPI; 2004-676151/66.

XX Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody
 PT capable of inhibiting binding of TNF alpha to TNF receptor, useful for
 PT treating TNF-related diseases such as obesity or rheumatoid arthritis.

XX Claim 2; SEQ ID NO 14; 45pp; English.

XX The present invention relates to a mammalian anti-tumour necrosis factor
 CC (TNF) antibody capable of inhibiting binding of TNF alpha to TNF
 CC receptor. The invention is useful for diagnosing or treating an anti-TNF
 CC related condition in a cell, tissue, organ or animal and in

CC immunotherapy. The invention is also useful for treating TNF related
 CC diseases chosen from obesity, immune related disease such as rheumatoid
 CC arthritis, cardiovascular disease such as stroke, malignant disease such
 CC as leukemia, neurological disease such as multiple sclerosis and
 CC bacterial or viral infections such as hepatitis. The present sequence is
 CC the human anti-TNF antibody light chain complementarity determining
 CC region 3 (CDR3) peptide.

XX Sequence 10 AA;
 SQ

Query Match 100.0%; Score 50; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 DB 1 QQRSNWPP 8

RESULT 9
 ADW07089
 ID ADW07089 standard; peptide; 10 AA.

XX
 AC ADW07089;
 XX
 DT 07-APR-2005 (first entry)

XX Anti-PsAa-antibody 9A7 VK CDR3.

XX antibacterial; antiinflammatory; immunosuppressive; antibody engineering;
 KW pharmaceutical; infection; pneumonia; meningitis; sepsis;
 KW pneumococcal surface adhesin A; PsAa; light chain variable region;
 KW complementarity determining region 3; CDR3; db.

XX Homo sapiens.

XX WO2005003174-A1.

XX 13-JAN-2005.

XX 08-JUL-2004; 2004WO-DK000492.

XX 08-JUL-2003; 2003DK-00001044.

XX 11-JUL-2003; 2003US-0486647P.

XX (GENE-) GENESTO AS.

XX Sorensen AP, Benfield TL, Lundgren JD, Kempe TD;

DR WPI; 2005-101476/11.

DR N-PSDB; ADW07088.

XX New binding member towards Streptococcus pneumoniae surface adhesin A
 PT protein, useful for treating or preventing pneumonia, meningitis and/or
 PT sepsis.

XX Disclosure; SEQ ID NO 38; 137pp; English.

XX The invention describes an isolated binding member comprising at least
 CC one binding domain capable of specifically binding Streptococcus
 CC pneumoniae surface adhesin A (PsAa) protein, the binding domain having a
 CC dissociation constant Kd for PsAa which is less than 1 x10⁻⁶ M. Also
 CC described are: an isolated nucleic acid molecule encoding at least a part
 CC of the binding member described above; a vector comprising the nucleic
 CC acid molecule of (1); a host cell comprising the nucleic acid molecule of
 CC (1); a cell line engineered to express the binding member described above
 CC ; detecting or diagnosing a disease or disorder associated with
 CC pneumococcus in an individual; a kit comprising at least one binding
 CC member described above, the antibody being labeled; and a pharmaceutical
 CC composition comprising at least one binding member described above. The
 CC binding member is useful for producing a pharmaceutical composition for
 CC the treatment of pneumococcus infection. The binding member, methods and
 CC composition are useful for treating or preventing an individual suffering

CC from disorders or diseases associated with S. pneumoniae, e.g. pneumonia,
 CC meningitis and/or sepsis. This sequence encodes anti-pneumococcal surface
 CC adhesin A (PsAa)-antibody 9A7 kappa light chain variable region
 CC complementarity determining region 3 (CDR3).

XX Sequence 10 AA;

Query Match 100.0%; Score 50; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 DB 1 QQRSNWPP 8

RESULT 10
 AEB01051
 ID AEB01051 standard; peptide; 10 AA.

XX
 AC AEB01051;

XX 08-SEP-2005 (first entry)

XX Human IP10 antibody light chain variable region, CDR3, SEQ ID NO 79.

XX antibody; IP-10; inflammation; immune disorder; dermatological disease;
 KW respiratory disease; neurological disease; degeneration; infection;
 KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;
 KW Gastrointestinal-Gen.; Antiulcer; Dermatological; Immunosuppressive;
 KW Antiadipatic; Antipsoriatic; Antithyroid; Antiasthmatic;
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
 KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Vitucide;
 KW Antibacterial.

XX Homo sapiens.

XX WO2005058815-A2.

XX 30-JUN-2005.

XX 10-DEC-2004; 2004WO-US041506.

XX 10-DEC-2003; 2003US-0529180P.

XX (MEDA-) MEDAREX INC.

XX Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;

XX WPI; 2005-467095/47.

XX Isolated human monoclonal antibody or an antigen-binding portion, which
 PT specifically binds to human interferon gamma inducible protein 10 (IP-
 PT 10), useful for treating viral or bacterial infection, or inflammatory or
 PT autoimmune diseases.

XX Claim 15; SEQ ID NO 79; 179pp; English.

XX The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human ITAC. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type 1 diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,

CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative
 CC glomerulonephritis, rapidly progressive glomerulonephritis), or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the amino acid sequence of a human IP10 monoclonal
 CC antibody light chain variable region, CDR3.

XX Sequence 10 AA;

Query Match 100.0%; Score 50; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 |||||
 Db 1 QQRSNWPP 8

RESULT 11

ID AEB01046 standard; peptide; 10 AA.

XX AEB01046;

AC 08-SEP-2005 (first entry)

DE Human IP10 antibody light chain variable region, CDR3, SEQ ID NO 74.

XX antibody; IP-10; inflammation; immune disorder; dermatological disease;
 KW respiratory disease; neurological disease; degeneration; infection;
 KW Neuroprotective; Antiarthritic; Antirheumatic; Anti-inflammatory;
 KW Gastrointestinal-Gen.; Antitumor; Dermatological; Immunosuppressive;
 KW Antidiabetic; Antiproliferative; Antithyroid; Anticancer;
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
 KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Virucide;
 KW Antibacterial.

OS Homo sapiens.

XX WO2005058915-A2.

PN 30-JUN-2005.

XX 10-DEC-2004; 2004WO-US041506.

XX 10-DEC-2003; 2003US-0529180P.

XX (MEDA-) MEDAREX INC.

XX Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;

PI Passmore D, Rangan VS, Lane TS, Keirstead HS, Liu MT;

XX WPI; 2005-467095/47.

XX Isolated human monoclonal antibody or an antigen-binding portion, which
 PT specifically binds to human interferon gamma inducible protein 10 (IP-
 PT 10), useful for treating viral or bacterial infection, or inflammatory or
 PT autoimmune diseases.

XX Claim 15; SEQ ID NO 74; 179pp; English.

XX The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human ITAC. The isolated human monoclonal antibody is

CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
 CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative
 CC glomerulonephritis, rapidly progressive glomerulonephritis), or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the amino acid sequence of a human IP10 monoclonal
 CC antibody light chain variable region, CDR3.

XX Sequence 10 AA;

Query Match 100.0%; Score 50; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 |||||
 Db 1 QQRSNWPP 8

RESULT 12

ADSS2368
 ID ADSS2368 standard; peptide; 11 AA.

XX ADSS2368;

XX 16-DEC-2004 (first entry)

DE Fab targeting HLA-A2/Tax11-19, T3E3, light chain CDR 3.

XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KW major histocompatibility complex; MHC class I; viral infection;
 KW human T lymphotropic virus-1 infection; viral oncoprotein;
 KW mycoplasma infection; bacterial infection; fungal infection;
 KW protozoal infection; phage display; light chain; CDR;
 KW complementarity determining region.

XX Homo sapiens.

XX US2004191260-A1.

XX 30-SEP-2004.

XX 26-MAR-2003; 2003US-00396578.

XX 26-MAR-2003; 2003US-00396578.

XX (TECR) TECHNION RES & DEV FOUND LTD.

XX Reiter Y, Cohen C;

XX WPI; 2004-735863/72.

XX New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.

XX Claim 5; SEQ ID NO 19; 68pp; English.

XX The invention relates to a composition-of-matter comprising (a multimeric
 CC form of) an antibody or antibody fragment including an antigen-binding
 CC region capable of specifically binding an antigen-presenting portion of a

CC complex composed of a human antigen-presenting molecule and an antigen
 CC derived from a pathogen. Also included are an isolated polynucleotide
 CC comprising a nucleic acid sequence encoding an antibody fragment (the
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule and an antigen derived from a
 CC pathogen), a nucleic acid construct comprising the isolated
 CC polynucleotide above (and a promoter sequence for directing transcription
 CC of the isolated polynucleotide in a host cell), a host cell comprising
 CC the nucleic acid construct above, a host virus comprising the nucleic
 CC acid construct above, a virus comprising a coat protein fused to the
 CC antibody fragment, detecting an antigen-presenting portion of a complex
 CC composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen, a method of diagnosing an infection by a pathogen in an
 CC individual, a method of killing or damaging a target cell
 CC expressing/displaying an antigen-presenting portion of a complex
 CC (composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC detectable moiety is a recognition sequence of a biotin protein ligase, a
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polyhistidine tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC Pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
 CC The antigen derived from a pathogen is restricted by the antigen-
 CC presenting molecule and is a polypeptide selected from a segment of a
 CC viral oncoprotein or a segment of a tax protein. A pharmaceutical
 CC composition comprising as an active ingredient the composition-of-matter
 CC is useful in a method for treating a disease associated with a pathogen
 CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
 CC protozoans. The composition-of-matter or the methods are useful for
 CC diagnosing an infection by a pathogen in an individual and for killing or
 CC damaging a target cell expressing or displaying an antigen-presenting
 CC portion of a complex composed of a human antigen-presenting molecule and
 CC an antigen derived from a pathogen. A phage displayed library of human
 CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC sequences compared. The present sequence is a CDR from the light chain of
 CC an isolated Fab clone.

XX Sequence 11 AA;

Query Match 100.0%; Score 50; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 |||||
 Db 1 QQRSNWPP 8

RESULT 13

AEA46154
 ID AEA46154 standard; peptide; 11 AA.

XX AEA46154;

AC AEA46154;

XX 11-AUG-2005 (first entry)

DE Apolipoprotein E C-terminal domain antibody VL-CDR3 peptide #130.

XX Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
 KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen.; Apolipoprotein E;
 KW Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
 -KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;

KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
 KW motor neurone disease; chronic obstructive pulmonary disease.

XX Homo sapiens.

PN GB2408508-A.

XX 01-JUN-2005.

XX 26-NOV-2004; 2004GB-00026043.

XX 28-NOV-2003; 2003US-0525174P.

PA (ASTR) ASTRAZENECA AB.

PA (DYAX-) DYAX CORP.

XX Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
 PI Hufton S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;

XX WPI; 2005-408785/42.

XX New human antibody or antibody fragment which binds to a sequence of the
 PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
 PT manufacturing a medicament for treating or preventing an amyloid disorder
 PT e.g. Alzheimers disease.

XX Example 23; Page 111; 392pp; English.

XX The present invention relates to a human antibody or antibody fragment,
 CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD);
 CC A2A44803) and also to human plaques. The antibody or its fragment is
 CC useful for manufacturing a medicament for treating or preventing an
 CC amyloid disorder such as Alzheimers disease, primary systemic
 CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
 CC familial amyloid polynuropathy 1, familial amyloid polynuropathy II,
 CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
 CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
 CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
 CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
 CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
 CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
 CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
 CC disease, Gerstmann-Strausler-Scheinker Disease (GSS), Kuru, Parkinsons
 CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
 CC chronic obstructive pulmonary disease. The present sequence was used to
 CC illustrate the invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 50; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 |||||
 Db 1 QQRSNWPP 8

RESULT 14

AE28693

ID AEB28693 standard; peptide; 11 AA.

XX AEB28693;

XX 22-SEP-2005 (first entry)

DE Human CDR3 of T3E3 Fab specifically binding HLA-A2/Tax11-19, SEQ: 19.

XX Diagnosis; therapeutic; infection; antimicrobial; light chain; T3E3.

XX Homo sapiens.

XX US2005152912-A1.

PN

XX PD 14-JUL-2005.
 XX PF 09-MAR-2005; 2005US-00074803.
 XX PR 26-MAR-2003; 2003US-00396578.
 XX PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX PI Reiter Y, Cohen C;
 XX DR WPI; 2005-496781/50.
 XX PS New composition-of-matter capable of specifically binding an antigen-presenting molecule and a pathogen-derived antigen complexes, useful for treating diseases associated with a pathogen.
 XX CC Claim 5; SEQ ID NO 19; 65pp; English.
 XX CC The present invention relates to a composition-of-matter which comprises an antibody or antibody fragment or a multimeric form of an antibody or antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule (APM) and an antigen derived from a pathogen. The invention is useful for the specific detection of the antigen-presenting portion of the complex and for diagnosing/treating various types of diseases associated with a pathogen infection by killing/damaging pathogen infected cells. The present sequence is a complementarity determining regions (CDR) of Fab light chain antibody specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex. Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-1).
 XX SQ Sequence 11 AA;
 Query Match 100.0%; Score 50; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;
 Qy 1 QQRSNWPP 8
 Db 1 QQRSNWPP 8
 RESULT 15
 ADY33961
 ID ADY33961 standard; protein; 102 AA.
 AC ADY33961;
 DT 19-MAY-2005 (first entry)
 DE Anti-Tie 1 antibody PD10 light chain variable region protein.
 XX Receptor tyrosine kinase; Tie 1; light chain variable region;
 KW antibody engineering; angiogenesis; drug discovery;
 KW angiogenesis disorder; antiangiogenic; cardiovascular disease; cancer;
 KW cyostatic; neoplasm; inflammation; antiinflammatory;
 KW rheumatoid arthritis; antiarthritic; antirheumatic; immune disorder;
 KW musculoskeletal disease; psoriasis; antipsoriatic;
 KW dermatological disease; antibody.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO2005019267-A2.
 PN 03-MAR-2005.
 PD 12-AUG-2004; 2004WO-US026116.
 XX PF 12-AUG-2003; 2003US-0494713P.
 XX PR 12-AUG-2003; 2003US-0494713P.
 XX PA (DAND) DANA FARBER CANCER INST INC.

PA (DYAX-) DYAX CORP.
 XX Hufton SE, Hoet R, Pieters H, Kent RB, Rookey K;
 XX WPI; 2005-202607/21.
 DR N-PSDB; ADY33960.
 XX PT New isolated proteins comprising heavy and light chain immunoglobulin variable domain sequences and that bind to Tie1 ectodomain, useful for diagnosing, preventing or treating angiogenesis-related disorders or inflammation.
 XX PS Example 3; SEQ ID NO 38; 171pp; English.
 XX CC The invention relates to an isolated protein that binds to Tie1 (receptor tyrosine kinase) ectodomain. The protein comprises heavy and light chain immunoglobulin variable domain sequences. Also included an isolated nucleic acid comprising a coding sequence that encodes a polypeptide comprising an immunoglobulin heavy chain (HC) or light chain (LC) variable domain sequence (where the coding sequence is at least 85% identical to a reference sequence that encodes the HC variable domain of clone E3, G2, p-A1, p-A10, p-B1, p-B3, p-C6, p-D12, p-F3, p-F4, p-G3, s-A10, s-H1, s-A2, s-B2, s-B9, s-C10, s-C2, s-C7, s-D11, s-E11, s-G10, or s-H4, or the coding sequence hybridizes to the reference sequence or its complement), a host cell that contains the nucleic acid nucleic acid, a pharmaceutical composition comprising the above protein and a pharmaceutical carrier, methods of modulating angiogenesis or endothelial cell activity in the subject and methods for detecting the presence of a Tie1 protein, in a sample. The composition and methods are useful for diagnosing, preventing or treating angiogenesis-related disorders (e.g. cancer) of inflammatory disorders, such as rheumatoid arthritis or psoriasis. These may also be used in drug screening procedures. The present sequence represents the light chain variable region of an antibody that binds to human receptor tyrosine kinase Tie 1.
 XX SQ Sequence 102 AA;
 Query Match 100.0%; Score 50; DB 9; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QQRSNWPP 8
 Db 90 QQRSNWPP 97
 RESULT 16
 AEB12772
 ID AEB12772 standard; protein; 106 AA.
 AC AEB12772;
 DT 08-SEP-2005 (first entry)
 DE Antibody 80R light chain variable region SEQ ID NO 20.
 XX virutide; respiratory-gen.; vaccine; monoclonal antibody;
 KW antibody production; diagnosis; therapeutic;
 KW Severe acute respiratory syndrome; SARS coronavirus infection; antiviral;
 KW respiratory disease; infection; single chain antibody; 80R;
 KW light chain variable region.
 XX OS Homo sapiens.
 OS WO2005060520-A2.
 PN 07-JUL-2005.
 PD 24-NOV-2004; 2004WO-US039750.
 XX PF 25-NOV-2003; 2003US-0524840P.
 XX PR (DAND) DANA FARBER CANCER INST INC.

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XX Marasco W, Sui J;
PI
XX WPI; 2005-488568/49.
DR
XX Novel monoclonal or scFv antibody capable of binding to epitope on region
PT of spike protein of severe acute respiratory syndrome coronavirus (SARS-
PT CoV) and neutralizing SARS-CoV, useful for treating SARS-CoV infection.
XX
XX Example 2; SEQ ID NO 20; 93pp; English.
PS
XX The invention describes a monoclonal antibody (I) capable of neutralizing
CC SARS-CoV, binding to an epitope on a region of the spike protein of SARS-
CC CoV and neutralizing SARS-CoV, or an scFv antibody (II) capable of
CC neutralizing SARS-CoV, binding to an epitope on a region of the spike
CC protein of SARS-CoV and neutralizing SARS-CoV. Also described are:
CC vaccinating (M1) a patient against SARS-CoV; a composition (III)
CC comprising (I) and a carrier; a kit (IV) comprising (III) in one or more
CC containers; a passive vaccine (V) against SARS-CoV, comprising (III);
CC screening (M2) for compounds that modulate the interaction between SARS-
CC CoV and the SARS-CoV receptor ACE2; and enhancing (M3) the neutralization
CC activity of MAb or scFv 80R. (I) or (II) is useful for preventing a
CC disease or disorder caused by a coronavirus. (I) or (II) is useful for
CC treating a coronavirus-related disease or disorder. (I) is useful for
CC diagnosing a coronavirus-related disease or disorder. The coronavirus-
CC related disease or disorder is SARS. (I) is useful for detecting the
CC presence of a coronavirus in a sample, which involves contacting the
CC sample with (I), and detecting the presence or absence of an antibody-
CC antigen complex, thus detecting the presence of a coronavirus in a
CC sample. (I) is useful for identifying compounds useful to treat a SARS-
CC CoV-related disease or disorder. The at least one SARS-CoV protein is
CC provided as a SARS-CoV molecule. The at least one SARS-CoV protein is
CC provided in a cell infected with the SARS-CoV (M1) is useful for
CC vaccinating a patient against SARS-CoV. This is the amino acid sequence
CC of anti-SARS-CoV spike protein N-terminal single chain (scFv) antibody
CC 80R light chain variable region.
XX
SQ Sequence 106 AA;
Query Match 100.0%; Score 50; DB 9; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db |||||
88 QQRSNWPP 95

RESULT 17
ABR54916
ID ABR54916 standard; protein; 107 AA.
XX
XX ABR54916;
AC
XX
XX 30-JUN-2003 (first entry)
DT
XX
XX Light chain clone HBPAXK9b 3E7 SEQ ID NO:142.
DE
XX Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.
XX
XX Homo sapiens.
OS Synthetic.
XX WO2003025202-A2.
FN
XX 27-MAR-2003.
PD
XX 19-SEP-2002; 2002WO-US029889.
PF
XX 19-SEP-2001; 2001US-0323455P.
PR
XX (ALEX-) ALEXION PHARM INC.
PA

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XX Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
PI
XX WPI; 2003-313359/30.
DR
XX Amplifying nucleic acid by contacting engineered nucleic acid strand
PT having predetermined sequence at one end and sequence complementary to
PT predetermined sequence at other end, with primer having predetermined
PT sequence.
XX
XX Example 3; Fig 8b-c; 68pp; English.
PS
XX The present invention describes a method (M1) for amplifying a nucleic
CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other, and contacting (S) with a
CC primer having the predetermined sequence in the presence of a polymerase
CC and nucleotides under conditions suitable for polymerisation of the
CC nucleotides. Also described is an engineered nucleic acid strand (I)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other end. M1 is useful for
CC amplifying a nucleic acid. M1 can be used for producing an antibody
CC library. M1 is useful for preparing amplified products that can be
CC ligated into a suitable expression vector, where the vector can be used
CC to transform an appropriate host organism to produce the polypeptide or
CC protein encoded by the target sequence. M1 is useful to amplify a family
CC of related sequences to build a complex library such as, for example an
CC antibody library. M1 is useful not only for producing large amounts of
CC one target nucleic acid sequence, but also for amplifying simultaneously
CC more than one different target nucleic acid sequence located on the same
CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
CC ABR54998 represent sequence used in the exemplification of the present
CC invention
XX
SQ Sequence 107 AA;
Query Match 100.0%; Score 50; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db |||||
89 QQRSNWPP 96

RESULT 18
ABE19292
ID ABE19292 standard; protein; 107 AA.
XX
XX ABE19292;
AC
XX
XX 08-SEP-2005 (first entry)
DT
XX
XX IgG kappa light chain variable region polypeptide HBPAXK9b SEQ ID 142.
DE
XX DNA amplification; expression; light chain variable region.
XX
XX Homo sapiens.
OS
XX WO2005060641-A2.
FN
XX 07-JUL-2005.
PD
XX 15-DEC-2004; 2004WO-US041945.
PF
XX 15-DEC-2003; 2003US-00737252.
PR
XX (ALEX-) ALEXION PHARM INC.
PA
XX Maruyama T, Frederickson S, Bowdish KS, Renshaw M, Lin Y;
XX WPI; 2005-488575/49.
XX

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PT Amplifying nucleic acid encoding portion of antibody, by annealing primer
 PT to template encoding antibody, synthesizing polynucleotide complementary
 PT to template, annealing template to polynucleotide and amplifying
 XX polynucleotide.

XX Disclosure; SEQ ID NO 142; 76pp; English.

XX The invention describes a method of amplifying a nucleic acid encoding a
 CC portion of an antibody, involving annealing a primer to a template that
 CC encodes a portion of the antibody, synthesizing a polynucleotide that is
 CC complementary to the portion of the template, separating the synthesized
 CC polynucleotide, annealing a template oligonucleotide to the synthesized
 CC polynucleotide, extending the synthesized polynucleotide and amplifying
 CC the polynucleotide. Also described are: producing (M2) an antibody
 CC library, involves providing a diverse population of templates that encode
 CC a portion of an IgA antibody, contacting the diverse population of
 CC templates with a primer, which has a first portion which anneals to the
 CC templates and a second portion of predetermined sequence which does not
 CC anneal to the templates, and carrying out steps (b)-(f) of (M1); a
 CC library of IgA antibodies prepared by (M2); identifying (M3) an antibody
 CC having a desired binding specificity, involves preparing a library of IgA
 CC antibodies by (M2), and screening the library to identify one or more IgA
 CC antibodies having a desired binding specificity; and an IgA antibody
 CC identified by (M3). (M1) is useful for amplifying nucleic acid encoding a
 CC portion of an antibody, and for producing an antibody library. (M2) is
 CC useful for identifying an antibody having a desired binding specificity.
 CC (M1) enables an improved nucleic acid amplification with decreased mis-
 CC priming and amplification of sequences other than the target sequence.
 CC This is the amino acid sequence of an IGG kappa light chain variable
 CC region comprising framework 1-CDRI-framework 2-CDR2.

XX Sequence 107 AA;

Query Match 100.0%; Score 50; DB 9; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 Db 89 QQRSNWPP 96
 |||||

RESULT 19

AA72884
 ID AAB72884 standard; protein; 108 AA.

XX AC AAB72884;

XX DT 10-MAY-2001 (first entry)

XX DE Human anti-HER2/neu antibody 2-E8 light chain.

XX KW Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;
 KW 1-D2; 2-E8; growth factor receptor.

XX OS Homo sapiens.

XX FN WO200109187-A2.

XX PD 08-FEB-2001.

XX PF 25-JUL-2000; 2000WO-US020272.

XX PR 29-JUL-1999; 99US-0146313P.

XX PR 10-MAR-2000; 2000US-0188539P.

XX PA (MEDA-) MEDAREX INC.

XX PI Keler T, Deo Y;

XX DR WPI; 2001-168698/17.

XX DR N-PSDB; AAF75590.

XX

PT New human monoclonal antibody that specifically binds to growth factor
 PT receptor HER2/neu, for treating, preventing or diagnosing diseases
 PT characterized by aberrant HER2/neu expression e.g. cancers.

XX PS Disclosure; Page 110; 113pp; English.

XX CC The present invention provides the protein and coding sequences for human
 CC monoclonal antibodies which bind specifically to the HER2/neu growth
 CC factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
 CC and 2-E8. They can be used in the immunotherapy-based treatment and
 CC prognosis of cancers, particularly adenocarcinomas such as salivary
 CC gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
 CC and ovarian cancer. The present sequence is part of an antibody of the
 CC invention

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 4; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 Db 89 QQRSNWPP 96
 |||||

RESULT 20

AA51165

ID AA51165 standard; protein; 108 AA.

XX AC AA51165;

XX DT 10-JUN-2002 (first entry)

XX DE Anti-tumour necrosis factor antibody light chain variable region.

XX KW Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;
 KW complementarity determining region; antirheumatic; antiarthritic;
 KW antitumor; antidiabetic; antiallergic; antiinflammatory; antiskidling;
 KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
 KW antianginal; cardiant; antibacterial; virucide; fungicide; antileptotic;
 KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
 KW human; diagnosis; therapy.

XX OS Homo sapiens.

XX FN WO200212502-A2.

XX PD 14-FEB-2002.

XX PF 07-AUG-2001; 2001WO-US024785.

XX PR 07-AUG-2000; 2000US-0223360P.

XX PR 29-SEP-2000; 2000US-0236826P.

XX PR 01-AUG-2001; 2001US-00920137.

XX PA (CENZ) CENTOCOR INC.

XX

XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
PI WPI; 2002-217194/27.
XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT angina pectoris, myocardial infarction, leprosy.
XX Claim 9; Page 129-130; 131pp; English.
XX The present sequence is that of the light chain variable region of an
CC anti-tumour necrosis factor (TNF) antibody of the invention. The
CC invention provides isolated human, primate, rodent, mammalian, chimeric,
CC humanised and/or complementarity determining region (CDR)-grafted anti-
CC TNF antibodies, immunoglobulins, cleavage products and other specified
CC portions and variants, as well as anti-TNF antibody compositions,
CC encoding or complementary nucleic acids, vectors, host cells,
CC compositions, formulations, devices, transgenic animals, transgenic
CC plants, and methods of making and using them. The anti-TNF antibody
CC comprises at least a portion of an immunoglobulin molecule, especially
CC the heavy chain and/or light chain variable regions given in AAM51164 and
CC in the present sequence, or either all of the CDRs of the heavy chain
CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC 63). The antibody may inhibit TNF-induced cell adhesion molecules,
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC in a mouse model. It is useful for diagnosing or treating a TNF related
CC condition in a cell, tissue, organ or animal (claimed) such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, a cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC myocardial infarction, an infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma and multiple myeloma, or a neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC Creutzfeldt-Jakob disease
XX Sequence 108 AA;
XX
XX Query Match 100.0%; Score 50; DB 5; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 0.63;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 QQRSNWPP 8
XX |||||
XX Db 89 QQRSNWPP 96
XX
XX RESULT 21
XX AAM51173
XX ID AAM51173 standard; protein; 108 AA.
XX AC AAM51173;
XX XX 10-JUN-2002 (first entry)
XX DE Human Vg/38K-type light chain variable region.
XX
XX Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;
KW complementarity determining region; antirheumatic; antiarthritic;
KW antileucic; antiasthmatic; anti allergic; antiinflammatory; antisickling;
KW antidiabetic; antiarteriosclerotic; antithrombotic; vasotropic;
KW antianginal; cardiac; antibacterial; virucide; fungicide; antileprotic;
KW protozoacide; cyostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy; Vg/38K.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..23
XX FT /label= FR1
XX FT 24..34
XX . FT

FT Region /label= CDR1
FT 35..49
FT /label= FR2
FT 50..56
FT /label= CDR2
FT 57..88
FT /label= FR3
FT 89..98
FT /label= CDR3
FT 99..108
FT /label= J3
XX
XX WO200212502-A2.
XX
XX 14-FEB-2002.
XX
XX 07-AUG-2001; 2001WO-US024785.
XX
XX 07-AUG-2000; 2000US-0223360P.
XX 29-SEP-2000; 2000US-0236826P.
XX 01-AUG-2001; 2001US-00920137.
XX (CENZ) CENTOCOR INC.
XX
XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
XX
XX WPI; 2002-217194/27.
XX N-PSDB; ABL53513.
XX
XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
XX angina pectoris, myocardial infarction, leprosy.
XX
XX Example 3; Fig 5; 131pp; English.
XX
XX The present sequence is that of a human Vg/38K-type light chain variable
XX region encoded by a human germline gene in a transgenic mouse used in
XX human monoclonal antibody (mab) construction. A Genviv fusion was
XX performed using spleen cells from a hybrid mouse containing human
XX variable and constant region antibody transgenes that was immunised with
XX recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were
XX obtained that bound immobilised human TNF alpha with apparently high
XX avidity. These mAbs had a totally human IgG1, kappa isotype. The mature
XX portion of the light chain variable region of 2 of the mAbs, TNV14 and
XX TNV15, were identical (see AAM51174) to the present sequence, while the
XX light chain variable region of 2 others, TNV14(8) and TNV156 (see
XX AAM51175), differed by a single amino acid residue. The invention
XX provides human, primate, rodent, mammalian, chimeric, humanised and/or
XX complementarity determining region (CDR)-grafted anti-TNF antibodies,
XX immunoglobulins, and cleavage products and variants, as well as anti-TNF
XX antibody compositions, encoding or complementary nucleic acids, vectors,
XX host cells, compositions, formulations, devices, transgenic animals,
XX transgenic plants, and methods of making and using them. The anti-TNF
XX antibody comprises at least a portion of an immunoglobulin molecule,
XX especially the heavy chain and/or light chain variable regions given in
XX the present sequence and in AAM51165, or either all of the CDRs of the
XX heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see
XX AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion
XX molecules, inhibit TNF binding to receptor, or provide Arthritic Index
XX improvement in a mouse model. They are useful for diagnosing or treating
XX a TNF related condition in a cell, tissue, organ or animal (claimed) such
XX as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,
XX Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular
XX disease such as arteriosclerosis, atherosclerosis, restenosis, angina
XX pectoris or myocardial infarction, an infectious disease in a cell such
XX as bacterial, viral, and fungal infections, pneumonia, leprosy and
XX malaria, a malignant disease such as leukaemia, chronic myelocytic
XX leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological
XX disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,
XX Alzheimer's disease and Creutzfeldt-Jakob disease
XX Sequence 108 AA;
XX SQ

Query Match 100.0%; Score 50; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSNWPP 8
 |||||
 DB 89 QORSNWPP 96

RESULT 22

ID AAU76334
 AC AAU76334;

DT 21-MAY-2002 (first entry)

DE Human anti-dual integrin antibody complete variable region #2.

KW Human; antibody; dual integrin; HC CDR; variable region; LC CDR;
 KW medical device; immune related disease; rheumatoid arthritis;
 KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
 KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
 KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
 KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
 KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
 KW neurological disease; multiple sclerosis; Parkinson's disease;
 KW Alzheimer's disease; Creutzfeldt-Jakob disease.

OS Homo sapiens.

XX WO200212501-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024784.

XX 07-AUG-2000; 2000US-0223363P.

XX 01-AUG-2001; 2001US-00920267.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Heavner G, Snyder L, Trikha M;

XX WPI; 2002-217193/27.

XX Novel isolated mammalian anti-dual integrin antibody, useful for
 PT diagnosing or treating dual integrin related condition such as rheumatoid
 PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

XX Claim 1; Page 134; 144pp; English.

XX The invention relates to an isolated mammalian anti-dual integrin
 CC antibody having at least one of the human heavy chain or light chain
 CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
 CC included are the nucleic acids encoding the CDRs, a vector comprising the
 CC nucleic acids, a host cell comprising the vector, an anti-idiotypic
 CC antibody that binds to the anti-dual integrin, a medical device comprising
 CC the antibody suitable for administration by parenteral, subcutaneous,
 CC intramuscular, intravenous, intrarticular, intrabronchial,
 CC intraabdominal, intracapsular, intracartilaginous, intracavitary,
 CC intracerebellar, or other routes as given in specification. The antibody
 CC is useful for diagnosing or treating a dual integrin related condition in
 CC an animal for example, immune related disease such as rheumatoid
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
 CC sickle cell anaemia, diabetes, cardiovascular disease such as
 CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
 CC myocardial infarction, infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma, multiple myeloma; neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
 CC Creutzfeldt-Jakob disease and many other diseases given in the

CC specification. The present sequence is an anti-dual integrin human
 CC variable region containing at least one of the six CDRs listed above
 CC (AAU76327-AAU76332)
 XX SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 5; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSNWPP 8
 |||||
 DB 89 QORSNWPP 96

RESULT 23

ID ADJ73533 standard; protein; 108 AA.

XX AC ADJ73533;

XX 06-MAY-2004 (first entry)

DE Erythropoietin light chain mimetibody SeqID 989.

XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 KW erythropoietin.

XX Synthetic.

XX WO2003084477-A2.

XX 16-OCT-2003.

XX 24-MAR-2003; 2003WO-US009139.

XX 29-MAR-2002; 2002US-0368791P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Knight DM, Scallion BJ, Ghayeb J;

XX WPI; 2003-804237/75.

XX New CDR mimetibody comprising a portion of a heavy or light chain
 PT variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.

XX Example 2; SEQ ID NO 989; 97pp; English.

XX This invention relates to novel mammalian CDR mimetibodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC mimetibodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetibody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC polypeptide sequence is an erythropoietin light chain mimetibody of the
 XX invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 7; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.63; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QQRSNWPP 8
 Db 89 QQRSNWPP 96

RESULT 24

ADJ73534
 ID ADJ73534 standard; protein; 108 AA.

XX AC ADJ73534;

DT 06-MAY-2004 (first entry)

XX Erythropoietin light chain mimetibody SeqID 990.

DE XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KW cardiovascular; infectious; malignant; neurogenic disease; anaemia;
 KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 KW erythropoietin.

XX OS Synthetic.

XX PN W02003084477-A2.

XX PD 16-OCT-2003.

XX PF 24-MAR-2003; 2003WO-US009139.

XX PR 29-MAR-2002; 2002US-0368791P.

XX PA (CENZ) CENTOCOR INC.

XX PI Heavner GA, Knight DM, Scallion BJ, Ghrayeb J;

XX WPI; 2003-804237/75.

XX New CDR mimetibody comprising a portion of a heavy or light chain
 PT variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.

PS Example 2; SEQ ID NO 990; 97pp; English.

XX This invention relates to novel mammalian CDR mimetibodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC mimetibodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetibody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC polypeptide sequence is an erythropoietin light chain mimetibody of the
 CC invention.

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 7; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.63; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QQRSNWPP 8
 Db 89 QQRSNWPP 96

RESULT 25

ADJ22138

ID ADJ22138 standard; protein; 108 AA.

XX AC ADJ22138;

DT 22-APR-2004 (first entry)

XX Anti-platelet autoantibody related light chain amino acid L76 SEQ:101.

DE XX anti-platelet autoantibody; autoantibody; blood clotting inhibition;
 KW thrombus; platelet adhesion inhibition;
 KW thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
 KW idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
 KW thrombolytic; human.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN W02004005890-A2.

XX PD 15-JAN-2004.

XX PF 03-JUL-2003; 2003WO-US021304.

XX PR 03-JUL-2002; 2002US-0394352P.

XX PR 18-SEP-2002; 2002US-0411694P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Siegel DL;

XX WPI; 2004-142998/14.

XX DR N-PSDB; ADI22085.

XX PS Claim 12; SEQ ID NO 101; 232pp; English.

XX The present invention describes a method (M1) for identifying an anti-
 CC platelet autoantibody (I) in a mammal. The autoantibody is detected by
 CC producing an antibody phage display library from B-lymphocytes obtained
 CC from the mammal, and screening the library to detect a phage that
 CC specifically binds with a platelet component, where the screening
 CC comprises panning the phage on intact platelets using competitive cell-
 CC surface panning. Also described: (1) an autoantibody identified by (M1);
 CC (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)
 CC inhibiting (M2) blood clotting in a mammal having a thrombus or at risk
 CC of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a
 CC mammal having a thrombus or at risk of thrombus formation; (5) inhibiting
 CC (M4) binding of an anti-platelet autoantibody with a platelet component;
 CC (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)
 CC thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)
 CC platelet aggregation; (9) inhibiting (M8) platelet activation; (10)
 CC inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an
 CC anti-platelet autoantibody, or its biologically active fragment with a
 CC platelet; (12) identifying (M11) a peptide that inhibits binding of an
 CC anti-platelet autoantibody with a platelet; (13) a peptide identified by
 CC the method of (12); (14) a peptide that specifically binds with an anti-
 CC platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic
 CC purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood
 CC clotting, inhibiting platelet aggregation, inhibiting platelet function
 CC or inhibiting platelet activation comprising an amount of an anti-
 CC platelet autoantibody, or its biologically active fragment that
 CC specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or
 CC its fragment comprises an antigen binding region derived from an H44L4
 CC anti-platelet autoantibody, the kit further comprising a peptide
 CC inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator
 CC and an instructions for use. (I) has haemostatic, anticoagulant and
 CC thrombolytic activities. The autoantibodies (I) are useful for diagnosing
 CC and for developing therapeutics for diseases mediated by autoantibody
 CC binding with platelet antigens. (M6) and (M12) are useful for treating
 CC thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic
 CC purpura, respectively. (M2) and (M3) are useful for inhibiting blood

CC clotting. The present sequence is used in the exemplification of the
 CC present invention.

XX Sequence 108 AA;

Query Match 100.0%; Score 50; DB 8; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

QY 1 QORSNWPP 8

|||||||
 89 QORSNWPP 96

RESULT 26

ADSI9298
 ID ADS19298 standard; protein; 108 AA.

XX AC ADS19298;

XX DT 18-NOV-2004 (first entry)

XX DE Light chain variable region of human mAb 3G6 antibody protein SeqID 9.

XX KW human; antibody; mAb 3G6; lymphocyte migration;

XX KW inflammatory bowel disease; Crohn's disease; gastroenteritis;

XX KW pulmonary inflammatory disease; asthma; chronic bronchitis;

XX KW graft rejection; psoriasis; eczema; urticaria; scleroderma;

XX KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;

XX KW autoimmune thyroiditis; Behcet's syndrome; viral infection; cancer;

XX KW neoplastic disease; leukaemia; lymphoma; antiinflammatory; antiasthmatic;

XX KW immunosuppressive; antipsoriatic; dermatological; neuroprotective;

XX KW antidiabetic; nephrotropic; virucide; cytostatic; vasotropic;

XX KW alphaE integrin; CD103; alphaE-beta7.

XX OS Homo sapiens.

XX XX US2003232387-A1.

XX PN 18-DEC-2003.

XX PD 14-JUN-2002; 2002US-00173551.

XX PF 14-JUN-2002; 2002US-00173551.

XX PR 14-JUN-2002; 2002US-00173551.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lu C;

XX XX WPI; 2004-178738/17.

XX DR N-PSDB; ADS19297.

XX XX Novel antibody which binds activated alpha-E integrin, specifically to

XX PT activation-induced epitope on integrin alpha-E chain (CD103), useful for

XX PT treating inflammatory bowel diseases e.g., Crohn's disease,

XX PT gastroenteritis.

XX PS Disclosure; SEQ ID NO 9; 67pp; English.

XX XX This invention relates to novel antibody and antigen-binding fragments of

XX CC antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically,

XX CC it refers to the binding of activation induced epitopes present on

XX CC activated alphaE integrins, where these integrins are activated by

XX CC exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable

XX CC growth factors and/ or mitogens. The present invention describes the

XX CC alphaE-beta7 integrin as a homing receptor that mediates lymphocyte

XX CC migration to mucosal epithelium. As such, compositions of this invention

XX CC are useful for treating a subject having an inflammatory bowel disease

XX CC such as Crohn's disease or gastroenteritis or pulmonary inflammatory

XX CC diseases such as asthma and chronic bronchitis. Furthermore, such

XX CC compositions can be used for inhibiting graft rejection, psoriasis,

XX CC eczema, urticaria, scleroderma, autoimmune diseases such as multiple

XX CC sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's

XX CC

CC syndrome, viral infections, cancer and/or neoplastic diseases such as
 CC leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory,
 CC antiasthmatic, immunosuppressive, antipsoriatic, dermatological,
 CC neuroprotective, antidiabetic, nephrotropic, virucide, cytostatic and
 CC vasotropic activities. This polypeptide sequence is a human antibody that
 XX binds the integrin alphaE chain of the invention.

SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 8; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;

QY 1 QORSNWPP 8

|||||||
 89 QORSNWPP 96

RESULT 27

ADSI9308
 ID ADS19308 standard; protein; 108 AA.

XX AC ADS19308;

XX DT 18-NOV-2004 (first entry)

XX DE Light chain variable region of human mAb 5E4 antibody protein SeqID 19.

XX KW human; antibody; mAb 5E4; lymphocyte migration;

XX KW inflammatory bowel disease; Crohn's disease; gastroenteritis;

XX KW pulmonary inflammatory disease; asthma; chronic bronchitis;

XX KW graft rejection; psoriasis; eczema; urticaria; scleroderma;

XX KW autoimmune disease; multiple sclerosis; diabetes; glomerulonephritis;

XX KW autoimmune thyroiditis; Behcet's syndrome; viral infection; cancer;

XX KW neoplastic disease; leukaemia; lymphoma; antiinflammatory; antiasthmatic;

XX KW immunosuppressive; antipsoriatic; dermatological; neuroprotective;

XX KW antidiabetic; nephrotropic; virucide; cytostatic; vasotropic;

XX KW alphaE integrin; CD103; alphaE-beta7.

XX OS Homo sapiens.

XX XX US2003232387-A1.

XX PN 18-DEC-2003.

XX PD 14-JUN-2002; 2002US-00173551.

XX PF 14-JUN-2002; 2002US-00173551.

XX PR 14-JUN-2002; 2002US-00173551.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lu C;

XX XX WPI; 2004-178738/17.

XX DR N-PSDB; ADS19307.

XX XX Novel antibody which binds activated alpha-E integrin, specifically to

XX PT activation-induced epitope on integrin alpha-E chain (CD103), useful for

XX PT treating inflammatory bowel diseases e.g., Crohn's disease,

XX PT gastroenteritis.

XX PS Disclosure; SEQ ID NO 19; 67pp; English.

XX XX This invention relates to novel antibody and antigen-binding fragments of

XX CC antibodies that bind alphaE-beta7 integrin chains (CD103). Specifically,

XX CC it refers to the binding of activation induced epitopes present on

XX CC activated alphaE integrins, where these integrins are activated by

XX CC exposure to divalent cations (e.g. Mn2+), to phorbol esters or suitable

XX CC growth factors and/ or mitogens. The present invention describes the

XX CC alphaE-beta7 integrin as a homing receptor that mediates lymphocyte

XX CC migration to mucosal epithelium. As such, compositions of this invention

XX CC are useful for treating a subject having an inflammatory bowel disease

XX CC such as Crohn's disease or gastroenteritis or pulmonary inflammatory

XX CC

CC diseases such as asthma and chronic bronchitis. Furthermore, such
 CC compositions can be used for inhibiting graft rejection, psoriasis,
 CC eczema, urticaria, scleroderma, autoimmune diseases such as multiple
 CC sclerosis, diabetes, glomerulonephritis, autoimmune thyroiditis, Behcet's
 CC syndrome, viral infections, cancer and/or neoplastic diseases such as
 CC leukaemias and lymphomas. Accordingly, they exhibit antiinflammatory,
 CC antiasthmatic, immunosuppressive, antipsoriatic, dermatological,
 CC neuroprotective, antidiabetic, nephroprotective, virucide, cytostatic and
 CC vasotrophic activities. This polypeptide sequence is a human antibody that
 CC binds the integrin alphaE chain of the invention.
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 8; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 DB 89 QQRSNWPP 96
 |||||

RESULT 28
 ADW07091
 ID ADW07091 standard; protein; 108 AA.

AC ADW07091;

XX 07-APR-2005 (first entry)

XX Anti-Psaa-antibody 9A7 VK.

XX antibacterial; antiinflammatory; immunosuppressive; antibody engineering;
 KW pharmaceutical; infection; pneumonia; meningitis; sepsis;
 KW pneumococcal surface adhesin A; PsaA; light chain variable region.

XX Homo sapiens.

XX WO2005003174-A1.

XX 13-JAN-2005.

XX 08-JUL-2004; 2004WO-DK000492.

XX 08-JUL-2003; 2003DK-00001044.

XX 11-JUL-2003; 2003US-0486647P.

XX (GENE-) GENESTO AS.

XX Sorensen AP, Benfield TL, Lundgren JD, Kempe TD;

XX WPI; 2005-101476/11.

XX N-PSDB; ADW07090.

XX New binding member towards Streptococcus pneumoniae surface adhesin A
 PT protein, useful for treating or preventing pneumonia, meningitis and/or
 PT sepsis.

XX Disclosure; SEQ ID NO 40; 137pp; English.

XX The invention describes an isolated binding member comprising at least
 CC one binding domain capable of specifically binding Streptococcus
 CC pneumoniae surface adhesin A (psaa) protein, the binding domain having a
 CC dissociation constant Kd for PsaA which is less than 1 x10⁻⁶ M. Also
 CC described are: an isolated nucleic acid molecule encoding at least a part
 CC of the binding member described above; a vector comprising the nucleic
 CC acid molecule of (1); a host cell comprising the nucleic acid molecule of
 CC (1); a cell line engineered to express the binding member described above
 CC ; detecting or diagnosing a disease or disorder associated with
 CC Pneumococcus in an individual; a kit comprising at least one binding
 CC member described above, the antibody being labeled; and a pharmaceutical
 CC composition comprising at least one binding member described above. The
 CC binding member is useful for producing a pharmaceutical composition for

CC the treatment of Pneumococcus infection. The binding member, methods and
 CC composition are useful for treating or preventing an individual suffering
 CC from disorders or diseases associated with S. pneumoniae, e.g. pneumonia,
 CC meningitis and/or sepsis. This is the amino acid sequence of anti-
 CC pneumococcal surface adhesin A (psaa)-antibody 9A7 kappa light chain
 CC variable region.
 XX

SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 9; Length 108;

Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 DB 89 QQRSNWPP 96
 |||||

RESULT 29
 ADX01832
 ID ADX01832 standard; protein; 108 AA.

XX ADX01832;

XX 21-APR-2005 (first entry)

XX SARS coronavirus antibody light chain SEQ ID NO 88.

XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 KW respiratory disease; infection; antibody; light chain.

XX SARS coronavirus.

XX WO2005012360-A2.

XX 10-FEB-2005.

XX 21-JUL-2004; 2004WO-EP051568.

XX 22-JUL-2003; 2003WO-EP050328.

XX 01-SEP-2003; 2003WO-EP050391.

XX 16-OCT-2003; 2003WO-EP050723.

XX 24-NOV-2003; 2003WO-EP050883.

XX 04-DEC-2003; 2003WO-EP050943.

XX 02-FEB-2004; 2004WO-EP050067.

XX 13-FEB-2004; 2004WO-EP050127.

XX 19-MAR-2004; 2004WO-EP050334.

XX 07-APR-2004; 2004WO-EP050464.

XX 14-APR-2004; 2004WO-EP050516.

XX 29-APR-2004; 2004WO-EP050643.

XX (CRUC-) CRUCELL HOLLAND BV.

XX Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;

XX WPI; 2005-142879/15.

XX N-PSDB; ADX01831.

XX New binding molecules that specifically bind to severe acute respiratory
 PT syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 PT treating conditions resulting from SARS-CoV.

XX Disclosure; SEQ ID NO 88; 633pp; English.

XX The invention relates to a binding molecule, or its variant, capable of
 CC specifically binding to a severe acute respiratory syndrome (SARS)-
 CC coronavirus (CoV). The composition (including the binding molecule or its
 CC functional variant, or the immunconjugate) is useful as a medicament for
 CC the diagnosis, prophylaxis or treatment of a condition resulting from a
 CC SARS-CoV, or in the preparation of the medicament. The present sequence
 CC represents a SARS coronavirus binding molecule light chain.

XX Sequence 108 AA;

Query Match 100.0%; Score 50; DB 9; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 | | | | | | | |
 DB 89 QQRSNWPP 96

RESULT 30
 AEB01057
 ID AEB01057 standard; protein; 108 AA.
 XX
 AC AEB01057;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Human IP10 antibody light chain variable region, SEQ ID NO 85.
 XX
 KW antibody; IP-10; inflammation; immune disorder; dermatological disease;
 KW respiratory disease; neurological disease; degeneration; infection;
 KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;
 KW Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;
 KW Antidiabetic; Antipariatic; Antichyroid; Antiasthmatic;
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
 KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Virucide;
 KW Antibacterial; light chain variable region.
 XX
 OS Homo sapiens.
 XX
 PN WO2005058815-A2.
 XX
 PD 30-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-US041506.
 XX
 PR 10-DEC-2003; 2003US-0529180P.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
 XX
 DR WPI; 2005-467095/47.
 DR N-PSDB; AEB01083.
 XX
 PS Isolated human monoclonal antibody or an antigen-binding portion, which
 XX specifically binds to human interferon gamma inducible protein 10 (IP-
 XX 10), useful for treating viral or bacterial infection, or inflammatory or
 XX autoimmune diseases.
 XX
 PS Claim 35; SEQ ID NO 85; 179pp; English.
 XX
 CC The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human ITAC. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
 CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative

CC glomerulonephritis, rapidly progressive glomerulonephritis), or
 CC atherosclerosis. It is also useful for treating a viral or bacterial
 CC infection involving unwanted IP-10 activity in a subject, where the viral
 CC infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present
 CC sequence represents the amino acid sequence of a human IP10 monoclonal
 CC antibody light chain variable region.
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 50; DB 9; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 | | | | | | | |
 DB 89 QQRSNWPP 96

RESULT 31
 AEB01062
 ID AEB01062 standard; protein; 108 AA.
 XX
 AC AEB01062;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE Human IP10 antibody light chain variable region, SEQ ID NO 90.
 XX
 KW antibody; IP-10; inflammation; immune disorder; dermatological disease;
 KW respiratory disease; neurological disease; degeneration; infection;
 KW Neuroprotective; Antiarthritic; Antirheumatic; Antiinflammatory;
 KW Gastrointestinal-Gen.; Anticancer; Dermatological; Immunosuppressive;
 KW Antidiabetic; Antipariatic; Antichyroid; Antiasthmatic;
 KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
 KW Antiparkinsonian; Antiangiogenic; Antiarteriosclerotic; Virucide;
 KW Antibacterial; light chain variable region.
 XX
 OS Homo sapiens.
 XX
 PN WO2005058815-A2.
 XX
 PD 30-JUN-2005.
 XX
 PF 10-DEC-2004; 2004WO-US041506.
 XX
 PR 10-DEC-2003; 2003US-0529180P.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
 PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
 XX
 DR WPI; 2005-467095/47.
 DR N-PSDB; AEB01088.
 XX
 PS Isolated human monoclonal antibody or an antigen-binding portion, which
 XX specifically binds to human interferon gamma inducible protein 10 (IP-
 XX 10), useful for treating viral or bacterial infection, or inflammatory or
 XX autoimmune diseases.
 XX
 PS Claim 35; SEQ ID NO 90; 179pp; English.
 XX
 CC The invention relates to an isolated human monoclonal antibody or an
 CC antigen-binding portion, which specifically binds to human IP-10 and
 CC exhibits at least one property selected from: inhibits binding of IP-10
 CC to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced
 CC cell migration; cross-reacts with rhesus monkey IP-10; does not cross-
 CC react with mouse IP-10; does not cross-react with human MIG; or does not
 CC cross-react with human ITAC. The isolated human monoclonal antibody is
 CC useful for treating an inflammatory or autoimmune disease including
 CC multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease
 CC (e.g., ulcerative colitis, Crohn's disease), systemic lupus
 CC erythematosus, Type I diabetes, inflammatory skin disorders (e.g.,
 CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves'
 CC disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary
 CC inflammation (e.g., asthma, chronic obstructive pulmonary disease,
 CC pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection,
 CC spinal cord injury, brain injury (e.g., stroke), neurodegenerative
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis,
 CC gene therapy-induced inflammation, diseases of angiogenesis, inflammatory
 CC kidney disease (e.g., IgA nephropathy, membranoproliferative

CC psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves' disease, Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary inflammation (e.g., asthma, chronic obstructive pulmonary disease, pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection, spinal cord injury, brain injury (e.g., stroke), neurodegenerative diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis, gene therapy-induced inflammation, diseases of angiogenesis, inflammatory kidney disease (e.g., IGA nephropathy, membranoproliferative glomerulonephritis, rapidly progressive glomerulonephritis), or atherosclerosis. It is also useful for treating a viral or bacterial infection involving unwanted IP-10 activity in a subject, where the viral infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present sequence represents the amino acid sequence of a human IP10 monoclonal antibody light chain variable region.

XX Sequence 108 AA;

Query Match 100.0%; Score 50; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db |||||

89 QQRSNWPP 96

RESULT 32

ADA89232
ID ADA89232 standard; protein; 109 AA.

XX AC ADA89232;

DT 20-NOV-2003 (first entry)

DE Human antibody T3F1 light chain amino acid sequence SEQ ID NO:76.

XX immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW cancer.

XX Synthetic.
OS Homo sapiens.

XX WO2003070752-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005128.

XX 20-FEB-2002; 2002US-0358994P.

XX (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.

XX Hoogenboom HRJM, Reiter Y;

XX WPI; 2003-663847/62.
DR N-PSDB; ADA89231.

XX New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.

PS Disclosure; Fig 18A; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL) domain. The protein binds a complex comprising a major histocompatibility complex (MHC) and a peptide, and does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide in the absence of the MHC. The peptide is a peptide fragment of gp100, MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition

CC comprising the novel protein and a carrier; (2) a cytotoxic T cell comprising one or more nucleic acids for expressing the Ig that binds a complex having an MHC and a peptide, does not substantially bind the MHC in the absence of the bound peptide, and does not substantially bind the peptide in the absence of the MHC; (3) an isolated nucleic acid comprising a first segment that encodes the Ig variable domain; (4) a host cell comprising heterologous nucleic acid sequences that encodes the novel protein; (5) a transgenic animal whose genome includes heterologous nucleic acid sequences that encode the protein; (6) identifying the protein that specifically binds the MHC-peptide complex; (7) expressing an antigen-binding protein; (8) ablating or killing a target cell that displays a peptide on a surface MHC molecule; (9) treating or preventing a cancerous disorder in a subject; and (10) detecting an MHC-peptide complex in a sample. A protein of the invention has cytostatic activity, and can be used in gene therapy. The protein is useful for preparing a composition for treating or preventing a cancerous disorder. The present sequence represents the light chain of an antibody which binds to an MHC-peptide complex where the peptide component in as peptide fragment of TAX.

XX Sequence 109 AA;

Query Match 100.0%; Score 50; DB 6; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8

Db |||||

88 QQRSNWPP 95

RESULT 33

ADA89228
ID ADA89228 standard; protein; 109 AA.

XX AC ADA89228;

DT 20-NOV-2003 (first entry)

DE Human antibody T3E3 light chain amino acid sequence SEQ ID NO:72.

XX immunoglobulin; Ig; heavy chain variable domain;
KW light chain variable domain; major histocompatibility complex; MHC;
KW gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
KW cancer.

XX Synthetic.
OS Homo sapiens.

XX WO2003070752-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005128.

XX 20-FEB-2002; 2002US-0358994P.

XX (DYAX-) DYAX CORP.
PA (TECR) TECHNION RES & DEV FOUND LTD.

XX Hoogenboom HRJM, Reiter Y;

XX WPI; 2003-663847/62.
DR N-PSDB; ADA89227.

XX New protein comprising an immunoglobulin heavy chain variable (VH) domain and an immunoglobulin light chain variable (VL) domain, useful for preparing a composition for treating or preventing a cancerous disorder.
PS Disclosure; Fig 17A; 224pp; English.

XX The present invention describes a protein comprising an immunoglobulin (Ig) heavy chain variable (VH) domain and an Ig light chain variable (VL)

CC domain. The protein binds a complex comprising a major histocompatibility
 CC complex (MHC) and a peptide, does not substantially bind the MHC in the
 CC absence of the bound peptide, and does not substantially bind the peptide
 CC in the absence of the MHC. The peptide is a peptide fragment of gp100,
 CC MUC1, TAX or hTERT. Also described: (1) a pharmaceutical composition
 CC comprising the novel protein and a carrier; (2) a cytotoxic T cell
 CC comprising one or more nucleic acids for expressing the Ig that binds a
 CC complex having an MHC and a peptide, does not substantially bind the MHC
 CC in the absence of the bound peptide, and does not substantially bind the
 CC peptide in the absence of the MHC; (3) an isolated nucleic acid
 CC comprising a first segment that encodes the Ig variable domain; (4) a
 CC host cell comprising heterologous nucleic acid sequences that encodes the
 CC novel protein; (5) a transgenic animal whose genome includes heterologous
 CC nucleic acid sequences that encode the protein; (6) identifying the
 CC protein that specifically binds the MHC-peptide complex; (7) expressing
 CC an antigen-binding protein; (8) ablating or killing a target cell that
 CC displays a peptide on a surface MHC molecule; (9) treating or preventing
 CC a cancerous disorder in a subject; and (10) detecting an MHC-peptide
 CC complex in a sample. A protein of the invention has cytostatic activity,
 CC and can be used in gene therapy. The protein is useful for preparing a
 CC composition for treating or preventing a cancerous disorder. The present
 CC sequence represents the light chain of an antibody which binds to an MHC-
 CC peptide complex where the peptide component in as peptide fragment of
 CC TAX.

Sequence 109 AA;

Query Match 100.0%; Score 50; DB 6; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.64;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 |||||
 Db 88 QQRSNWPP 95

RESULT 34

ADFI1411
 ID ADFI1411 standard; protein; 109 AA.

AC ADFI1411;

DT 12-FEB-2004 (first entry)

DE 15E1 anti-OPGL antibody kappa chain variable region SEQ ID NO:24.

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

OS Homo sapiens.

XX WO2003086289-A2.

PN 23-OCT-2003.

XX 07-APR-2003; 2003WO-US010749.

XX 05-APR-2002; 2002US-0370407P.

PR (AMGE-) AMGEN INC.

XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX WPI; 2003-845253/78.

XX N-PSDB; ADFI1410.

XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.

XX Claim 6; SEQ ID NO 24; 156pp; English.

XX

CC The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.

Sequence 109 AA;

Query Match 100.0%; Score 50; DB 7; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.64;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 |||||
 Db 89 QQRSNWPP 96

RESULT 35

ADFI1395
 ID ADFI1395 standard; protein; 109 AA.

AC ADFI1395;

XX 12-FEB-2004 (first entry)

XX 22B3 anti-OPGL antibody kappa chain variable region SEQ ID NO:8.

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

XX Homo sapiens.

XX WO2003086289-A2.

XX 23-OCT-2003.

XX 07-APR-2003; 2003WO-US010749.

XX 05-APR-2002; 2002US-0370407P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX WPI; 2003-845253/78.

XX N-PSDB; ADFI1394.

XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.

XX Claim 6; SEQ ID NO 8; 156pp; English.

XX The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody

CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 109 AA;

Query Match 100.0%; Score 50; DB 7; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.64;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 Db 89 QQRSNWPP 96
 |||||

RESULT 36

ADX02205
 ID ADX02205 standard; protein; 110 AA.

XX AC ADX02205;

XX DT 21-APR-2005 (first entry)

XX SARS coronavirus antibody light chain SEQ ID NO 461.

XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 XX respiratory disease; infection; antibody; light chain.

XX OS SARS coronavirus.

XX PN WO2005012360-A2.

XX PD 10-FEB-2005.

XX PF 21-JUL-2004; 2004WO-EP051568.

XX PR 22-JUL-2003; 2003WO-EP050328.

XX PR 01-SEP-2003; 2003WO-EP050391.

XX PR 16-OCT-2003; 2003WO-EP050723.

XX PR 24-NOV-2003; 2003WO-EP050883.

XX PR 04-DEC-2003; 2003WO-EP050943.

XX PR 02-FEB-2004; 2004WO-EP050067.

XX PR 13-FEB-2004; 2004WO-EP050127.

XX PR 19-MAR-2004; 2004WO-EP050334.

XX PR 07-APR-2004; 2004WO-EP050464.

XX PR 14-APR-2004; 2004WO-EP050516.

XX PR 29-APR-2004; 2004WO-EP050643.

XX PA (CRUC-) CRUCELL HOLLAND BV.

XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;

XX WPI; 2005-142879/15.

XX DR N-PSDB; ADX02204.

XX New binding molecules that specifically bind to severe acute respiratory
 XX syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 XX treating conditions resulting from SARS-CoV.

XX Disclosure; SEQ ID NO 461; 633pp; English.

XX The invention relates to a binding molecule, or its variant, capable of
 XX specifically binding to a severe acute respiratory syndrome (SARS) -
 XX coronavirus (CoV). The composition (including the binding molecule or its
 XX functional variant, or the immunoconjugate) is useful as a medicament for
 XX the diagnosis, prophylaxis or treatment of a condition resulting from a
 XX SARS-CoV, or in the preparation of the medicament. The present sequence
 XX represents a SARS coronavirus binding molecule light chain.

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 50; DB 9; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.64;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
 Db 89 QQRSNWPP 96
 |||||

RESULT 37

ADX02049
 ID ADX02049 standard; protein; 110 AA.

XX AC ADX02049;

XX DT 21-APR-2005 (first entry)

XX SARS coronavirus antibody light chain SEQ ID NO 305.

XX severe acute respiratory syndrome; diagnosis; Respiratory-Gen.; Virucide;
 XX respiratory disease; infection; antibody; light chain.

XX OS SARS coronavirus.

XX PN WO2005012360-A2.

XX PD 10-FEB-2005.

XX PF 21-JUL-2004; 2004WO-EP051568.

XX PR 22-JUL-2003; 2003WO-EP050328.

XX PR 01-SEP-2003; 2003WO-EP050391.

XX PR 16-OCT-2003; 2003WO-EP050723.

XX PR 24-NOV-2003; 2003WO-EP050883.

XX PR 04-DEC-2003; 2003WO-EP050943.

XX PR 02-FEB-2004; 2004WO-EP050067.

XX PR 13-FEB-2004; 2004WO-EP050127.

XX PR 19-MAR-2004; 2004WO-EP050334.

XX PR 07-APR-2004; 2004WO-EP050464.

XX PR 14-APR-2004; 2004WO-EP050516.

XX PR 29-APR-2004; 2004WO-EP050643.

XX PA (CRUC-) CRUCELL HOLLAND BV.

XX PI Ter Meulen JH, De Kruif CA, Van Den Brink EN, Goudsmit J;

XX WPI; 2005-142879/15.

XX DR N-PSDB; ADX02048.

XX New binding molecules that specifically bind to severe acute respiratory
 XX syndrome (SARS)-coronavirus (CoV), useful for diagnosing, preventing or
 XX treating conditions resulting from SARS-CoV.

XX Disclosure; SEQ ID NO 305; 633pp; English.

XX The invention relates to a binding molecule, or its variant, capable of
 XX specifically binding to a severe acute respiratory syndrome (SARS) -
 XX coronavirus (CoV). The composition (including the binding molecule or its
 XX functional variant, or the immunoconjugate) is useful as a medicament for
 XX the diagnosis, prophylaxis or treatment of a condition resulting from a
 XX SARS-CoV, or in the preparation of the medicament. The present sequence
 XX represents a SARS coronavirus binding molecule light chain.

Qy 1 QQRSNWPP 8

```

Db          89 QQRSNWPP 96
|||||
RESULT 38
ADJ73528
ID ADJ73528 standard; protein; 128 AA.
XX
XX ADJ73528;
XX
XX 06-MAY-2004 (first entry)
XX
XX Erythropoietin light chain mimetibody SeqID 984.
XX
XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW erythropoietin.
XX
XX Synthetic.
XX
XX WO2003084477-A2.
XX
XX 16-OCT-2003.
XX
XX 24-MAR-2003; 2003WO-US009139.
XX
XX 29-MAR-2002; 2002US-0368791P.
XX
XX (CENZ ) CENTOCOR INC.
XX
XX Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
XX
XX WPI; 2003-804237/75.
XX
XX New CDR mimetibody comprising a portion of a heavy or light chain
XX variable region comprising human framework or ligand binding region,
XX useful for preparing a composition for treating e.g., immune,
XX cardiovascular or neurologic disease.
XX
XX Example 2; SEQ ID NO 984; 97pp; English.
XX
XX This invention relates to novel mammalian CDR mimetibodies, specific
XX portions or variants thereof. Specifically, it refers to an antibody
XX fragment where a protein has been inserted into, or replaces a portion
XX of, one or more CDR regions, such that each CDR mimetibody comprises at
XX least one portion of a heavy chain or light chain variable region, which
XX itself comprises at least one human framework region and at least one
XX ligand binding region (fBR). The present invention describes human
XX mimetibodies, including modified immunoglobulins and cleavage products
XX that can be useful in gene therapy and the generation of transgenic
XX plants and animals. Furthermore, the CDR mimetibody is useful for
XX preparing compositions for modulating, treating or reducing the symptoms
XX of immune, cardiovascular, infectious, malignant and/or neurologic
XX diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
XX cardiant, antimicrobial, cytostatic and neuroprotective activities. This
XX polypeptide sequence is an erythropoietin light chain mimetibody of the
XX invention.
XX
XX Sequence 128 AA;
Query Match 100.0%; Score 50; DB 7; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQRSNWPP 8
|||||
Db 109 QQRSNWPP 116
|||||
RESULT 39
ADM41547
ID ADM41547 standard; protein; 128 AA.
XX
XX ADM41547;
XX
XX 03-JUN-2004 (first entry)
XX
XX Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.
XX
XX Human; monoclonal antibody; antibody; interleukin-1; receptor;
XX antiathmatic; antiinflammatory; dermatological; antiallergic;
XX protozoacide; antirheumatic; antiarthritic; osteopathic; vasotropic;
XX analgesic; antidiabetic; nephrotropic; antianaemic; nootropic;
XX anticonvulsant; dermatological; antiparkinsonian; antidiabetic;
XX cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004022718-A2.
XX
XX 18-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027978.
XX
XX 06-SEP-2002; 2002US-0408719P.
XX
XX (AMGE-) AMGEN INC.
XX
XX Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
XX Elliott G;
XX
XX WPI; 2004-248462/23.
XX
XX N-PSDB; ADM41546.
XX
XX Isolated human antibody that specifically binds interleukin-1 receptor
XX type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
XX rheumatoid arthritis, osteoarthritis and inflammatory conditions.
XX
XX Claim 2; SEQ ID NO 12; 179pp; English.
XX
XX The present sequence is that of human anti-interleukin-1 receptor type 1
XX (IL-1R1) monoclonal antibody (Mab) 26F5 kappa chain variable region.
XX Human Mabs to IL-1R1 were prepared using the HCo7 strain of transgenic
XX mice, which expresses human antibody genes. These mice were immunised
XX with purified recombinant IL-1R1, and splenocytes from immunised mice
XX were fused to a mouse myeloma cell line to generate hybridomas.
XX Hybridomas which secreted a Mab that bound with high avidity to IL-1R1
XX were selected. The Mabs inhibit IL-1 signalling by competing with IL-
XX 1beta and IL-1alpha binding to IL-1R. These Mabs, as well as single chain
XX antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies
XX and (Fab')2 antibodies derived from them, are used in methods of treating
XX IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.
XX IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral
XX sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,
XX atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
XX Clostridium associated illnesses, coronary conditions, cancer including
XX leukaemia and tumour metastasis, diabetes, endometriosis, fever,
XX fibromyalgia, glomerulonephritis, graft versus host disease,
XX osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
XX ischaemia, Kawasaki's disease, learning impairment, lung diseases,
XX multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
XX periodontal disease, pre-term labour, psoriasis, reperfusion injury,
XX septic shock, side effects of radiation therapy, temporal mandibular
XX joint disease, sleep disturbance, uveitis, or an inflammatory condition
XX resulting from strain, sprain, cartilage damage, trauma, orthopaedic
XX surgery, infection or other disease processes.
XX
XX Sequence 128 AA;
Query Match 100.0%; Score 50; DB 8; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QQRSNWPP 8
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Db      109 QQRSNWPP 116
RESULT 40
ID      AAM51174
XX      AAM51174 standard; protein; 129 AA.
AC      AAM51174;
XX      AAM51174;
DT      10-JUN-2002 (first entry)
XX      Human recombinant mAb TNV14, TNV15 light chain variable region.
XX
XX      Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
KW      complementarity determining region; antirheumatic; antiarthritic;
KW      antitumor; antitasthmatic; antiallergic; antiinflammatory; antisickling;
KW      antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW      antidyslipidemic; antidiabetic; antitubercular; virucide; fungicide; antileptotic;
KW      protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW      human; diagnosis; therapy; TNV14; TNV15; monoclonal antibody; mAb.
XX
OS      Homo sapiens.
XX
XX      Key Location/Qualifiers
FH      Peptide 1..20
FT      /label= Signal_peptide
FT      Protein 20..129
FT      /label= Mature_protein
FT      Region 21..43
FT      /label= FR1
FT      Region 44..54
FT      /label= CDR1
FT      Region 55..69
FT      /label= FR2
FT      Region 70..76
FT      /label= CDR2
FT      Region 77..108
FT      /label= FR3
FT      Region 109..118
FT      /label= CDR3
FT      Region 119..129
FT      /label= J3
XX
XX      W0200212502-A2.
XX
XX      14-FEB-2002.
XX
XX      07-AUG-2001; 2001WO-US024785.
XX
XX      07-AUG-2000; 2000US-0223360P.
XX
XX      29-SEP-2000; 2000US-0236826P.
XX
XX      01-AUG-2001; 2001US-00920137.
XX
XX      (CENZ ) CENTOCOR INC.
XX
XX      Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
XX
XX      WPI; 2002-217194/27.
XX
XX      N-PSDB; ABL53514.
XX
XX      Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
XX      treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
XX      angina pectoris, myocardial infarction, leprosy.
XX
XX      Example 3; Fig 5; 131pp; English.
XX
XX      The present sequence is that of the light chain variable region of anti-
XX      tumour necrosis factor (TNF) human recombinant monoclonal antibodies
XX      (mAbs) TNV14 and TNV15. These are human mAbs produced from a GenIV
XX      fusion using spleen cells from a hybrid mouse containing human variable
XX      and constant region antibody transgenes that was immunised with human TNF
XX      alpha. The human mAbs bind immobilised human TNF alpha with high avidity
XX      and have a totally human IgG1, kappa isotype. The mature portion of the

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CC      light chain variable region is identical to that of the Vg/38-type light
CC      chain germline sequence (see AAM51173). The light chain variable regions
CC      of 2 other human mAbs (see AAM51175) show a single amino acid difference.
CC      The invention provides human, primate, mammalian, rodent, chimeric, anti-
CC      TNF antibodies, immunoglobulins, cleavage products and other specified
CC      portions and variants, as well as anti-TNF antibody compositions,
CC      encoding or complementary nucleic acids, vectors, host cells,
CC      compositions, formulations, devices, transgenic animals, transgenic
CC      plants, and methods of making and using them. The anti-TNF antibody
CC      comprises at least a portion of an immunoglobulin molecule, especially
CC      the heavy chain and/or light chain variable regions given in the present
CC      sequence and in AAM51165, or either all of the CDRs of the heavy chain
CC      (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC      63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC      inhibit TNF binding to receptor, or provide Arthritic index improvement
CC      in a mouse model. They are useful for diagnosing or treating a TNF
CC      related condition in a cell, tissue, organ or animal (claimed) such as
CC      rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC      pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC      as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC      myocardial infarction, an infectious disease in a cell such as bacterial,
CC      viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC      disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC      lymphoma and multiple myeloma, or a neurological disease such as multiple
CC      sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC      Creutzfeldt-Jakob disease
XX
XX      Sequence 129 AA;

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Query Match      100.0%; Score 50; DB 5; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 QQRSNWPP 8
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Db      109 QQRSNWPP 116

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Search completed: December 14, 2005, 07:25:30
Job time : 46.5172 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:38 : Search time 11.7241 Seconds
(without alignments)
56.414 Million cell updates/sec

Title: US-10-720-323-6

Perfect score: 50

Sequence: 1 QQRNWP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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- 2: /cgm2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgm2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgm2_6/ptodata/1/iaa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	224	2	US-09-456-090A-46
2	50	100.0	224	2	US-09-453-234-46
3	45	90.0	107	2	US-09-438-954-40
4	43	86.0	95	2	US-10-194-975-86
5	43	86.0	107	2	US-09-434-870-2
6	43	86.0	115	1	US-08-053-131-179
7	43	86.0	115	1	US-08-096-762-179
8	43	86.0	115	2	US-09-042-353-42
9	43	86.0	115	2	US-08-758-417A-307
10	43	86.0	224	2	US-09-456-090A-36
11	43	86.0	224	2	US-09-453-234-36
12	40	80.0	107	1	US-07-634-278-34
13	40	80.0	107	1	US-08-477-728-34
14	40	80.0	107	1	US-08-474-040-34
15	40	80.0	107	1	US-08-487-200-34
16	40	80.0	107	2	US-08-484-537-34
17	40	80.0	117	2	US-09-203-768A-4
18	40	80.0	224	2	US-09-456-090A-82
19	40	80.0	224	2	US-09-456-090A-84
20	40	80.0	224	2	US-09-456-090A-88
21	40	80.0	224	2	US-09-456-090A-90
22	40	80.0	224	2	US-09-453-234-82
23	40	80.0	224	2	US-09-453-234-84
24	40	80.0	224	2	US-09-453-234-88
25	40	80.0	224	2	US-09-453-234-90
26	39	78.0	96	1	US-08-276-852-113
27	39	78.0	96	1	US-08-899-575-113

28	39	78.0	96	1	US-08-899-575-113	Sequence 113, App
29	39	78.0	96	4	PCT-US95-08743-113	Sequence 113, App
30	38	76.0	100	2	US-09-899-896-2	Sequence 2, Appli
31	38	76.0	738	2	US-09-712-363-238	Sequence 238, App
32	38	76.0	3174	1	US-08-477-451-3	Sequence 3, Appli
33	37	74.0	234	2	US-09-848-832-4	Sequence 4, Appli
34	37	74.0	467	2	US-09-252-991A-18296	Sequence 18296, A
35	36	72.0	95	2	US-10-194-975-87	Sequence 87, Appl
36	36	72.0	108	2	US-09-726-219A-240	Sequence 240, App
37	36	72.0	108	2	US-09-196-522-240	Sequence 240, App
38	36	72.0	110	1	US-08-828-009-2	Sequence 2, Appli
39	36	72.0	115	1	US-08-053-131-181	Sequence 181, App
40	36	72.0	115	1	US-08-096-762-181	Sequence 181, App
41	36	72.0	115	2	US-08-042-353-44	Sequence 44, Appl
42	36	72.0	115	2	US-08-758-417A-309	Sequence 309, App
43	36	72.0	139	2	US-09-832-129-53	Sequence 53, Appl
44	36	72.0	160	2	US-09-252-991A-21803	Sequence 21803, A
45	36	72.0	188	2	US-09-252-991A-28878	Sequence 28878, A
46	36	72.0	261	2	US-09-949-016-9885	Sequence 9885, Ap
47	36	72.0	439	2	US-08-252-991A-17127	Sequence 17127, A
48	35	70.0	9	2	US-09-798-689-36	Sequence 36, Appl
49	35	70.0	106	2	US-09-513-999C-7939	Sequence 7939, Ap
50	35	70.0	135	2	US-09-252-991A-16677	Sequence 16677, A
51	35	70.0	139	2	US-09-252-991A-22432	Sequence 22432, A
52	35	70.0	145	2	US-09-732-210-411	Sequence 411, App
53	35	70.0	147	2	US-09-252-991A-19420	Sequence 19420, A
54	35	70.0	169	2	US-09-252-991A-31389	Sequence 31389, A
55	35	70.0	205	2	US-09-252-991A-17234	Sequence 17234, A
56	35	70.0	234	2	US-08-311-731A-60	Sequence 60, Appl
57	35	70.0	247	2	US-09-252-991A-26736	Sequence 26736, A
58	35	70.0	294	2	US-09-355-160D-8	Sequence 8, Appli
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60	35	70.0	299	2	US-09-149-476-396	Sequence 396, App
61	35	70.0	338	1	US-09-004-502-5	Sequence 5, Appli
62	35	70.0	338	2	US-09-360-125-5	Sequence 5, Appli
63	35	70.0	376	2	US-09-270-767-42071	Sequence 42071, A
64	35	70.0	424	2	US-09-149-476-555	Sequence 555, App
65	35	70.0	568	2	US-09-248-796A-22993	Sequence 22993, A
66	35	70.0	635	2	US-09-252-991A-23203	Sequence 23203, A
67	35	70.0	633	2	US-09-252-991A-23497	Sequence 23497, A
68	35	70.0	1658	1	US-08-609-049A-13	Sequence 13, Appl
69	35	70.0	1658	2	US-09-170-996-13	Sequence 13, Appl
70	35	70.0	1686	2	US-09-355-160D-2	Sequence 2, Appli
71	35	70.0	1686	2	US-10-092-219-2	Sequence 2, Appli
72	35	70.0	1726	1	US-08-609-049A-30	Sequence 30, Appl
73	35	70.0	1726	2	US-09-170-996-30	Sequence 30, Appl
74	34	68.0	141	2	US-09-252-991A-20019	Sequence 20019, A
75	34	68.0	169	2	US-09-252-991A-28109	Sequence 28109, A
76	34	68.0	209	2	US-09-252-991A-18317	Sequence 18317, A
77	34	68.0	268	2	US-09-252-991A-23249	Sequence 23249, A
78	34	68.0	282	2	US-09-252-991A-29124	Sequence 29124, A
79	34	68.0	329	1	US-09-004-502-3	Sequence 3, Appli
80	34	68.0	329	2	US-09-360-125-3	Sequence 3, Appli
81	34	68.0	329	2	US-10-146-710-2	Sequence 2, Appli
82	34	68.0	347	1	US-09-004-502-1	Sequence 1, Appli
83	34	68.0	347	2	US-09-360-125-1	Sequence 1, Appli
84	34	68.0	399	2	US-09-252-991A-21957	Sequence 21957, A
85	34	68.0	400	2	US-09-252-991A-18589	Sequence 18589, A
86	34	68.0	544	2	US-08-591-685-9	Sequence 9, Appli
87	33	66.0	81	2	US-09-252-991A-17044	Sequence 17044, A
88	33	66.0	93	2	US-10-330-613A-68	Sequence 68, Appl
89	33	66.0	93	2	US-10-330-613A-76	Sequence 76, Appl
90	33	66.0	95	2	US-10-194-975-84	Sequence 84, Appl
91	33	66.0	95	2	US-10-194-975-85	Sequence 85, Appl
92	33	66.0	95	2	US-10-330-613A-75	Sequence 75, Appl
93	33	66.0	95	2	US-10-330-613A-79	Sequence 79, Appl
94	33	66.0	95	2	US-10-330-613A-82	Sequence 82, Appl
95	33	66.0	105	2	US-10-330-613A-80	Sequence 80, Appl
96	33	66.0	107	2	US-10-330-613A-6	Sequence 6, Appli
97	33	66.0	107	2	US-10-330-613A-34	Sequence 34, Appl
98	33	66.0	107	2	US-10-330-613A-67	Sequence 67, Appl
99	33	66.0	116	2	US-08-311-731A-330	Sequence 330, App
100	33	66.0	139	2	US-09-472-087-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-456-090A-46

Query Match 100.0%; Score 50; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 89 QQRSNWPP 96

RESULT 2

US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match 100.0%; Score 50; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 89 QQRSNWPP 96

RESULT 3

US-09-438-954-40

; Sequence 40, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-YuIl
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of human antibody (X82934)
US-09-438-954-40

Query Match 90.0%; Score 45; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QQRSNWPP 8
Db 89 QQRSNWPP 95

RESULT 4

US-10-194-975-86
; Sequence 86, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-86

Query Match 86.0%; Score 43; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 7
Db 89 QQRSNWPP 95

RESULT 5

US-09-434-870-2
; Sequence 2, Application US/09434870
; Patent No. 6849425
; GENERAL INFORMATION:
; APPLICANT: Huse, William
; APPLICANT: Watkins, Jeffry
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-06352
; CURRENT APPLICATION NUMBER: US/09/434,870

;; CURRENT FILING DATE: 2001-08-20
;; PRIOR APPLICATION NUMBER: 60/159,689
;; PRIOR FILING DATE: 1999-10-14
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-434-870-2

Query Match 86.0%; Score 43; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 89 QORSNWP 95

RESULT 6
US-08-053-131-179
; Sequence 179, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992

PRIOR APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-053-131-179

Query Match 86.0%; Score 43; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 109 QORSNWP 115

RESULT 7
US-08-096-762-179
; Sequence 179, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993

PRIOR APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-096-762-179

Query Match 86.0%; Score 43; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 109 QORSNWP 115

RESULT 8
US-09-042-353-42

; Sequence 42, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-042-353-42

Query Match 86.0%; Score 43; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
Db 109 QQRSNWP 115

RESULT 9
US-08-758-417A-307
; Sequence 307, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303

; REFERENCE/DOCKET NUMBER: 014643-0090300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 307:
US-08-758-417A-307

Query Match 86.0%; Score 43; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSNWP 7
Db 109 QORSNWP 115

RESULT 10

US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M1-1L
US-09-456-090A-36

Query Match 86.0%; Score 43; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSNWP 7
Db 89 QORSNWP 95

RESULT 11

US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 36
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-453-234-36

Query Match 86.0%; Score 43; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QORSNWP 7
Db 89 QORSNWP 95

RESULT 12

US-07-634-278-34
; Sequence 34, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..107
; OTHER INFORMATION: /note= "Amino acid sequence of the
; OTHER INFORMATION: light chain for humane Lay antibody."

US-07-634-278-34

Query Match 80.0%; Score 40; DB 1; Length 107;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 ||:||||
 Db 89 QQYNNWPP 96

RESULT 13

US-08-477-728-34
 ; Sequence 34, Application US/08477728
 ; Patent No. 5585089
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,728
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..107
 ; OTHER INFORMATION: /note= "Amino acid sequence of the
 ; light chain for humane Lay antibody."
 ; US-08-477-728-34

Query Match 80.0%; Score 40; DB 1; Length 107;
 Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 0; Gaps 0;

QY 1 QQRSNWPP 8
 ||:||||
 Db 89 QQYNNWPP 96

RESULT 14

US-08-474-040-34
 ; Sequence 34, Application US/08474040
 ; Patent No. 5693761
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELING, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/474,040
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..107
 ; OTHER INFORMATION: /note= "Amino acid sequence of the
 ; light chain for humane Lay antibody."
 ; US-08-474-040-34

Query Match 80.0%; Score 40; DB 1; Length 107;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QQRSNWPP 8
 Db 89 QQYNNWPP 96

RESULT 15
 US-08-487-200-34
 ; Sequence 34, Application US/08487200
 ; Patent No. 5693762
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,200
 ; FILING DATE: 7-JUN-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/634,278
 ; FILING DATE: 19-DEC-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002610
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..107
 ; OTHER INFORMATION: /note= "Amino acid sequence of the
 ; OTHER INFORMATION: light chain for humane Lay antibody."
 US-08-487-200-34

Query Match 80.0%; Score 40; DB 1; Length 107;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQRSNWPP 8
 Db 89 QQYNNWPP 96

Db 89 QQYNNWPP 96

RESULT 16
 US-08-484-537-34
 ; Sequence 34, Application US/08484537
 ; Patent No. 6180370
 ; GENERAL INFORMATION:
 ; APPLICANT: QUEEN, Cary L.
 ; APPLICANT: CO, Man Sung
 ; APPLICANT: SCHNEIDER, William P.
 ; APPLICANT: LANDOLFI, Nicholas F.
 ; APPLICANT: COELINGH, Kathleen L.
 ; APPLICANT: SELICK, Harold E.
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 113
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,537
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/634,278
 ; FILING DATE: 19-DEC-1990
 ; APPLICATION NUMBER: US 07/590,274
 ; FILING DATE: 28-SEP-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/310,252
 ; FILING DATE: 13-FEB-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/290,975
 ; FILING DATE: 28-DEC-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William M
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 11823-002600
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..107
 ; OTHER INFORMATION: /note= "Amino acid sequence of the
 ; OTHER INFORMATION: light chain for humane Lay antibody."
 US-08-484-537-34

Query Match 80.0%; Score 40; DB 2; Length 107;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQRSNWPP 8
 Db 89 QQYNNWPP 96

```
RESULT 17
US-09-203-768A-4
; Sequence 4, Application US/09203768A
; Patent No. 6787638
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Watkins, Jeffery D.
; TITLE OF INVENTION: Tumor Specific Human Monoclonal Antibodies and Methods
; TITLE OF INVENTION: of Use
; FILE REFERENCE: P-IX 2947
; CURRENT APPLICATION NUMBER: US/09/203,768A
; CURRENT FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-768A-4

Query Match      80.0%; Score 40; DB 2; Length 117;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      97 QQYNNWPP 104
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RESULT 18
US-09-456-090A-82
; Sequence 82, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 7
Db      89 QORTNWP 95
      ||:||||

RESULT 19
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-84

Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 7
Db      89 QORTNWP 95
      ||:||||

RESULT 20
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 7
Db      89 QORNWNP 95
      ||:||||

RESULT 21
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90
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Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 89 QORTNWP 95

RESULT 22
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; CURRENT APPLICATION NUMBER: US/09/453,234
; FILE REFERENCE: 020015-000110US
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 89 QORTNWP 95

RESULT 23
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84

Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 89 QORTNWP 95

RESULT 24
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88

Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 89 QORTNWP 95

RESULT 25
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match      80.0%; Score 40; DB 2; Length 224;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
Db 89 QORTNWP 95

```

```
Db      89 QORTNWP 95

RESULT 26
US-08-276-852-113
; Sequence 113, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,852
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,302
; FILING DATE: 30-SEP-1993
; NAME: Fitting, Thomas
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCR1452P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-852-113

Query Match      78.0%; Score 39; DB 1; Length 96;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      76 QOYDNWPP 83

RESULT 27
US-08-899-575-113
; Sequence 113, Application US/08899575
; Patent No. 5770440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

Query Match      78.0%; Score 39; DB 1; Length 96;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      76 QOYDNWPP 83

RESULT 28
US-08-899-575-113
; Sequence 113, Application US/08899575
; Patent No. 5804440
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-899-575-113

Query Match 78.0%; Score 39; DB 1; Length 96;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
||| ||||
Db 76 QQYDNWPP 83

RESULT 29
PCT-US95-08743-113
Sequence 113, Application PC/TUS9508743
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08743-113

Query Match 78.0%; Score 39; DB 4; Length 96;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
||| ||||
Db 76 QQYDNWPP 83

RESULT 30
US-09-899-896-2
Sequence 2, Application US/09899896
Patent No. 6569431
GENERAL INFORMATION:
APPLICANT: von Bdingen, Hans-Christian
APPLICANT: Genain, Claude P.
APPLICANT: Hauser, Stephen L.
TITLE OF INVENTION: Recombinant Antibody Fragments as Autoantibody
TITLE OF INVENTION: Antagonists
FILE REFERENCE: SF01-025-2
CURRENT APPLICATION NUMBER: US/09/899,896
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/691,654
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 100
TYPE: PRT
ORGANISM: human
US-09-899-896-2

Query Match 76.0%; Score 38; DB 2; Length 100;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
||| ||||
Db 89 QQYSSWPP 96

RESULT 31
US-09-712-363-238
Sequence 238, Application US/09712363
Patent No. 8892139
GENERAL INFORMATION:
APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 238
LENGTH: 738
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-712-363-238

Query Match 76.0%; Score 38; DB 2; Length 738;


```

RESULT 36
US-09-726-219A-240
; Sequence 240, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-240

Query Match          72.0%; Score 36; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
      ||||:|
Db      88 QQRSSYP 95

RESULT 37
US-09-196-522-240
; Sequence 240, Application US/09196522
; Patent No. 6916605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC DISORDERS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

```

```

; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-240

Query Match          72.0%; Score 36; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
      ||||:|
Db      88 QQRSSYP 95

RESULT 38
US-08-828-009-2
; Sequence 2, Application US/08828009
; Patent No. 5914394
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Friemer, Nelson, B.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC DISORDERS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,009
; FILING DATE: 27-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-828-009-2

Query Match 72.0%; Score 36; DB 1; Length 110;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
   |::|||
Db 10 QRESHWPP 17

RESULT 39
US-08-053-131-181
; Sequence 181, Application US/08053131
; Patent No. 5661016
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
; PRODUCE Heterologous Antibodies
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,131
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
```

```
; REFERENCE/DOCKET NUMBER: 14643-9-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-053-131-181

Query Match 72.0%; Score 36; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNW 6
   |||||
Db 109 QQRSNW 114

RESULT 40
US-08-096-762-181
; Sequence 181, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; PRODUCE Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-096-762-181

Query Match 72.0%; Score 36; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNW 6
| | | | |
Db 109 QQRSNW 114

Search completed: December 14, 2005, 07:33:23
Job time : 12.7241 secs

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:54 ; Search time 36.6897 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-720-323-6

Perfect score: 50

Sequence: 1 QQRSNWPP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	8	3	US-09-920-267C-6
2	50	100.0	8	4	US-10-720-323-6
3	50	100.0	10	4	US-10-173-551-12
4	50	100.0	10	4	US-10-173-551-22
5	50	100.0	10	4	US-10-656-769-74
6	50	100.0	10	4	US-10-394-471B-14
7	50	100.0	10	5	US-10-954-900A-6
8	50	100.0	10	6	US-11-009-731-74
9	50	100.0	10	6	US-11-009-731-79
10	50	100.0	10	6	US-11-102-403-50
11	50	100.0	11	4	US-10-396-578-19
12	50	100.0	11	6	US-11-074-803-19
13	50	100.0	102	5	US-10-916-840-38
14	50	100.0	107	4	US-10-251-085B-142
15	50	100.0	107	4	US-10-737-252-142
16	50	100.0	108	3	US-09-920-267C-8
17	50	100.0	108	4	US-10-305-347A-8
18	50	100.0	108	4	US-10-173-551-9
19	50	100.0	108	4	US-10-173-551-19
20	50	100.0	108	4	US-10-720-323-8
21	50	100.0	108	5	US-10-954-900A-8
22	50	100.0	108	6	US-11-009-731-85
23	50	100.0	108	6	US-11-009-731-90
24	50	100.0	108	6	US-11-021-715-101
25	50	100.0	108	6	US-11-102-403-9
26	50	100.0	108	6	US-11-102-403-11
27	50	100.0	109	4	US-10-371-942-72
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					Sequence 6, Appli
					Sequence 12, Appl
					Sequence 22, Appl
					Sequence 74, Appl
					Sequence 14, Appl
					Sequence 6, Appli
					Sequence 74, Appl
					Sequence 79, Appl
					Sequence 59, Appl
					Sequence 19, Appl
					Sequence 19, Appl
					Sequence 38, Appl
					Sequence 142, App
					Sequence 142, App
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 9, Appli
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 85, Appl
					Sequence 90, Appl
					Sequence 101, App
					Sequence 9, Appli
					Sequence 11, Appl
					Sequence 72, Appl
					Sequence 76, Appl
					Sequence 24, Appl
					Sequence 12, Appl
					Sequence 16, Appl
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					Sequence 4914, A
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					Sequence 24, Appl
					Sequence 114, App
					Sequence 12, Appl
					Sequence 8, Appli
					Sequence 130, App
					Sequence 57, Appl
					Sequence 85, Appl
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					Sequence 93, Appl
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					Sequence 33, Appl
					Sequence 86, Appl
					Sequence 33, Appl
					Sequence 33, Appl
					Sequence 93, Appl
					Sequence 96, Appl
					Sequence 30, Appl
					Sequence 46, Appl
					Sequence 99, Appl
					Sequence 69, Appl
					Sequence 71, Appl
					Sequence 2, Appli
					Sequence 8, Appli
					Sequence 141, App
					Sequence 2, Appli
					Sequence 14, Appl
					Sequence 21, Appl
					Sequence 91, Appl
					Sequence 65, Appl
					Sequence 14, Appl
					Sequence 18, Appl
					Sequence 98, Appl
					Sequence 3, Appli
					Sequence 2, Appli
					Sequence 4, Appli
					Sequence 94, Appl
					Sequence 21, Appl
					Sequence 21, Appl
					Sequence 16, Appl
					Sequence 110, App
					Sequence 4, Appli
					Sequence 8, Appli
					Sequence 57, Appl
					Sequence 31, Appl
					Sequence 19, Appl
					Sequence 25, Appl
					Sequence 55, Appl

ALIGNMENTS

```
RESULT 1
US-09-920-267C-6
; Sequence 6, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920.267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-6

Query Match      100.0%; Score 50; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 QQRSNWPP 8
      |||||
Db      1 QQRSNWPP 8

RESULT 2
US-10-720-323-6
; Sequence 6, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720.323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-6

Query Match      100.0%; Score 50; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 QQRSNWPP 8
      |||||
Db      1 QQRSNWPP 8

RESULT 3
US-10-173-551-12
; Sequence 12, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-12

Query Match      100.0%; Score 50; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 QQRSNWPP 8
      |||||
Db      1 QQRSNWPP 8

RESULT 4
US-10-173-551-22
; Sequence 22, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-551-22

Query Match      100.0%; Score 50; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 QQRSNWPP 8
      |||||
Db      1 QQRSNWPP 8

RESULT 5
US-10-656-769-74
; Sequence 74, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-74
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Query Match 100.0%; Score 50; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
Db 1 QORSNWPP 8

RESULT 6
US-10-394-471B-14
; Sequence 14, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, JILL; CARTON, JILL; SCALLON, BERNARD J.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-14

Query Match 100.0%; Score 50; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
Db 1 QORSNWPP 8

RESULT 7
US-10-954-900A-6
; Sequence 6, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, JILL
; APPLICANT: DAVID SHEALY
; APPLICANT: DAVID KNIGHT
; APPLICANT: BERNIE SCALLON
; APPLICANT: GEORGE HEAVNER
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-6

Query Match 100.0%; Score 50; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
Db 1 QORSNWPP 8

Db 1 QORSNWPP 8

RESULT 8
US-11-009-731-74
; Sequence 74, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, SHIRKANT
; APPLICANT: HUANG, HAICHUN
; APPLICANT: SRINIVASAN, MOHAN
; APPLICANT: CARDARELLI, JOSEPHINE M.
; APPLICANT: WANG, CHANGYU
; APPLICANT: PASSMORE, DAVID
; APPLICANT: RANGAN, VANGIPURAM
; APPLICANT: LANE, THOMAS E.
; APPLICANT: KEIRSTEAD, HANS S.
; APPLICANT: LIU, MICHAEL T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-74

Query Match 100.0%; Score 50; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
Db 1 QORSNWPP 8

RESULT 9
US-11-009-731-79
; Sequence 79, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, SHIRKANT
; APPLICANT: HUANG, HAICHUN
; APPLICANT: SRINIVASAN, MOHAN
; APPLICANT: CARDARELLI, JOSEPHINE M.
; APPLICANT: WANG, CHANGYU
; APPLICANT: PASSMORE, DAVID
; APPLICANT: RANGAN, VANGIPURAM
; APPLICANT: LANE, THOMAS E.
; APPLICANT: KEIRSTEAD, HANS S.
; APPLICANT: LIU, MICHAEL T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-79

Query Match 100.0%; Score 50; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QQRSNWPP 8
Db 1 QQRSNWPP 8

RESULT 10
US-11-102-403-50
; Sequence 50, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PAREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STERNER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STREIN, PAMELA
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUUT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 50
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-50

Query Match 100.0%; Score 50; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 1 QQRSNWPP 8

RESULT 11
US-10-396-578-19
; Sequence 19, Application US/10396578
; Publication No. US2004019260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Taxil-19 complex.
US-10-396-578-19

Query Match 100.0%; Score 50; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.27;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 1 QQRSNWPP 8

RESULT 12
US-11-074-803-19
; Sequence 19, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Taxil-19 complex.
US-11-074-803-19

Query Match 100.0%; Score 50; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 1 QQRSNWPP 8

RESULT 13
US-10-916-840-38
; Sequence 38, Application US/10916840
; Publication No. US20050136053A1
; GENERAL INFORMATION:
; APPLICANT: Hufton, Simon E.
; APPLICANT: Hoet, Rene
; APPLICANT: Pieters, Henk
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Rookey, Kristen
; TITLE OF INVENTION: TIE1-BINDING LIGANDS
; FILE REFERENCE: 10280-083001
; CURRENT APPLICATION NUMBER: US/10/916,840
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/494,713
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-916-840-38

Query Match 100.0%; Score 50; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 90 QQRSNWPP 97
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; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-8

Query Match      100.0%; Score 50; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      89 QORSNWPP 96

RESULT 17
US-10-305-347A-8
; Sequence 8, Application US/10305347A
; Publication No. US20030143603A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Bernie Scallon
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5005
; CURRENT APPLICATION NUMBER: US/10/305,347A
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.0
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-347A-8

Query Match      100.0%; Score 50; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      89 QORSNWPP 96

RESULT 18
US-10-173-551-9
; Sequence 9, Application US/10173551
; Publication No. US2003023287A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafin
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855.2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
US-10-173-551-9

; Sequence 142, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Matuyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-142

Query Match      100.0%; Score 50; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      89 QORSNWPP 96

RESULT 15
US-10-737-252-142
; Sequence 142, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Matuyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-737-252-142

Query Match      100.0%; Score 50; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      89 QORSNWPP 96

RESULT 16
US-09-920-267C-8
; Sequence 8, Application US/09920267C
```

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDR1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)...(56)
; OTHER INFORMATION: CDR2
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)...(98)
; OTHER INFORMATION: CDR3
US-10-173-551-9

Query Match      100.0%; Score 50; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      89 QQRSNWPP 96

RESULT 19
US-10-173-551-19
; Sequence 19, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafon
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1855-2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDR1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)...(56)
; OTHER INFORMATION: CDR2
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)...(98)
; OTHER INFORMATION: CDR3
US-10-173-551-19

Query Match      100.0%; Score 50; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      89 QQRSNWPP 96

RESULT 20
US-10-720-323-8
; Sequence 8, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian

; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 C1PNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-8

Query Match      100.0%; Score 50; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      89 QQRSNWPP 96

RESULT 21
US-10-954-900A-8
; Sequence 8, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallion
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 Div-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-8

Query Match      100.0%; Score 50; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      89 QQRSNWPP 96

RESULT 22
US-11-009-731-85
; Sequence 85, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkan
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
```

; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; PRIOR FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-85

Query Match 100.0%; Score 50; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 89 QQRSNWPP 96

RESULT 23
US-11-009-731-90
; Sequence 90, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkan
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-90

Query Match 100.0%; Score 50; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 89 QQRSNWPP 96

RESULT 24
US-11-021-715-101
; Sequence 101, Application US/11021715
; Publication No. US20050208596A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: 053893-5050
; CURRENT APPLICATION NUMBER: US/11/021,715

; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: PCT/US03/21304
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,352
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-715-101

Query Match 100.0%; Score 50; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 89 QQRSNWPP 96

RESULT 25
US-11-102-403-9
; Sequence 9, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PARREN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102,403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-403-9

Query Match 100.0%; Score 50; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 89 QQRSNWPP 96

RESULT 26
US-11-102-403-11
; Sequence 11, Application US/11102403
; Publication No. US20050226876A1
; GENERAL INFORMATION:
; APPLICANT: GRAUS, YVO
; APPLICANT: HIMBER, JACQUES
; APPLICANT: JANSEN-MOLENAAR, MIRANDA

```
; APPLICANT: KLING, DOROTHEE
; APPLICANT: KOPETZKI, ERHARD
; APPLICANT: PARRIN, PAUL
; APPLICANT: REBERS, FRANK
; APPLICANT: STEINER, BEAT
; APPLICANT: STERN, ANNE
; APPLICANT: STREIN, PAMELA
; APPLICANT: STUBENRAUCH, KAY-GUNNAR
; APPLICANT: VAN DE WINKEL, JAN
; APPLICANT: VAN VUGT, MARTINE
; TITLE OF INVENTION: ANTI-P SELECTIN ANTIBODIES
; FILE REFERENCE: 22354
; CURRENT APPLICATION NUMBER: US/11/102.403
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: EP 04008722.3
; PRIOR FILING DATE: 2004-04-13
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 11
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-102-403-11

Query Match      100.0%; Score 50; DB 6; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      89 QQRSNWPP 96

RESULT 27
US-10-371-942-72
; Sequence 72, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371.942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-371-942-72

Query Match      100.0%; Score 50; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      88 QQRSNWPP 95

RESULT 28
US-10-371-942-76
; Sequence 76, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371.942
```

```
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-371-942-76

Query Match      100.0%; Score 50; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      88 QQRSNWPP 95

RESULT 29
US-10-408-901-8
; Sequence 8, Application US/10408901
; Publication No. US20040023131A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MEHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-408-901-8

Query Match      100.0%; Score 50; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      89 QQRSNWPP 96

RESULT 30
US-10-408-901-24
; Sequence 24, Application US/10408901
; Publication No. US20040023131A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: MEHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 109
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-24

Query Match      100.0%; Score 50; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      89 QORSNWPP 96

RESULT 31
US-10-656-769-12
; Sequence 12, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-12

Query Match      100.0%; Score 50; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      109 QORSNWPP 116

RESULT 32
US-10-394-471B-16
; Sequence 16, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallion, Bernard J.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 16
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-16

Query Match      100.0%; Score 50; DB 4; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      109 QORSNWPP 116
```

```
RESULT 33
US-10-408-901-32
; Sequence 32, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliott, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-32

Query Match      100.0%; Score 50; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      89 QORSNWPP 96

RESULT 34
US-10-408-901-48
; Sequence 48, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliott, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-48

Query Match      100.0%; Score 50; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QORSNWPP 8
Db      89 QORSNWPP 96

RESULT 35
US-09-453-234-46
; Sequence 46, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
```

```
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match      100.0%; Score 50; DB 3; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      89 QQRSNWPP 96

RESULT 36
US-10-656-769-38
; Sequence 38, Application US/10656769
; Publication No. US20040097712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-38

Query Match      100.0%; Score 50; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      109 QQRSNWPP 116

RESULT 37
US-10-961-567A-6
; Sequence 6, Application US/10961567A
; Publication No. US20050095244A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Hefta, Laura
; APPLICANT: Santoro, Marc
; APPLICANT: Ganguly, Subinay
; TITLE OF INVENTION: FULLY HUMAN ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: 10060 NP
; CURRENT APPLICATION NUMBER: US/10/961,567A
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 60/510193
```

```
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pD16gate-20H4.9.LC amino acid sequence
US-10-961-567A-6

Query Match      100.0%; Score 50; DB 5; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
Db      109 QQRSNWPP 116

RESULT 38
US-09-833-245-237
; Sequence 237, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 237
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (80)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (97)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (112)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (117)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-237

Query Match      92.0%; Score 46; DB 3; Length 236;
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Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 109 QQRXNWPP 116
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    ||| |||

RESULT 39
US-10-233-996-40
; Sequence 40, Application US/10233996
; Publication No. US20030096976A1
; GENERAL INFORMATION:
; APPLICANT: HONG, HYO JEONG
; APPLICANT: PARK, SUNG SUP
; APPLICANT: KANG, YOUNG JUN
; APPLICANT: KANG, CHANG-YUIL
; APPLICANT: YOON, SUNG KWAN
; TITLE OF INVENTION: HUMANIZED ANTIBODIES LB-00503 AND LB-00506 SPECIFIC FOR HUMAN 4-1
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING SAID HUMANIZED ANTIBODIES
; FILE REFERENCE: 4363-0102P
; CURRENT APPLICATION NUMBER: US/10/233,996
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of human antibody (X82934)
US-10-233-996-40

Query Match 90.0%; Score 45; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QQRSNWPP 8
Db 89 QQRXNWPP 95
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RESULT 40
US-10-450-763-44914
; Sequence 44914, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44914
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (69)..(110)
; OTHER INFORMATION: EGG-LAYING HORMONE domain identified by eMATRIX, accession
; OTHER INFORMATION: number DM01813B, p-value=1.956e-09, raw score of 17.93
US-10-450-763-44914

Query Match 90.0%; Score 45; DB 5; Length 148;
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Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 114 QQRSSWPP 121
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    ||| |||

Search completed: December 14, 2005, 07:37:54
Job time : 36.6897 secs
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1940

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:25:44 : Search time 2.48276 Seconds
(without alignments)
21.698 Million cell updates/sec

Title: US-10-720-323-6

Perfect score: 50

Sequence: 1 QQRNWP 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB pep.*
- 5: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	6	US-10-997-201A-39
2	50	100.0	9	7	US-11-093-274-18
3	50	100.0	56	6	US-10-997-201A-20
4	50	100.0	107	7	US-11-093-274-24
5	47	94.0	10	7	US-11-093-274-17
6	47	94.0	108	7	US-11-093-274-23
7	43	86.0	95	7	US-11-054-669-86
8	43	86.0	95	7	US-11-084-554-138
9	43	86.0	128	6	US-10-721-763-31
10	43	86.0	129	6	US-10-721-763-19
11	43	86.0	251	7	US-11-054-515-1049
12	40	80.0	10	7	US-11-093-274-16
13	40	80.0	108	7	US-11-093-274-22
14	40	80.0	251	7	US-11-054-515-1238
15	38	76.0	129	6	US-10-721-763-23
16	36	72.0	94	7	US-11-093-274-33
17	36	72.0	95	7	US-11-054-669-87
18	36	72.0	95	7	US-11-084-554-131
19	34	68.0	9	6	US-10-925-366A-45
20	34	68.0	347	6	US-10-821-234-1379
21	33	66.0	95	7	US-11-054-669-84
22	33	66.0	95	7	US-11-054-669-85
23	33	66.0	95	7	US-11-084-554-127
24	33	66.0	95	7	US-11-084-554-130
25	33	66.0	246	7	US-11-054-515-1268

26	33	66.0	250	7	US-11-054-515-1952	Sequence 1952, Ap
27	33	66.0	372	7	US-11-131-212-71	Sequence 71, Appl
28	32	64.0	223	7	US-11-050-440-17	Sequence 17, Appl
29	32	64.0	305	6	US-10-502-972-4	Sequence 4, Appl
30	31	62.0	405	6	US-10-821-234-1357	Sequence 1357, Ap
31	31	62.0	499	6	US-10-508-263-94	Sequence 94, Appl
32	31	62.0	1548	7	US-11-108-172-1095	Sequence 1095, Ap
33	30	60.0	108	6	US-10-925-366A-97	Sequence 97, Appl
34	30	60.0	223	7	US-11-050-440-18	Sequence 18, Appl
35	30	60.0	224	7	US-11-050-440-4	Sequence 4, Appl
36	30	60.0	259	7	US-11-056-825-7	Sequence 7, Appl
37	30	60.0	261	7	US-11-056-825-2	Sequence 2, Appl
38	30	60.0	295	6	US-10-510-386-58	Sequence 58, Appl
39	30	60.0	413	6	US-10-821-234-989	Sequence 989, App
40	30	60.0	1311	6	US-10-509-422-5	Sequence 5, Appl
41	29	58.0	75	6	US-10-986-501-139	Sequence 139, App
42	29	58.0	194	7	US-11-108-172-1126	Sequence 1126, Ap
43	29	58.0	292	7	US-11-082-389-16	Sequence 16, Appl
44	29	58.0	1892	7	US-11-075-185-6	Sequence 6, Appl
45	28	56.0	9	7	US-11-108-135-12	Sequence 12, Appl
46	28	56.0	18	7	US-11-054-515-2726	Sequence 2726, Ap
47	28	56.0	65	6	US-10-467-657-9029	Sequence 9029, Ap
48	28	56.0	107	7	US-11-108-135-18	Sequence 18, Appl
49	28	56.0	107	7	US-11-108-135-20	Sequence 20, Appl
50	28	56.0	107	7	US-11-108-135-22	Sequence 22, Appl
51	28	56.0	107	7	US-11-108-135-26	Sequence 26, Appl
52	28	56.0	144	6	US-10-467-657-2602	Sequence 2602, Ap
53	28	56.0	253	7	US-11-054-515-1349	Sequence 1349, Ap
54	28	56.0	292	6	US-10-510-386-74	Sequence 74, Appl
55	28	56.0	305	6	US-10-518-341-2	Sequence 2, Appl
56	28	56.0	359	7	US-11-087-227-8	Sequence 8, Appl
57	28	56.0	404	7	US-11-087-227-6	Sequence 6, Appl
58	28	56.0	482	6	US-10-821-234-372	Sequence 372, App
59	28	56.0	525	7	US-11-082-389-36	Sequence 36, Appl
60	28	56.0	545	7	US-11-082-389-34	Sequence 34, Appl
61	28	56.0	552	6	US-10-131-826A-332	Sequence 332, App
62	28	56.0	983	7	US-11-113-424-59	Sequence 59, Appl
63	28	56.0	7102	7	US-11-143-980-48	Sequence 48, Appl
64	27	54.0	9	6	US-10-925-366A-72	Sequence 72, Appl
65	27	54.0	86	6	US-10-467-657-5730	Sequence 5730, Ap
66	27	54.0	107	7	US-11-010-954-3	Sequence 3, Appl
67	27	54.0	107	7	US-11-053-750-3	Sequence 3, Appl
68	27	54.0	107	7	US-11-053-749-3	Sequence 3, Appl
69	27	54.0	108	6	US-10-925-366A-237	Sequence 237, App
70	27	54.0	125	6	US-10-793-626-3264	Sequence 3264, Ap
71	27	54.0	126	6	US-10-821-234-1311	Sequence 1311, Ap
72	27	54.0	174	7	US-11-113-424-185	Sequence 185, App
73	27	54.0	177	6	US-10-793-626-2532	Sequence 2532, Ap
74	27	54.0	239	7	US-11-054-515-1882	Sequence 1882, Ap
75	27	54.0	239	7	US-11-054-515-1922	Sequence 1922, Ap
76	27	54.0	241	7	US-11-054-515-1889	Sequence 1889, Ap
77	27	54.0	241	7	US-11-054-515-1901	Sequence 1901, Ap
78	27	54.0	241	7	US-11-054-515-1948	Sequence 1948, Ap
79	27	54.0	243	7	US-11-054-515-1883	Sequence 1883, Ap
80	27	54.0	243	7	US-11-054-515-1935	Sequence 1935, Ap
81	27	54.0	243	7	US-11-054-515-1945	Sequence 1945, Ap
82	27	54.0	243	7	US-11-054-515-2063	Sequence 2063, Ap
83	27	54.0	245	7	US-11-054-515-1900	Sequence 1900, Ap
84	27	54.0	245	7	US-11-054-515-1902	Sequence 1902, Ap
85	27	54.0	246	7	US-11-054-515-1920	Sequence 1920, Ap
86	27	54.0	246	7	US-11-054-515-2062	Sequence 2062, Ap
87	27	54.0	247	7	US-11-054-515-1969	Sequence 1969, App
88	27	54.0	247	7	US-11-054-515-1177	Sequence 1177, App
89	27	54.0	247	7	US-11-054-515-1923	Sequence 1923, Ap
90	27	54.0	247	7	US-11-054-515-3242	Sequence 3242, Ap
91	27	54.0	248	7	US-11-054-515-1008	Sequence 1008, Ap
92	27	54.0	248	7	US-11-054-515-1421	Sequence 1421, Ap
93	27	54.0	248	7	US-11-054-515-1700	Sequence 1700, Ap
94	27	54.0	248	7	US-11-054-515-1771	Sequence 1771, Ap
95	27	54.0	248	7	US-11-054-515-1778	Sequence 1778, Ap
96	27	54.0	249	7	US-11-054-515-918	Sequence 918, App
97	27	54.0	249	7	US-11-054-515-919	Sequence 919, App
98	27	54.0	249	7	US-11-054-515-926	Sequence 926, App

99 27 54.0 249 7 US-11-054-515-1188 Sequence 1188, Ap
100 27 54.0 250 7 US-11-054-515-932 Sequence 932, App

ALIGNMENTS

RESULT 1
US-10-997-201A-39
; Sequence 39, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-39

Query Match 100.0%; Score 50; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | | | | |
Db 1 QQRSNWPP 8

RESULT 2
US-11-093-274-18
; Sequence 18, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-18

Query Match 100.0%; Score 50; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.9e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | | | | |
Db 1 QQRSNWPP 8

RESULT 3
US-10-997-201A-20
; Sequence 20, Application US/10997201A

; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-20

Query Match 100.0%; Score 50; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | | | | |
Db 44 QQRSNWPP 51

RESULT 4
US-11-093-274-24
; Sequence 24, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-24

Query Match 100.0%; Score 50; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | | | | |
Db 89 QQRSNWPP 96

RESULT 5
US-11-093-274-17
; Sequence 17, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274

; CURRENT FILING DATE: 2005-03-28
 ; PRIOR APPLICATION NUMBER: 60/557,741
 ; PRIOR FILING DATE: 2004-03-29
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 17
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-093-274-17

Query Match 94.0%; Score 47; DB 7; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.0027;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRNWP 8
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 Db 1 QQRNWP 8

RESULT 6
 US-11-093-274-23
 ; Sequence 23, Application US/11093274
 ; Publication No. US20050266008A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Graziano, Robert
 ; APPLICANT: Cardarelli, Josephine M.
 ; APPLICANT: Kempe, Thomas
 ; APPLICANT: Cutter, Beth
 ; APPLICANT: Srinivasan, Mohan
 ; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
 ; FILE REFERENCE: 04280/1201101-US1
 ; CURRENT APPLICATION NUMBER: US/11/093,274
 ; CURRENT FILING DATE: 2005-03-28
 ; PRIOR APPLICATION NUMBER: 60/557,741
 ; PRIOR FILING DATE: 2004-03-29
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 23
 ; LENGTH: 108
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-093-274-23

Query Match 94.0%; Score 47; DB 7; Length 108;
 Best Local Similarity 87.5%; Pred. No. 0.022;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRNWP 8
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 Db 89 QQRNWP 96

RESULT 7
 US-11-054-669-86
 ; Sequence 86, Application US/11054669
 ; Publication No. US20050261480A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Foote, Jefferson
 ; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
 ; FILE REFERENCE: 30219/US/3
 ; CURRENT APPLICATION NUMBER: US/11/054,669
 ; CURRENT FILING DATE: 2005-02-08
 ; PRIOR APPLICATION NUMBER: US 10/194,975
 ; PRIOR FILING DATE: 2002-07-12
 ; PRIOR APPLICATION NUMBER: US 60/305,111
 ; PRIOR FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 124
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO 86
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-11-054-669-86

Query Match 86.0%; Score 43; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRNWP 7
 |||:||||
 Db 89 QQRNWP 95

RESULT 8
 US-11-084-554-138
 ; Sequence 138, Application US/11084554
 ; Publication No. US20050260679A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kellermann, Sirid-Ai
 ; APPLICANT: Green, Larry L.
 ; APPLICANT: Korver, Wouter
 ; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
 ; FILE REFERENCE: AGENIX.100A
 ; CURRENT APPLICATION NUMBER: US/11/084,554
 ; CURRENT FILING DATE: 2005-03-17
 ; PRIOR APPLICATION NUMBER: 60/554,372
 ; PRIOR FILING DATE: 2004-03-19
 ; PRIOR APPLICATION NUMBER: 60/574,661
 ; PRIOR FILING DATE: 2004-05-24
 ; NUMBER OF SEQ ID NOS: 266
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 138
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-084-554-138

Query Match 86.0%; Score 43; DB 7; Length 95;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRNWP 7
 |||:||||
 Db 89 QQRNWP 95

RESULT 9
 US-10-721-763-31
 ; Sequence 31, Application US/10721763
 ; Publication No. US20050249729A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
 ; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
 ; FILE REFERENCE: PH-1573-PCT
 ; CURRENT APPLICATION NUMBER: US/10/721,763
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: JP2001-150213
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: JP2001-243040
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: JP2001-314489
 ; PRIOR FILING DATE: 2001-10-11
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 128
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-721-763-31

Query Match 86.0%; Score 43; DB 6; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 QQRSNWP 7
Db 109 QQRSNWP 115

RESULT 10
US-10-721-763-19
; Sequence 19, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19

Query Match 86.0%; Score 43; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
Db 109 QQRSNWP 115

RESULT 11
US-11-054-515-1049
; Sequence 1049, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT

; ORGANISM: Homo sapiens
US-11-054-515-1049

Query Match 86.0%; Score 43; DB 7; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
Db 231 QQRSNWP 237

RESULT 12
US-11-093-274-16
; Sequence 16, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-16

Query Match 80.0%; Score 40; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 0.049;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWP 8
Db 1 QQLNNWP 8

RESULT 13
US-11-093-274-22
; Sequence 22, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-22

Query Match 80.0%; Score 40; DB 7; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 QQRSNWPP 8
      ||:||||
Db      89 QQLNWWPP 96

RESULT 14
US-11-054-515-1238
; Sequence 1238, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1238
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1238

Query Match      80.0%; Score 40; DB 7; Length 251;
Best Local Similarity 75.0%; Pred. No. 0.85;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
      ||:||||
Db      231 QQYNNWPP 238

RESULT 15
US-10-721-763-23
; Sequence 23, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 129
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-721-763-23

Query Match      76.0%; Score 38; DB 6; Length 129;
Best Local Similarity 85.7%; Pred. No. 1.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 7
      ||||:|
Db      109 QQRSDWP 115

RESULT 16
US-11-093-274-33
; Sequence 33, Application US/11093274
; Publication No. US2005026608A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-33

Query Match      72.0%; Score 36; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNW 6
      |||||
Db      89 QQRSNW 94

RESULT 17
US-11-054-669-87
; Sequence 87, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-87

Query Match      72.0%; Score 36; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNW 6
      |||||
```


Query Match 66.0%; Score 33; DB 7; Length 95;
Best Local Similarity 71.4%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|| :|||
Db 89 QOYNNWP 95

RESULT 22

US-11-054-669-85
; Sequence 85, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-85

Query Match 66.0%; Score 33; DB 7; Length 95;
Best Local Similarity 71.4%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|| :|||
Db 89 QOYNNWP 95

RESULT 23

US-11-084-554-127
; Sequence 127, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ARGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-127

Query Match 66.0%; Score 33; DB 7; Length 95;
Best Local Similarity 71.4%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|| :|||
Db 89 QOYNNWP 95

Query Match 66.0%; Score 33; DB 7; Length 95;
Best Local Similarity 71.4%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|| :|||
Db 89 QOYNNWP 95

US-11-084-554-130
; Sequence 130, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ARGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-130

Query Match 66.0%; Score 33; DB 7; Length 95;
Best Local Similarity 71.4%; Pred. No. 6.5;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|| :|||
Db 89 QOYNNWP 95

RESULT 25

US-11-054-515-1268
; Sequence 1268, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1268
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1268

Query Match 66.0%; Score 33; DB 7; Length 246;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
Db 227 QQYNNWP 233

RESULT 26
US-11-054-515-1952
; Sequence 1952, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1952
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1952

Query Match 66.0%; Score 33; DB 7; Length 250;
Best Local Similarity 71.4%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
Db 231 QQYNNWP 237

RESULT 27
US-11-131-212-71
; Sequence 71, Application US/11131212
; Publication No. US20050262593A1
; GENERAL INFORMATION:
; APPLICANT: Yutaka KANDA
; APPLICANT: Mitsuo SATOH
; APPLICANT: Kazuyasu NAKAMURA
; APPLICANT: Kazuhisa UCHIDA
; APPLICANT: Toyohide SHINKAWA
; APPLICANT: Naoko YAMANE
; APPLICANT: MOTOO YANASAKI
; APPLICANT: MOTOO HANAI
; TITLE OF INVENTION: ANTIBODY COMPOSITION-PRODUCING CELL
; FILE REFERENCE: 249-202
; CURRENT APPLICATION NUMBER: US/11/131,212
; CURRENT FILING DATE: 2005-05-18

; PRIOR APPLICATION NUMBER: US/09/971,773
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: JP 2000-308526
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/268,926
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Cricetus griseus
US-11-131-212-71

Query Match 66.0%; Score 33; DB 7; Length 372;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 340 QQKLNWKP 347

RESULT 28
US-11-050-440-17
; Sequence 17, Application US/11050440
; Publication No. US2005025530A1
; GENERAL INFORMATION:
; APPLICANT: KEEFER, CAROL L.
; APPLICANT: BISCHOFF, STEVEN R.
; APPLICANT: HE, SHUYANG
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF PLURIPOTENCY
; TITLE OF INVENTION: DETERMINING FACTORS
; FILE REFERENCE: 0108172.00116
; CURRENT APPLICATION NUMBER: US/11/050,440
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,498
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 17
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-440-17

Query Match 64.0%; Score 32; DB 7; Length 223;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QQRSNWP 7
Db 89 QQKLNWPP 94

RESULT 29
US-10-502-972-4
; Sequence 4, Application US/10502972
; Publication No. US20050255573A1
; GENERAL INFORMATION:
; APPLICANT: Chambers, Ian
; APPLICANT: Smith, Austin G.
; TITLE OF INVENTION: Pluripotency determining factors and uses thereof
; FILE REFERENCE: 2325.0020000/RWE/BAS
; CURRENT APPLICATION NUMBER: US/10/502,972
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-502-972-4

Query Match 64.0%; Score 32; DB 6; Length 305;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QRSNWP 7
 : : : : :
 Db 154 QKNWPP 159

RESULT 30

US-10-821-234-1357
 ; Sequence 1357, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 1357
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1357

Query Match 62.0%; Score 31; DB 6; Length 405;
 Best Local Similarity 57.1%; Pred. No. 54;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
 : : : : :
 Db 259 RRGWPP 265

RESULT 31

US-10-508-263-94
 ; Sequence 94, Application US/10508263
 ; Publication No. US20050260754A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BASF Plant Science GmbH
 ; TITLE OF INVENTION: Constructs and methods for regulating gene expression
 ; FILE REFERENCE: 53262-20085.00
 ; CURRENT APPLICATION NUMBER: US/10/508,263
 ; CURRENT FILING DATE: 2004-09-20
 ; NUMBER OF SEQ ID NOS: 126
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 94
 ; LENGTH: 499
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-508-263-94

Query Match 62.0%; Score 31; DB 6; Length 499;
 Best Local Similarity 37.5%; Pred. No. 65;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QORSNWP 8
 : : : : :
 Db 464 BEKKRWPP 471

RESULT 32

US-11-108-172-1095
 ; Sequence 1095, Application US/11108172
 ; Publication No. US20050260177A1

; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Secrist, Heather
 ; APPLICANT: Benson, Darin R.
 ; APPLICANT: Meagher, Madeleine Joy
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Jiang, Yudi
 ; APPLICANT: Smith, Carole L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Clapper, Jonathan D.
 ; APPLICANT: Skeiky, Yasir A. W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick Thomas S.
 ; APPLICANT: Carter, Darick
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
 ; FILE REFERENCE: 210121.471C15
 ; CURRENT APPLICATION NUMBER: US/11/108,172
 ; CURRENT FILING DATE: 2005-04-15
 ; PRIOR APPLICATION NUMBER: US 10/025,380
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: US 09/922,217
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: US 09/833,263
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: US 09/649,811
 ; PRIOR FILING DATE: 2000-08-28
 ; PRIOR APPLICATION NUMBER: US 09/609,448
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 09/575,251
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 09/519,444
 ; PRIOR FILING DATE: 2000-03-06
 ; PRIOR APPLICATION NUMBER: US 09/504,629
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: US 09/480,321
 ; PRIOR FILING DATE: 2000-01-10
 ; PRIOR APPLICATION NUMBER: US 09/476,296
 ; PRIOR FILING DATE: 1999-12-30
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1130
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1095
 ; LENGTH: 1548
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-108-172-1095

Query Match 62.0%; Score 31; DB 7; Length 1548;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
 : : : : :
 Db 153 QRSRWD 159

RESULT 33

US-10-925-366A-97
 ; Sequence 97, Application US/10925366A
 ; Publication No. US20050271663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ignatovich, Olga
 ; APPLICANT: Dewildt, Rudolph M.T.
 ; APPLICANT: Benjamin, Woolven
 ; APPLICANT: Grant, Steven
 ; APPLICANT: Jones, Philip
 ; APPLICANT: Baaran, Amrik
 ; APPLICANT: Brewis, Neil
 ; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders

FILE REFERENCE: 8039/2105
CURRENT APPLICATION NUMBER: US/10/925.366A
SEQUENCE 4, Application US/10/925.366A
PUBLICATION NO. US2005025530A1
GENERAL INFORMATION:
APPLICANT: KEEFER, CAROL L.
APPLICANT: BISCHOFF, STEVEN R.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF PLURIPOTENCY
TITLE OF INVENTION: DETERMINING FACTORS
FILE REFERENCE: 0108172.00116
CURRENT APPLICATION NUMBER: US/11/050.440
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,498
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 97
LENGTH: 108
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Antibody Domain
US-10-925-366A-97

Query Match 60.0%; Score 30; DB 6; Length 108;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
| | | | |
Db 89 QQRWRWP 95

RESULT 34
US-11-050-440-18
Sequence 18, Application US/11050440
Publication No. US2005025530A1
GENERAL INFORMATION:
APPLICANT: KEEFER, CAROL L.
APPLICANT: BISCHOFF, STEVEN R.
APPLICANT: HE, SHUYANG
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF PLURIPOTENCY
TITLE OF INVENTION: DETERMINING FACTORS
FILE REFERENCE: 0108172.00116
CURRENT APPLICATION NUMBER: US/11/050.440
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,498
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 18
LENGTH: 223
TYPE: PRT
ORGANISM: Capra hircus
US-11-050-440-18

Query Match 60.0%; Score 30; DB 7; Length 223;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QQRSNWP 7
| | | | |
Db 89 QQRWRWP 94

RESULT 35
US-11-050-440-4
Sequence 4, Application US/11050440
Publication No. US2005025530A1
GENERAL INFORMATION:
APPLICANT: KEEFER, CAROL L.
APPLICANT: BISCHOFF, STEVEN R.
APPLICANT: HE, SHUYANG
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF PLURIPOTENCY
TITLE OF INVENTION: DETERMINING FACTORS
FILE REFERENCE: 0108172.00116
CURRENT APPLICATION NUMBER: US/11/050.440
CURRENT FILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: 60/542,498
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 4
LENGTH: 224
TYPE: PRT
ORGANISM: Capra hircus
FEATURE:
NAME/KEY: MOD RES
LOCATION: (224)
OTHER INFORMATION: Variable amino acid
US-11-050-440-4

Query Match 60.0%; Score 30; DB 7; Length 224;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QQRSNWP 7
| | | | |
Db 89 QQRWRWP 94

RESULT 36
US-11-056-825-7
Sequence 7, Application US/11056825
Publication No. US20050255109A1
GENERAL INFORMATION:
APPLICANT: Feilding-Habermann, Brunhilde
APPLICANT: Janda, Kim D.
APPLICANT: Saven, Alan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
FILE REFERENCE: SCRP-0042
CURRENT APPLICATION NUMBER: US/11/056.825
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: US 60/626,726
PRIOR FILING DATE: 2004-11-10
PRIOR APPLICATION NUMBER: US 60/544,807
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 259
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-11-056-825-7

Query Match 60.0%; Score 30; DB 7; Length 259;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QQRSNWP 8
| | | | |
Db 228 QQRWRWP 234

RESULT 37

```
US-11-056-825-2
; Sequence 2, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SCRP-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-825-2

Query Match 60.0%; Score 30; DB 7; Length 261;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
Db 228 QGTHWP 234

RESULT 38
US-10-510-386-58
; Sequence 58, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-58

Query Match 60.0%; Score 30; DB 6; Length 296;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSNWP 7
Db 271 RKNWP 276

RESULT 39
US-10-821-234-989
; Sequence 989, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan

US-11-056-825-2
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 989
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-989

Query Match 60.0%; Score 30; DB 6; Length 413;
Best Local Similarity 62.5%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QRSNWP 8
Db 191 QGASWVP 198

RESULT 40
US-10-509-422-5
; Sequence 5, Application US/10509422
; Publication No. US20050244825A1
; GENERAL INFORMATION:
; APPLICANT: Liou, Simon
; TITLE OF INVENTION: Human BMP2 Inducible Kinases
; FILE REFERENCE: 004974.01015
; CURRENT APPLICATION NUMBER: US/10/509,422
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: PCT/EP03/080825
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/367,512
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/406,936
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1311
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-509-422-5

Query Match 60.0%; Score 30; DB 6; Length 1311;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
Db 1127 QGASWVP 1133

Search completed: December 14, 2005, 07:38:17
Job time : 3.48276 secs
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1. The first part of the document is a list of the names of the persons who have been appointed to the various positions of the Board of Directors of the company.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:38 ; Search time 8.68966 Seconds
(without alignments)
88.581 Million cell updates/sec

Title: US-10-720-323-6

Perfect score: 50

Sequence: 1 QQRSNWPP 8

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR_80:*

2: PIR1:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	92	2 S37512	Ig kappa chain V r
2	50	100.0	92	2 S37516	Ig kappa chain V r
3	50	100.0	107	2 S57444	Ig kappa chain V-J
4	50	100.0	108	2 G44151	Ig kappa chain V r
5	50	100.0	114	2 S54905	Ig kappa chain V r
6	50	100.0	128	2 S40345	Ig kappa chain V-J
7	43	86.0	86	2 S16834	Ig kappa chain V r
8	43	86.0	86	2 S16836	Ig kappa chain V r
9	43	86.0	92	2 S37522	Ig kappa chain V r
10	43	86.0	111	2 S23628	Ig kappa chain V r
11	43	86.0	115	1 K3HUVG	Ig kappa chain pre
12	43	86.0	128	2 A56701	Ig kappa chain V r
13	43	86.0	144	2 PLO106	Ig kappa chain pre
14	41	82.0	129	2 S29627	Ig kappa chain V r
15	40	80.0	92	2 S37506	Ig kappa chain V r
16	40	80.0	92	2 S37523	Ig kappa chain V r
17	40	80.0	98	2 I30608	Ig kappa chain V-I
18	40	80.0	108	1 K1HUIY	Ig kappa chain V-I
19	40	80.0	109	1 K1HUPM	Ig kappa chain V-I
20	39	78.0	92	2 S37504	Ig kappa chain V r
21	38	76.0	85	2 S16829	Ig kappa chain V r
22	38	76.0	86	2 S16826	Ig kappa chain V r
23	38	76.0	738	2 D70680	hypothetical prote
24	38	76.0	788	2 H96545	hypothetical prote
25	37	74.0	128	2 S40379	Ig kappa chain V-J
26	37	74.0	429	2 T23734	hypothetical prote
27	37	74.0	816	2 C59493	hypothetical prote
28	36	72.0	86	2 S16830	Ig kappa chain V r
29	36	72.0	86	2 S16833	Ig kappa chain V-I

30	36	72.0	91	2 S37521	Ig kappa chain V r
31	36	72.0	91	2 S17626	Ig kappa chain V r
32	36	72.0	115	2 S11697	Ig kappa chain pre
33	36	72.0	140	2 PLO013	Ig kappa chain pre
34	36	72.0	486	2 S66097	cell-cycle protein
35	36	72.0	508	2 T09046	proline-rich prote
36	36	72.0	1501	1 B29813	174K ninaC protein
37	36	72.0	2157	2 S71461	proline-rich prote
38	36	72.0	2649	2 T51023	hypothetical prote
39	35	70.0	106	2 PC4282	Ig kappa chain (an
40	35	70.0	125	2 S40344	Ig kappa chain V-J
41	35	70.0	131	2 S40328	Ig kappa chain - h
42	35	70.0	133	2 I45927	Ig kappa chain - h
43	35	70.0	145	1 R5PM18	membrane-bound imm
44	35	70.0	338	2 S37395	ribosomal protein
45	35	70.0	499	2 B86182	secretory carrier
46	35	70.0	684	2 T31640	hypothetical prote
47	35	70.0	1658	2 T42642	phosphoinositide 3
48	35	70.0	3530	2 A59266	unconventional myo
49	34	68.0	86	2 S16825	Ig kappa chain V r
50	34	68.0	103	2 A70749	hypothetical prote
51	34	68.0	116	2 B26555	Ig kappa chain V-I
52	34	68.0	128	2 PN0445	Ig kappa chain pre
53	34	68.0	215	2 JE0244	Ig kappa chain pre
54	34	68.0	347	2 T08826	Ig kappa chain NIG
55	34	68.0	371	2 T04017	secretory carrier
56	34	68.0	1595	2 T31082	hypothetical prote
57	33	66.0	84	2 S34099	endo-1,4-beta-xyla
58	33	66.0	86	2 S16837	Ig kappa chain V r
59	33	66.0	86	2 S16839	Ig kappa chain V r
60	33	66.0	86	2 S16832	Ig kappa chain V r
61	33	66.0	86	2 S16827	Ig kappa chain V r
62	33	66.0	86	2 S16831	Ig kappa chain V r
63	33	66.0	86	2 S16828	Ig kappa chain V r
64	33	66.0	86	2 S16835	Ig kappa chain V r
65	33	66.0	87	2 S34097	Ig kappa chain V r
66	33	66.0	87	2 S16841	Ig kappa chain V r
67	33	66.0	87	2 S34098	Ig kappa chain V r
68	33	66.0	91	2 S37525	Ig kappa chain V r
69	33	66.0	91	2 S37527	Ig kappa chain V r
70	33	66.0	92	2 S37509	Ig kappa chain V r
71	33	66.0	115	1 K3HUCI	Ig kappa chain pre
72	33	66.0	115	2 A30553	Ig kappa chain pre
73	33	66.0	117	2 S40362	Ig kappa chain - h
74	33	66.0	128	2 S40343	Ig kappa chain V-J
75	33	66.0	203	2 B70784	cytochrome-c oxida
76	33	66.0	282	2 A84594	hypothetical prote
77	33	66.0	323	2 D83708	phosphonates trans
78	33	66.0	365	2 T15660	hypothetical prote
79	33	66.0	494	2 S67314	regulatory protein
80	33	66.0	545	2 B88479	protein F47D12.9 [
81	33	66.0	608	2 S32823	somatotropin recep
82	33	66.0	608	2 I53269	prolactin receptor
83	33	66.0	767	2 S41479	DNA-binding protei
84	33	66.0	846	2 H70599	hypothetical prote
85	33	66.0	1009	2 T42925	DNA-directed DNA p
86	33	66.0	1097	1 DJBEMC	DNA-directed DNA p
87	33	66.0	1246	2 G90887	cryptic nitrate re
88	33	66.0	1246	2 B85730	cryptic nitrate re
89	33	66.0	1292	2 D84727	probable RAD50 DNA
90	33	66.0	1312	2 T30845	probable DNA repai
91	33	66.0	1488	2 T02856	probable membrane
92	33	66.0	1557	2 T02859	probable serine/th
93	33	66.0	1748	1 JQ1555	genome polypeptid
94	33	66.0	2282	2 T42717	DNA-binding protei
95	32	64.0	24	2 S43011	merD protein - fer
96	32	64.0	107	2 C45722	anti-glycoprotein
97	32	64.0	112	2 F83564	probable HIT fami
98	32	64.0	123	2 S40378	Ig kappa chain - h
99	32	64.0	125	1 A35350	protein kinase C i
100	32	64.0	129	2 S45368	protein kinase C i

ALIGNMENTS

```

RESULT 1
S37512
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37512
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37512
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: UNIPARC:UPI0000116570; EMBL:Z26599; NID:G405666; PIDN:CAA81353.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match      100.0%; Score 50; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
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Db     72 QQRSNWPP 79

RESULT 2
S37516
Ig kappa chain V region (V-kappa 3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37516
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37516
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: UNIPARC:UPI0000116588; EMBL:Z26624; NID:G405674; PIDN:CAA81377.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match      100.0%; Score 50; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
      |||||
Db     72 QQRSNWPP 79

RESULT 3
S57444
Ig kappa chain V-J region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
C:Accession: S57444
R;Pateron, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IGM antibodies cloned from motor neurop
A;Reference number: S57408
A;Accession: S57444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <PAT>
A;Cross-references: UNIPARC:UPI00001137AE; EMBL:X87898; NID:G871275; PIDN:CAA61149.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology

```

F;16-90/Domain: immunoglobulin homology <IMM>

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Query Match      100.0%; Score 50; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
      |||||
Db     89 QQRSNWPP 96

```

RESULT 4

```

G44151
Ig kappa chain V region (JW-10) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: G44151
R;Zbenedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pya
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A;Reference number: A44151; MUID:92228746; PMID:1373487
A;Accession: G44151
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-108 <ZEB>
A;Cross-references: UNIPARC:UPI00001139AC; GB:M88317; NID:G183968; PIDN:AAA35975.1; PID:
A;Note: nucleotide translation not given
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>

```

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Query Match      100.0%; Score 50; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
      |||||
Db     88 QQRSNWPP 95

```

RESULT 5

```

S54905
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S54905
R;Esposito, G.; Traboni, C.
submitted to the EMBL Data Library, November 1994
A;Description: Cloning and sequencing of cDNA coding for the variable domains of a human
A;Reference number: S54905
A;Accession: S54905
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-114 <ESP>
A;Cross-references: UNIPARC:UPI000011620A; EMBL:X82934; NID:G809554; PIDN:CAA58108.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```

```

Query Match      100.0%; Score 50; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QQRSNWPP 8
      |||||
Db     89 QQRSNWPP 96

```

RESULT 6

```

S40345
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

```


C;Accession: S40345
R.Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40345
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-128 <KLE>
A;Cross-references: UNIPARC:UPI000011615F; EMBL:X72455; NID:g441378; PIDN:CAA51123.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 50; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
|||||
Db 105 QORSNWPP 112

RESULT 7
S16834
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16834
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16834
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPARC:UPI0000176D5F; EMBL:X54832
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|||||
Db 80 QORSNWP 86

RESULT 8
S16836
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S16836
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16836
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPARC:UPI0000176D61; EMBL:X54834
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|||||
Db 80 QORSNWP 86

RESULT 9

S37522
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37522
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IGM(+) IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37522
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: UNIPARC:UPI0000116586; EMBL:Z26622; NID:g3405686; PIDN:CAA81375.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 86.0%; Score 43; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|||||
Db 72 QORSNWP 78

RESULT 10

S23628
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S23628
R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23628
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <OLE>
A;Cross-references: UNIPARC:UPI0000115F96; EMBL:X59705; NID:g34022; PIDN:CRA42226.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 43; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
|||||
Db 89 QORSNWP 95

RESULT 11

K3HUVG
Ig kappa chain precursor V-III region (Vg) - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01900
R;Pech, M.; Zachau, H.G.
Nucleic Acids Res. 12, 9229-9236, 1984
A;Title: Immunoglobulin genes of different subgroups are interdigitated within the V-K 1
A;Reference number: A93549; MUID:85087932; PMID:6440122
A;Accession: A01900
A;Molecule type: DNA

A;Residues: 1-115 <PC>
A;Cross-references: UNIPROT:P04433; UNIPARC:UPI0000116D05; GB:X01668; GB:X02768; NID:g33
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V-III region (Vg) #status predicted <MAT>
F;21-43/Region: framework 1
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;55-69/Region: framework 2
F;70-76/Region: complementarity-determining 2
F;77-108/Region: framework 3
F;109-115/Region: complementarity-determining 3
F;43-108/Disulfide bonds: #status predicted

Query Match 86.0%; Score 43; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
|||||
Db 109 QQRSNWP 115

RESULT 12
A56701
Ig kappa chain V region precursor (HuA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C;Accession: A56701
R;Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A;Title: Human and mouse monoclonal antibodies to blood group A substance, which are ne
A;Reference number: A56701; MUID:95279371; PMID:7759488
A;Accession: A56701
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <NIC>
A;Cross-references: UNIPARC:UPI0000113B26; GB:L41174; NID:g762823; PIDN:AAA64877.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 43; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
|||||
Db 109 QQRSNWP 115

RESULT 13
PL0106
Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A;Reference number: PL0106; MUID:89235583; PMID:2541221
A;Accession: PL0106
A;Molecule type: mRNA
A;Residues: 1-144 <SIL>

A;Cross-references: UNIPARC:UPI00001767A2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;116-127/Domain: J region <JRG>
F;128-144/Domain: C region (fragment) <CRE>

Query Match 86.0%; Score 43; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
|||||
Db 109 QQRSNWP 115

RESULT 14

S29627

Ig kappa chain V region (60.3 hybridoma) - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C;Accession: S34110; S29627

R;Walls, M.A.; Hsiao, K.; Harris, L.J.

Nucleic Acids Res. 21, 2921-2929, 1993

A;Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains with

A;Reference number: S34110; MUID:93324379; PMID:8332501

A;Accession: S34110

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <WA2>

A;Cross-references: UNIPARC:UPI000011649A; EMBL:Z17330; NID:g38511; PIDN:CAA78978.1; PID

A;Note: human sequences cloned and sequenced prior to expression in mouse myeloma cells

C;Keywords: heterotetramer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

C;Genetics: 17/1

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 82.0%; Score 41; DB 2; Length 129;

Best Local Similarity 75.0%; Pred. No. 2.7;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8

|||||

Db 109 QHRDNWPP 116

RESULT 15

S37506

Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37506

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A;Reference number: S37501

A;Accession: S37506

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-92 <KLE>

A;Cross-references: UNIPARC:UPI0000116576; EMBL:Z26606; NID:g405653; PIDN:CAA81359.1; PID

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 80.0%; Score 40; DB 2; Length 92;

Best Local Similarity 85.7%; Pred. No. 2.9;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQRSNWPP 7
 |||:||||
 Db 72 QQRTNWPP 78

RESULT 16
 S37523
 Ig kappa chain V region (V-kappa 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37523
 R:Klein, U.; Kueppers, R.; Rajewsky, K.
 submitted to the EMBL Data Library, September 1993
 A:Description: Human IgM(+) IgG(+) cells, the major B cell subset in the peripheral blood
 A:Reference number: S37501
 A:Accession: S37523
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <KLE>
 A:Cross-references: UNIPARC:UPI0000116585; EMBL:226621; NID:G405688; PIDN:CAA81374.1; PI
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 80.0%; Score 40; DB 2; Length 92;
 Best Local Similarity 75.0%; Pred. No. 2.9;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 |||:||||
 Db 72 QQYNNWPP 79

RESULT 17
 I30608
 Ig kappa chain V-III region (Les) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C:Accession: I30608
 J:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: I30608
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-98 <GON>
 A:Cross-references: UNIPARC:UPI0000176D78
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 40; DB 2; Length 98;
 Best Local Similarity 75.0%; Pred. No. 3;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 |||:||||
 Db 91 QQYNNWPP 98

RESULT 18
 KIHLUY
 Ig kappa chain V-I region (Lay) - human
 C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C:Accession: A01871; F30609
 R:Capra, J.D.; Klapper, D.G.
 Scand. J. Immunol. 5, 677-684, 1976
 A:Title: Complete amino acid sequence of the variable domains of two human IgM anti-gam
 A:Reference number: A01871; MUID:77038198; PMID:824717
 A:Accession: A01871

A:Molecule type: protein
 A:Residues: 1-108 <CAP>
 A:Cross-references: UNIPROT:P01605; UNIPARC:UPI000012E148
 A>Note: the second and third hypervariable regions of this chain are identical with those
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: F30609
 A:Molecule type: protein
 A:Residues: 1-104 <GON>
 A:Cross-references: UNIPARC:UPI0000173703
 C:Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
 C:Genetics:
 A:Gene: GDB:IGKV1
 A:Cross-references: GDB:I36264
 A:Map position: 2p12-2p12
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-90/Domain: immunoglobulin homology <IMM>
 F:23-88/Disulfide bonds: #status Predicted

Query Match 80.0%; Score 40; DB 1; Length 108;
 Best Local Similarity 75.0%; Pred. No. 3.4;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 |||:||||
 Db 89 QQYNNWPP 96

RESULT 19
 K3HUPM
 Ig kappa chain V-III region (Pom) - human (tentative sequence)
 C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
 C:Accession: A01897
 R:Klapper, D.G.; Capra, J.D.
 Ann. Immunol. (Inst. Pasteur) 127C, 261-271, 1976
 A:Title: The amino acid sequence of the variable regions of the light chains from two id
 A:Reference number: A01897
 A:Accession: A01897
 A:Molecule type: protein
 A:Residues: 1-109 <KLA>
 A:Cross-references: UNIPROT:P01624; UNIPARC:UPI000012E15F
 C:Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
 C:Genetics:
 A:Gene: GDB:IGKV3
 A:Cross-references: GDB:I36266
 A:Map position: 2p12-2p11
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer
 F:16-91/Domain: immunoglobulin homology <IMM>
 F:23-89/Disulfide bonds: #status Predicted

Query Match 80.0%; Score 40; DB 1; Length 109;
 Best Local Similarity 75.0%; Pred. No. 3.4;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
 |||:||||
 Db 90 QQYNNWPP 97

RESULT 20
 S37504
 Ig kappa chain V region (V-kappa 3) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C/Accession: S37504
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S37501
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-92 <KLE>
A/Cross-references: UNIPARC:UPI000011578; EMBL:Z26608; NID:9405649; PIDN:CAA81361.1; PIDN:CAA38593.1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 78.0%; Score 39; DB 2; Length 92;
Best Local Similarity 75.0%; Pred. No. 4.3; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 2; Indels 0; Gaps 0;

Qy 1 QQRNWP 8
Db 72 QQRNWP 79

RESULT 21
S16829
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S16829
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid factor
A/Reference number: S16823; MUID:91243737; PMID:1903706
A/Accession: S16829
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-86 <BLA>
A/Cross-references: UNIPARC:UPI0000176DAC; EMBL:X54827
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 38; DB 2; Length 86;
Best Local Similarity 85.7%; Pred. No. 6; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1 QQRNWP 7
Db 80 QQRNWP 86

RESULT 22
S16826
Ig kappa chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S16826; S34101
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A/Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid factor
A/Reference number: S16823; MUID:91243737; PMID:1903706
A/Accession: S16826
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-86 <BLA>
A/Cross-references: UNIPARC:UPI0000115E92; EMBL:X54824; NID:933653; PIDN:CAA38593.1; PIDN:CAA38593.1
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A/Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A/Reference number: S34076; MUID:93170387; PMID:8436174
A/Accession: S34101
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-86 <WAG>

C/Accession: S37504
R:Klein, U.; Kueppers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A/Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A/Reference number: S37501
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-92 <KLE>
A/Cross-references: UNIPARC:UPI000011578; EMBL:Z26608; NID:9405649; PIDN:CAA81361.1; PIDN:CAA38593.1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 76.0%; Score 38; DB 2; Length 86;
Best Local Similarity 85.7%; Pred. No. 6; Mismatches 0; Gaps 0;
Matches 6; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1 QQRNWP 7
Db 80 QQRNWP 86

RESULT 23
D70680
hypothetical protein Rv2438c - Mycobacterium tuberculosis (strain H37RV)
C/Species: Mycobacterium tuberculosis
C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C/Accession: D70680
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A/Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A/Reference number: A70500; MUID:98295987; PMID:9634230
A/Accession: D70680
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-738 <COL>
A/Cross-references: UNIPARC:UPI00001650F9; GB:Z81451; GB:AL123456; NID:93361662; PIDN:CAI
A/Experimental source: strain H37RV
C/Genetics:
A/Gene: RV2438c

Query Match 76.0%; Score 38; DB 2; Length 738;
Best Local Similarity 71.4%; Pred. No. 53; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
Db 655 ERGNWP 661

RESULT 24
H96545
hypothetical protein F8A12.11 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: H96545
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, A.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: H96545
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-788 <STO>
A/Cross-references: UNIPROT:Q9C6J1; UNIPARC:UPI000009EC58; GB:AE005173; NID:g11094685;
C/Genetics:
A/Gene: F8A12.11
A/Map position: 1
C/Superfamily: Arabidopsis thaliana hypothetical protein T24A18.10

Query Match 76.0%; Score 38; DB 2; Length 788;

```
Best Local Similarity 62.5%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 462 ENRGNWPP 469

RESULT 25
S40379
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40379
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40379
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: UNIPARC:UPI0000116181; EMBL:X72489; NID:G441446; PIDN:CAA51157.1; P1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:36-110/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 37; DB 2; Length 128;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWP 7
Db 109 QQRSKWP 115

RESULT 26
T23734
hypochemical protein M05D6.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23734
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19791
A:Accession: T23734
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-429 <WIL>
A:Cross-references: UNIPROT:Q21523; UNIPARC:UPI000007F5BF; EMBL:Z66523; PIDN:CAA91413.1;
A:Experimental source: clone M05D6
C:Genetics:
A:Gene: CESP:M05D6.4
A:Map position: 2.
A:Introns: 51/2; 225/1; 291/3; 370/3

Query Match 74.0%; Score 37; DB 2; Length 429;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 176 QQVFNWPP 183

RESULT 27
C69493
hypochemical protein AF1948 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: C69493
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
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Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: C69493
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-816 <KLE>
A:Cross-references: UNIPROT:Q28331; UNIPARC:UPI0000056B16; GB:AE000968; GB:AE000782; N1C

Query Match 74.0%; Score 37; DB 2; Length 816;
Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RSNWPP 8
Db 775 RTNWPP 780

RESULT 28
S16830
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16830
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16830
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176DA9; EMBL:X54828
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 36; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNW 6
Db 80 QQRSNW 85

RESULT 29
S16833
Ig kappa chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16833; S16838
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16833
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54831
A:Experimental source: clone bkiv17
A:Accession: S16838
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLW>
A:Cross-references: UNIPARC:UPI0000176DA7; EMBL:X54836
A:Experimental source: clone elkv14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 36; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNW 6
| | | | |
Db 80 QQRSNW 85

RESULT 30

S37521

Ig kappa chain V region (V-kappa 3) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37521

R;Klein, U.; Kueppers, R.; Rajewsky, K.

submitted to the EMBL Data Library, September 1993

A;Description: Human IGM(+)IgD(+) cells, the major B cell subset in the peripheral blood

A;Reference number: S37501

A;Accession: S37521

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-91 <KLE>

A;Cross-references: UNIPARC:UPI0000116587; EMBL:Z26623; NID:G405684; PIDN:CAA81376.1; PI

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 72.0%; Score 36; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNW 6
| | | | |
Db 72 QQRSNW 77

RESULT 31

S17626

Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S17626

R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A;Title: Making antibody fragments using phage display libraries.

A;Reference number: S17230; MUID:91326098; PMID:1907718

A;Accession: S17626

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-91 <CLA>

A;Cross-references: UNIPARC:UPI00001767F2

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;8-81/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 36; DB 2; Length 91;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | |
Db 80 QQRSSYP 87

RESULT 32

S11697

Ig kappa chain precursor V-III region - human

C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S11697

R;Pech, M.; Smola, H.; Pohlens, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.

J. Mol. Biol. 183, 291-299, 1985

A;Title: A large section of the gene locus encoding human immunoglobulin variable region

A;Reference number: S11697; MUID:85264787; PMID:3927006

A;Accession: S11697

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-115 <PEC>

A;Cross-references: UNIPARC:UPI0000115E41; EMBL:X17264; NID:G37898; PIDN:CAA35168.1; PID

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 36; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNW 6
| | | | |
Db 109 QQRSNW 114

RESULT 33

PL0013

Ig kappa chain precursor V region (4C11) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C;Accession: PL0013

R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.

Mol. Immunol. 25, 33-40, 1988

A;Title: Structural basis of stimulatory anti-idiotypic antibodies.

A;Reference number: PL0011; MUID:88142863; PMID:3125424

A;Accession: PL0013

A;Molecule type: mRNA

A;Residues: 1-140 <CHE>

A;Cross-references: UNIPARC:UPI00001767A6

A;Experimental source: cell line 4C11

C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-22/Domain: signal sequence #status predicted <SIG>

F;21-129/Product: Ig heavy chain V region (4C11) #status predicted <MAT>

F;38-111/Domain: immunoglobulin homology <IMM>

F;46-55/Region: complementarity-determining 1

F;71-77/Region: complementarity-determining 2

F;110-118/Region: complementarity-determining 3

F;130-140/Domain: constant region (fragment) #status predicted <COR>

Query Match 72.0%; Score 36; DB 2; Length 140;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
| | | | |
Db 110 QQRSSYP 117

RESULT 34

S66097

cell-cycle protein homolog yacA - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004

C;Accession: S66097; D69740

R;Ogasawara, N.; Nakai, S.; Yoshikawa, H.

DNA Res. 1, 1-14, 1994

A;Title: Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chrom

A;Reference number: S65967; MUID:96051385; PMID:7584024

A;Accession: S66097

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-486 <OGA>

A;Cross-references: UNIPROT:P37563; UNIPARC:UPI000016E923; EMBL:D26185; NID:g467326; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bexte C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrazi, E. Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seroz akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrast, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: D69740
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 'M', 16-486 <KUN>
 A;Cross-references: UNIPARC:UPI000005FDF1; GB:Z99104; GB:AL009126; NID:g2632267; PIDN:CA
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: yacA
 C;Superfamily: cell cycle control PP-loop ATPase MesJ/YaeO

Query Match 72.0%; Score 36; DB 2; Length 486;
 Best Local Similarity 71.4%; Pred. No. 78;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QORSNWP 7
 Db 433 QORDNWP 439
 RESULT 35
 T09046
 proline-rich protein F26K10.180 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T09046
 R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro submitted to the Protein Sequence Database, June 1999
 A;Reference number: Z16533
 A;Accession: T09046
 A;Molecule type: DNA
 A;Residues: 1-508 <BEV>
 A;Cross-references: UNIPROT:Q9MOH8; UNIPARC:UPI00000A8723; EMBL:AL049803; GSPDB:GN00062;
 A;Experimental source: cultivar Columbia; BAC clone F26K10
 C;Genetics:
 A;Gene: ATSP:F26K10.180
 A;Map position: 4
 A;Introns: 52/3; 160/3

Query Match 72.0%; Score 36; DB 2; Length 508;
 Best Local Similarity 62.5%; Pred. No. 82;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QORSNWP 8
 Db 304 QYQONWPP 311

RESULT 36
 B29813
 174K ninaC protein - fruit fly (*Drosophila melanogaster*)
 N;Contains: protein kinase (EC 2.7.1.-)
 C;Species: *Drosophila melanogaster*
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C;Accession: B29813
 R;Montell, C.; Rubin, G.M.

Cell 52, 757-772, 1998
 A;Title: The *Drosophila* ninaC locus encodes two photoreceptor cell specific proteins wit A;Reference number: A90898; MUID:88151067; PMID:2449973
 A;Accession: B29813
 A;Molecule type: mRNA
 A;Residues: 1-1501 <MON>
 A;Cross-references: UNIPROT:P10676; UNIPARC:UPI000016BCC3; GB:M20230; NID:gl57967; PIDN: C;Genetics:
 A;Gene: FlyBase:ninaC
 A;Cross-references: FlyBase:FBgn0002938
 C;Superfamily: ninaC protein; myosin motor domain homology; protein kinase homology
 C;Keywords: actin binding; alternative splicing; ATP; nucleotide binding; P-loop; phosph F;14-282/Domain: protein kinase homology <KIN>
 F;135-1022/Domain: myosin motor domain homology <MMOT>
 F;425-432/Region: nucleotide-binding motif A (P-loop)
 F;911-936/Region: actin binding #status Predicted
 F;1054-1501/Domain: carboxyl-terminal <CBT>
 F;45-60.145/Active site: Lys, Glu, Asp #status predicted
 F;431/Binding site: ATP (Lys) #status predicted

Query Match 72.0%; Score 36; DB 1; Length 1501;
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWP 8
 Db 1352 QORSNWP 1359

RESULT 37

S71461

proline-rich protein Rad9 - inky cap (*Coprinus cinereus*)C;Species: *Coprinus cinereus*

C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004

C;Accession: S71461; S78194

R;Seitz, L.C.; Tang, K.; Cummings, W.J.; Zolan, M.E.

Genetics 142, 1105-1117, 1996

A;Title: The rad9 gene of *Coprinus cinereus* encodes a proline-rich protein required for A;Reference number: S71461; MUID:96271528; PMID:8846891

A;Accession: S71461

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-2157 <SEI>

A;Cross-references: UNIPROT:Q00333; UNIPARC:UPI000006C489; EMBL:U34998; NID:gl353389; PI

A;Accession: S78194

A;Molecule type: mRNA

A;Residues: 1-2157 <SET>

C;Cross-references: UNIPARC:UPI000006C489; GB:U34998; NID:gl353389; PIDN: AAC49309.1; PID

C;Genetics:

A;Gene: rad9

A;Introns: 65/1; 151/2; 433/3; 472/1; 685/3; 844/3; 878/2; 1080/1; 1114/3; 1182/2; 1246/

/2; 2054/3

C;Keywords: DNA repair; meiosis

F;607-616/Region: nuclear location signal

Query Match 72.0%; Score 36; DB 2; Length 2157;
 Best Local Similarity 85.7%; Pred. No. 3.5e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWP 7
 Db 159 QOPSNWP 165

RESULT 38

T51023

hypothetical protein B7F21.40 [imported] - *Neurospora crassa*C;Species: *Neurospora crassa*

C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004

C;Accession: T51023

R;Schulze, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000

A;Reference number: Z25286

A;Accession: T51023
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2649 <SCH>
A;Cross-references: UNIPROT:Q9P3J0; UNIPARC:UPI0000017B4B0; EMBL:AL389901; GSPDB:GN00116;
A;Experimental source: BAC clone B7F21; strain OR74A
C;Genetics:
A;Gene: NCSP:B7F21.40
A;Map position: 6
A;Introns: 1619/3; 2584/1

Query Match 72.0%; Score 36; DB 2; Length 2649;
Best Local Similarity 62.5%; Pred. NO. 4.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 2251 QQQGWPP 2258

RESULT 39

PC4282
Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: PC4282; PC4284
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A;Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin
A;Reference number: PC4279; MUID:97236289; PMID:9125110
A;Accession: PC4282
A;Molecule type: protein
A;Residues: 1-106 <SU2>
A;Cross-references: UNIPARC:UPI00000176E92
A;Note: E-42
A;Accession: PC4284
A;Molecule type: protein
A;Residues: 1-106 <SU2>
A;Cross-references: UNIPARC:UPI00000176E92
A;Note: E-56
C;Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;14-88/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 35; DB 2; Length 106;
Best Local Similarity 71.4%; Pred. NO. 25;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 7
Db 87 QQRASWP 93

RESULT 40

S40344
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40344
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40344
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000011615E; EMBL:X72454; NID:G441376; PIDN:CAA51122.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 35; DB 2; Length 125;

Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 7
Db 109 QQRSYWP 115

Search completed: December 14, 2005, 07:31:54
Job time : 9.68966 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:28 ; Search time 43.1724 Seconds
(without alignments)
130.737 Million cell updates/sec

Title: US-10-720-323-6

Perfect score: 50

Sequence: 1 QQRSNWPP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_05_80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	86.0	115	1 KV31 HUMAN	P04433 homo sapien
2	42	84.0	271	2 Q7ACK8 GEOSL	Q7ACK8 geobacter s
3	41	82.0	2528	1 Q92217 COCHE	Q92217 cochllobolu
4	40	80.0	108	1 KV1M HUMAN	P01605 homo sapien
5	40	80.0	109	1 KV3F HUMAN	P01624 homo sapien
6	40	80.0	129	1 KV3H HUMAN	P04207 homo sapien
7	39	78.0	737	1 EXT1C_BRARE	Q5596 brachydanio
8	38	76.0	176	2 Q8RVH6 GROS1	Q8RVH6 populus tre
9	38	76.0	255	2 Q5B394 EMENI	Q5B394 aspergillus
10	38	76.0	532	2 Q00069 ASCIM	Q00069 ascobolus i
11	38	76.0	679	1 NADE MYCBO	P0517 mycobacteri
12	38	76.0	679	1 NADE MYCTU	P0516 mycobacteri
13	38	76.0	687	2 Q8AME0 DESPS	Q8AME0 desulfotale
14	38	76.0	788	2 Q9C6J1 ARATH	Q9C6J1 arabidopsis
15	38	76.0	2135	2 Q4S258 TETNG	Q4S258 tetraodon n
16	37	74.0	112	2 Q4K508 PSEF5	Q4K508 pseudomonas
17	37	74.0	112	2 Q8QRO0 PSEPK	Q8QRO0 pseudomonas
18	37	74.0	184	2 Q96CG3 HUMAN	Q96CG3 homo sapien
19	37	74.0	189	2 Q99IU7_92ZZZ	Q99IU7 uncultured
20	37	74.0	239	2 Q8BRN8 MOUSE	Q8BRN8 mus musculu
21	37	74.0	287	2 Q84JCO ARATH	Q84JCO arabidopsis
22	37	74.0	310	2 Q9FM44 ARATH	Q9FM44 arabidopsis
23	37	74.0	388	2 Q6ZV70 HUMAN	Q6ZV70 homo sapien
24	37	74.0	419	2 Q62L7L CAEBR	Q62L7L caenorhabdi
25	37	74.0	420	2 Q8CD19_MOUSE	Q8CD19 mus musculu
26	37	74.0	429	2 Q21523 CAEBL	Q21523 caenorhabdi
27	37	74.0	524	2 Q99YTI BACTN	Q99YTI bacteroides
28	37	74.0	731	2 Q5BGB8 EMENI	Q5BGB8 aspergillus
29	37	74.0	762	2 Q41MM5_GIBZE	Q41MM5 gibberella
30	37	74.0	796	2 Q7Q3S0_ANOGA	Q7Q3S0 anopheles g
31	37	74.0	816	2 Q28331_ARCFU	Q28331 archaeoglob

32	74.0	2568	2	Q5A4M0_CANAL	Q5A4M0 candida alb
33	74.0	4108	2	Q89U49_BRAJA	Q89U49 bradyrhizob
34	72.0	77	2	Q8RY18_ORYSA	Q8RY18 oryza sativ
35	72.0	121	2	Q51ZM4_MAGGR	Q51ZM4 magnaporthe
36	72.0	155	2	Q9HAG2_HUMAN	Q9HAG2 homo sapien
37	72.0	184	2	Q8WY67_HUMAN	Q8WY67 homo sapien
38	72.0	219	2	Q5TQ22_ANOGA	Q5TQ22 anopheles g
39	72.0	289	2	Q7Q5J5_ANOGA	Q7Q5J5 anopheles g
40	72.0	314	2	Q4PCJ6_USTMA	Q4PCJ6 ustilago ma
41	72.0	373	2	Q56949_HPV10	Q56949 human papil
42	72.0	385	2	Q7NL38_GLOVI	Q7NL38 gloeobacter
43	72.0	420	2	Q69MG4_ORYSA	Q69MG4 oryza sativ
44	72.0	463	2	Q52KW5_XENLA	Q52KW5 xenopus lae
45	72.0	468	2	Q6NUG9_RHOPA	Q6NUG9 rhodopseudo
46	72.0	472	1	TILS_BACSU	P37563 bacillus su
47	72.0	496	2	Q8VZR8_ARATH	Q8VZR8 arabidopsis
48	72.0	508	2	Q9M0H8_ARATH	Q9M0H8 arabidopsis
49	72.0	612	2	Q8RUM5_ORYSA	Q8RUM5 oryza sativ
50	72.0	612	2	Q941S9_ORYSA	Q941S9 oryza sativ
51	72.0	616	2	Q5KPK5_CRYNE	Q5KPK5 cryptococcu
52	72.0	689	2	Q4IR75_GIBZE	Q4IR75 gibberella
53	72.0	708	2	Q8SX98_DROME	Q8SX98 drosophila
54	72.0	751	2	Q8MLU0_DROME	Q8MLU0 drosophila
55	72.0	761	2	Q7KVL6_DROME	Q7KVL6 drosophila
56	72.0	764	2	Q4WVA7_ASPFU	Q4WVA7 aspergillus
57	72.0	844	2	Q5WRN0_CAEBL	Q5WRN0 caenorhabdi
58	72.0	856	2	Q6ZQD1_MOUSE	Q6ZQD1 mus musculu
59	72.0	923	2	Q441L5_GIBZE	Q441L5 gibberella
60	72.0	990	2	Q560K8_CRYNE	Q560K8 cryptococcu
61	72.0	1012	2	Q54KC6_DICDI	Q54KC6 dictyosteli
62	72.0	1059	2	Q8C5X1_MOUSE	Q8C5X1 mus musculu
63	72.0	1059	2	Q6PAL5_MOUSE	Q6PAL5 mus musculu
64	72.0	1070	1	Y0355_HUMAN	Q15063 homo sapien
65	72.0	1070	2	Q5REB5_PONPY	Q5REB5 pongo pygma
66	72.0	1070	2	Q4R3A1_WACPA	Q4R3A1 macaca fasc
67	72.0	1501	1	NINAC_DROME	P10676 drosophila
68	72.0	1696	2	Q6JDF3_XENLA	Q6JDF3 xenopus lae
69	72.0	2032	2	Q6JUM2_AEDAE	Q6JUM2 aedes aegypt
70	72.0	2157	1	NPBL_COPCI	Q00333 coprinus ci
71	72.0	2592	2	Q9P3J0_NEUCR	Q9P3J0 neurospora
72	72.0	73	2	Q9VLG1_BACSU	Q9VLG1 bacillus su
73	70.0	87	2	Q6K614_ORYSA	Q6K614 oryza sativ
74	70.0	109	2	Q5UL85_HUMAN	Q5UL85 homo sapien
75	70.0	126	2	Q93TD7_PSEYM	Q93TD7 pseudomonas
76	70.0	126	2	Q4ZWE6_PSESY	Q4ZWE6 pseudomonas
77	70.0	126	2	Q87WE1_PSESM	Q87WE1 pseudomonas
78	70.0	127	2	Q7NPR8_CHROV	Q7NPR8 chromobacte
79	70.0	133	2	Q28134_BOVIN	Q28134 bos taurus
80	70.0	137	2	Q6ZOT0_ORYSA	Q6ZOT0 oryza sativ
81	70.0	139	2	Q6DFZ6_BRARE	Q6DFZ6 brachydanio
82	70.0	145	1	RX18_PEA	P11891 pisum sativ
83	70.0	155	2	Q981I5_RHILO	Q981I5 rhizobium l
84	70.0	170	2	Q4Y1B6_PLACH	Q4Y1B6 plasmodium
85	70.0	180	2	Q4N9V7_THEPA	Q4N9V7 theileria p
86	70.0	203	1	COX3_NOCFA	Q5Y119 nocardia fa
87	70.0	206	2	Q6IAO3_HUMAN	Q6IAO3 homo sapien
88	70.0	206	2	Q9H616_HUMAN	Q9H616 homo sapien
89	70.0	206	2	Q96ED6_HUMAN	Q96ED6 homo sapien
90	70.0	222	2	Q6GY73_9NEOP	Q6GY73 mucrobacter
91	70.0	222	2	Q6GY94_9NEOP	Q6GY94 spilosmylus
92	70.0	223	1	CD79A_BOVIN	P40293 bos taurus
93	70.0	224	1	HES6_MOUSE	Q9Jhe6 mus musculu
94	70.0	234	2	Q5PPN0_RAT	Q5PPN0 rattus norv
95	70.0	249	2	Q9AGU6_PSEBX	Q9AGU6 pseudomonas
96	70.0	260	2	Q61W46_CAEBR	Q61W46 caenorhabdi
97	70.0	261	2	Q897G9_9HEMI	Q897G9 aleurochito
98	70.0	263	2	Q5D003_RAT	Q5D003 rattus norv
99	70.0	277	2	Q5GX20_XANOR	Q5GX20 xanthomonas
100	70.0	277	2	Q7VD52_PROMA	Q7VD52 prochloroco

ALIGNMENTS

```
RESULT 1
KV31 HUMAN
ID _KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within
the VK locus.";
RL Nucleic Acids Res. 12:9229-9236 (1984).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC NOT_ANNOTATED_CDS; Genomic_DNA.
DR EMBL; X01668; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR PIR; A01900; K3HUVG.
DR HSSP; P01625; 1EEQ.
DR SMR; P04433; 21-115.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV; 1_v.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 Ig kappa chain V-III region VG.
FT REGION 21 43 Framework-1.
FT REGION 44 54 Complementarity-determining-1.
FT REGION 55 69 Framework-2.
FT REGION 70 76 Complementarity-determining-2.
FT REGION 77 108 Framework-3.
FT REGION 109 115 Complementarity-determining-3.
FT DISULFD 43 108 By similarity.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 86.0%; Score 43; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QQRSNWP 7
Db 109 QQRSNWP 115

RESULT 2
Q74CK8 GEOSL
ID Q74CK8 GEOSL PRELIMINARY; PRT; 271 AA.
AC Q74CK8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Rhomboid family protein.
OS OrderedLocustNames=GSU1665;
OC Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.

Query Match 86.0%; Score 43; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QQRSNWP 7
Db 109 QQRSNWP 115
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OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=PCA / ATCC 51573;
RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupati R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Winn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Uutterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
environments.";
RL Science 302:1967-1969 (2003).
DR EMBL; AE017180; AAR35043.1; -; Genomic_DNA.
DR TIGR; GSU1665; -.
DR InterPro; IPR002610; Rhomboid_like.
DR Pfam; PF01694; Rhomboid; 1.
KW Complete proteome.
SQ SEQUENCE 271 AA; 28632 MW; 0B86DEDB16E54AB5 CRC64;

Query Match 84.0%; Score 42; DB 2; Length 271;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQRSNWP 8
Db 33 QQRSNWP 40

RESULT 3
Q92217 COCHE
ID Q92217 COCHE PRELIMINARY; PRT; 2528 AA.
AC Q92217;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyketide synthase.
GN Name=PKS1;
OS Cochliobolus heterostrophus (Drechslera maydis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5016;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C4;
RX MEDLINE=97112040; PubMed=8953776; DOI=10.1105/tpc.8.11.2139;
RA Yang G., Rose M.S., Turgeon B.G., Yoder O.C.;
RT "A polyketide synthase is required for fungal virulence and production
of the polyketide T-toxin.";
RL Plant Cell 8:2139-2150 (1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C4;
RA Turgeon B.G.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U68040; AAB08104.2; -; Genomic_DNA.
DR HSSP; P96202; IPQM.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac transferase.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR000794; ketoacyl_synth.
DR InterPro; IPR006163; Phspanteth_bind.
DR InterPro; IPR006162; Ppantnf_S.
DR Pfam; PF00698; Acyl_transf_1; 1.
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DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR PROSITE; PS50075; ACP DOMAIN; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN 1.
SQ SEQUENCE 2528 AA; 275260 MW; D58D4FD59C1075F7 CRC64;

Query Match      82.0%; Score 41; DB 2; Length 2528;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 2237 EARSNWPP 2244

RESULT 4
KVLM_HUMAN
ID_KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IGM
anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
RN [2]
RP PROTEIN SEQUENCE OF 1-104.
RX MEDLINE=89215279; PubMed=2496160;
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
Goni F.R., Solomon A., Mendez E., Frangione B.;
RA Carson D., Solomon A., Mendez E., Frangione B.;
RT "Structural and idiotypic characterization of the L chains of human
IGM autoantibodies with different specificities.";
RL J. Immunol. 142:3158-3163(1989).
RN [3]
RP ERRATUM.
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
RA Carson D., Solomon A., Mendez E., Frangione B.;
RL J. Immunol. 143:3864-3864(1989).
CC -!- MISCELLANEOUS: The second and third hypervariable regions of this
chain are identical with those of the human POM V-III kappa chain,
with which it shares certain idiotypic determinants.
CC -!- MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma
globulin activity.
-----
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-----
PIR; A01871; KIHULY.
DR HSSP; P01607; 1BWV.
DR SMR; P01605; 1-108.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
IMMUNOGLOBULIN V region.
KVLM_HUMAN 23
DIISULFID 89
FT NON TER 109 109 By similarity.
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match      80.0%; Score 40; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 89 QQYNNWPP 96

RESULT 5
KV3F_HUMAN
ID_KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: This chain was isolated from an IGM with anti-gamma
globulin activity.
-----
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-----
PIR; A01897; K3HUPM.
DR HSSP; P01625; 1LVE.
DR SMR; P01624; 1-109.
GO; GO:0005576; C:extracellular region; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain;
IMMUNOGLOBULIN V region.
KV3F_HUMAN 23
DIISULFID 89
FT NON TER 109 109 By similarity.
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match      80.0%; Score 40; DB 1; Length 109;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 90 QQYNNWPP 97

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DE 1 homolog c).
GN Name-extlc;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND DEVELOPMENTAL STAGE.
RX PubMed=15614771; DOI=10.1002/dvdy.20248;
RA Stekman A.F., Brand M.;
RT "Distinct tissue-specificity of three zebrafish extl genes encoding
RT proteoglycan modifying enzymes and their relationship to somitic Sonic
RT hedgehog signaling.";
RL Dev. Dyn. 232:498-505(2005).
CC -1- FUNCTION: Glycosyltransferase required for the biosynthesis of
CC heparan-sulfate (By similarity).
CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + beta-D-
CC glucuronosyl-(1->4)-N-acetyl-alpha-D-glucosaminyl-proteoglycan =
CC UDP + N-acetyl-alpha-D-glucosaminyl-(1->4)-beta-D-glucuronosyl-
CC (1->4)-N-acetyl-alpha-D-glucosaminyl-proteoglycan.
CC -1- CATALYTIC ACTIVITY: UDP-alpha-D-glucuronate + N-acetyl-alpha-D-
CC glucosaminyl-(1->4)-beta-D-glucuronosyl-proteoglycan = UDP + beta-
CC D-glucuronosyl-(1->4)-N-acetyl-alpha-D-glucosaminyl-(1->4)-beta-D-
CC glucuronosyl-proteoglycan.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed zygotically. First detected at the
CC beginning of somitogenesis. At the 16-somite stage, restricted to
CC posterior adaxial cells and, in the anterior, to cells adjacent to
CC the neural tube and to ventromedial regions of the somites. At 24
CC hours-post-fertilization (hpf), expressed in the ventral
CC rhombomeres, telencephalon and olfactory bulbs. At 48 hpf,
CC expressed in the brain, retina and fin buds.
CC -1- SIMILARITY: Belongs to the glycosyltransferase 47 family.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY734457; AAW29035.1; -; mRNA.
CC ZFIN; ZDB-GENE-050211-5; extlc.
CC GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
CC GO; GO:0050508; F:glucuronosyl-N-acetylglucosaminyl-proteogly. . .; ISS.
CC GO; GO:0050509; F:N-acetylglucosaminyl-proteoglycan 4-beta-gl. . .; ISS.
CC GO; GO:0015012; P:heparan sulfate proteoglycan biosynthesis; ISS.
CC InterPro; IPR004263; Exostosin.
CC Pfam; PF03016; Exostosin; 1.
CC Endoplasmic reticulum; Glycoprotein; Glycosyltransferase;
CC Signal-anchor; Transmembrane.
CC TOPO_DOM 1 6 Cytoplasmic (Potential).
CC TRANSMEM 7 27 Signal-anchor for type II membrane
CC protein (Potential).
CC TOPO_DOM 28 737 Luminal (Potential).
CC CARBOHYD 194 194 N-linked (GLCNAc. . .) (Potential).
CC CARBOHYD 322 322 N-linked (GLCNAc. . .) (Potential).
CC SQ SEQUENCE 737 AA; 85389 MW; 349EB644FB7AADB4 CRC64;

Query Match 78.0%; Score 39; DB 1; Length 737;
Best Local Similarity 85.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSNWPP 8
Db 517 QRSKWPP 523

RESULT 8
Q8RVH6_9ROSI
ID Q8RVH6_9ROSI PRELIMINARY; PRT; 176 AA.
AC Q8RVH6;

DE 1 homolog c).
GN Name-extlc;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], AND DEVELOPMENTAL STAGE.
RX PubMed=15614771; DOI=10.1002/dvdy.20248;
RA Stekman A.F., Brand M.;
RT "Distinct tissue-specificity of three zebrafish extl genes encoding
RT proteoglycan modifying enzymes and their relationship to somitic Sonic
RT hedgehog signaling.";
RL Dev. Dyn. 232:498-505(2005).
CC -1- FUNCTION: Glycosyltransferase required for the biosynthesis of
CC heparan-sulfate (By similarity).
CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + beta-D-
CC glucuronosyl-(1->4)-N-acetyl-alpha-D-glucosaminyl-proteoglycan =
CC UDP + N-acetyl-alpha-D-glucosaminyl-(1->4)-beta-D-glucuronosyl-
CC (1->4)-N-acetyl-alpha-D-glucosaminyl-proteoglycan.
CC -1- CATALYTIC ACTIVITY: UDP-alpha-D-glucuronate + N-acetyl-alpha-D-
CC glucosaminyl-(1->4)-beta-D-glucuronosyl-proteoglycan = UDP + beta-
CC D-glucuronosyl-(1->4)-N-acetyl-alpha-D-glucosaminyl-(1->4)-beta-D-
CC glucuronosyl-proteoglycan.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Endoplasmic
CC reticulum (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed zygotically. First detected at the
CC beginning of somitogenesis. At the 16-somite stage, restricted to
CC posterior adaxial cells and, in the anterior, to cells adjacent to
CC the neural tube and to ventromedial regions of the somites. At 24
CC hours-post-fertilization (hpf), expressed in the ventral
CC rhombomeres, telencephalon and olfactory bulbs. At 48 hpf,
CC expressed in the brain, retina and fin buds.
CC -1- SIMILARITY: Belongs to the glycosyltransferase 47 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; M12740; AAA58992.1; -; Genomic_DNA.
CC HSSP; P01625; LLVE.
CC SMR; P04207; 21-129.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin domain; Immunoglobulin V region; Signal.
CC SIGNAL 1 20
CC CHAIN 21 129 Ig kappa chain V-III region CLL.
CC REGION 21 43 Framework-1.
CC REGION 44 54 Complementarity-determining-1.
CC REGION 55 69 Framework-2.
CC REGION 70 76 Complementarity-determining-2.
CC REGION 77 108 Framework-3.
CC REGION 109 118 Complementarity-determining-3.
CC REGION 119 129 Jk1 segment.
CC DISULFID 43 108 By similarity.
CC NON_TER 129 129
CC SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 80.0%; Score 40; DB 1; Length 129;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQRSNWPP 8
Db 109 QQYNNWPP 116

RESULT 7
EXTIC BRARE
ID EXTIC BRARE STANDARD; PRT; 737 AA.
AC Q51GR6;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Exostosin-1c (EC 2.4.1.224) (EC 2.4.1.225) (Glucuronosyl-N-
DE acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-
DE alpha-N-acetylglucosaminyltransferase 1c) (Multiple exostosin protein
```

DT 01-JUN-2002 (TremBLrel. 21, Created)
 DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Aux/IAA protein.
 GN Name=IAA4;
 OS Populus tremula x Populus tremuloides.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosids; eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=47664;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cambial region;
 RA Schrader J., Moyle R., Stenberg A., Olsson O., Sandberg G.,
 RA Bhallerao R.P.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ306827; CAC84708.1; -; mRNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0046983; P:protein dimerization activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006445; P:regulation of translation; IEA.
 DR InterPro; IPR011525; AuxIAA_ARF_dimer.
 DR InterPro; IPR003311; AUX IAA.
 DR Pfam; PF02309; AUX IAA; 1.
 DR PROSITE; PS05962; IAA ARF; 1.
 SQ SEQUENCE 176 AA; 15641 MW; E3EF5E0BC6599553 CRC64;

 Query Match 76.0%; Score 38; DB 2; Length 176;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 1 QQRSNWPP 8
 DB 58 QQLSDWPP 65

 RESULT 9
 ID Q5B394_EMENI PRELIMINARY; PRT; 255 AA.
 AC Q5B394;
 DT 10-MAY-2005 (TremBLrel. 30, Created)
 DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN4986.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
 RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataranan V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,

RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACD01000084; EAA61064.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 255 AA; 28504 MW; 4B13955E977CA447 CRC64;

 Query Match 76.0%; Score 38; DB 2; Length 255;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 QQRSNWPP 8
 DB 20 QQPPNWPP 27

 RESULT 10
 ID Q00069_ASCIM PRELIMINARY; PRT; 532 AA.
 AC Q00069;
 DT 01-NOV-1996 (TremBLrel. 01, Created)
 DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
 DE Zinc finger protein.
 OS Ascombolus immersus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
 OC Pezizales; Ascobolaceae; Ascobolus.
 OX NCBI_TaxID=5191;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RN42;
 RA Goyon C.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X99094; CAA67549.1; -; Genomic_DNA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0008270; P:zinc ion binding; IEA.
 DR InterPro; IPR007087; ZnF_C2H2.
 DR SMART; SM00355; ZnF_C2H2; 4.
 SQ SEQUENCE 532 AA; 58367 MW; B97A7B7C66D8887A CRC64;

 Query Match 76.0%; Score 38; DB 2; Length 532;
 Best Local Similarity 62.5%; Pred. No. 4.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 QQRSNWPP 8
 DB 458 KKRKNWPP 465

 RESULT 11
 ID NADE_MYCBO STANDARD; PRT; 679 AA.
 AC POA5L7; P71911;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) (NAD(+) synthase
 DE [Glutamine-hydrolyzing]).
 GN Name=nade; OrderedLocNames=Mb2464c;
 OS Mycobacterium bovis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
 OC Mycobacterium tuberculosis complex.
 OX NCBI_TaxID=1765;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=AF2122/97;
 RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
 RA Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,

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RA Prvor M., Duchoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Ackin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewison R.G.;
RA "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
CC -1- FUNCTION: Can use both glutamine or ammonia as a nitrogen source
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + L-glutamine + H(2)O =
CC AMP + diphosphate + NAD(+) + L-glutamate.
CC -1- PATHWAY: NAD biosynthesis.
CC -1- SIMILARITY: In the C-terminal section; belongs to the NAD
CC synthetase family.
CC -1- SIMILARITY: Contains 1 CN hydrolase domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX248342; CAD97325.1; -; Genomic_DNA.
DR HAWAP; MF_00193; fused; 1.
DR InterPro; IPR003694; NAD_synthase.
DR Pfam; PF00795; CN_hydrolase; 1.
DR Pfam; PF02540; NAD_synthase; 1.
DR TIGRFAMs; TIGR00552; nadE; 1.
DR PROSITE; PS0263; CN_HYDROLASE; 1.
DR ATP-binding; Complete proteome; Ligase; NAD; Nucleotide-binding.
FT DOMAIN 12 298
FT NP_BIND 366 373 ATP (By similarity).
FT REGION 337 679 Ligase.
FT ACT_SITE 368 368 By similarity.
SQ SEQUENCE 679 AA; 74683 MW; 14AC29CE434A8B0D CRC64;

Query Match 76.0%; Score 38; DB 1; Length 679;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
Db 596 ERGNWP 602

RESULT 12
NADE MYCTU STANDARD; PRT; 679 AA.
AC POA5L6; P71911;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) (NAD(+) synthase
DE [glutamine-hydrolyzing]).
DE Name=nadE; OrderedLocusNames=Rv2438c, MT2513; ORFNames=MTCY428.08;
GN Mycobacterium tuberculosis.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=H37Rv;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA Harris D.E., Gordon S.V., Eiglmeter K., Gas S., Barry C.B. III,
RA Tekaiia F., Badcock K., Basham D., Brown D., Chillingworth T.,
RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA Rogers J., Rutter S., Seeger K., Skelton S., Squares R.,
RA Sultston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence."

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RL Nature 393:537-544 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CDC 1551 / Oshkosh;
RX DOI=10.1128/JB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Uterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98292757; PubMed=9620974;
RA Cantoni R., Branzoni M., Labo M., Rizzi M., Riccardi G.;
RT "The MTCY428.08 gene of Mycobacterium tuberculosis codes for NAD+
RT synthetase.";
RL J. Bacteriol. 180:3218-3221(1998).
CC -1- FUNCTION: Can use both glutamine or ammonia as a nitrogen source.
CC -1- CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + L-glutamine + H(2)O =
CC AMP + diphosphate + NAD(+) + L-glutamate.
CC -1- PATHWAY: NAD biosynthesis.
CC -1- SIMILARITY: In the C-terminal section; belongs to the NAD
CC synthetase family.
CC -1- SIMILARITY: Contains 1 CN hydrolase domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX842579; CAB03781.2; -; Genomic DNA.
DR EMBL; AE000516; AAK46810.1; ALT_INIT; Genomic_DNA.
DR TIGR; MT2513; -;
DR TubercuList; Rv2438c; -.
DR HAWAP; MF_00193; fused; 1.
DR InterPro; IPR003694; NAD_synthase.
DR Pfam; PF00795; CN_hydrolase; 1.
DR Pfam; PF02540; NAD_synthase; 1.
DR TIGRFAMs; TIGR00552; nadE; 1.
DR PROSITE; PS0263; CN_HYDROLASE; 1.
DR ATP-binding; Complete proteome; Ligase; NAD; Nucleotide-binding.
FT DOMAIN 12 298
FT NP_BIND 366 373 ATP (By similarity).
FT REGION 337 679 Ligase.
FT ACT_SITE 368 368 By similarity.
SQ SEQUENCE 679 AA; 74683 MW; 14AC29CE434A8B0D CRC64;

Query Match 76.0%; Score 38; DB 1; Length 679;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
Db 596 ERGNWP 602

RESULT 13
Q6AME0 DESPS
ID Q6AME0 DESPS PRELIMINARY; PRT; 687 AA.
AC Q6AME0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DPI756;
OS Desulfotalea psychrophila.

```

OC	Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC	Desulfobacterales; Desulfobacteraceae; Desulfotalea.
OX	NCBI_TaxID=84980;
[1]	
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=LSV54 / DSM 12343;
RA	PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RX	Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA	Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA	Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
KL	Klenk H.-P.;
RT	"The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT	from permanently cold Arctic sediments.";
RL	Environ. Microbiol. 6:887-902(2004).
DR	EMBL; CR522870; CAG36485.1; -; Genomic DNA.
KW	Complete proteome; Hypothetical protein.
SQ	SEQUENCE 687 AA; 77118 MW; 1CD38BEBF96FDA2D CRC64;
Query Match	76.0%; Score 38; DB 2; Length 687;
Best Local Similarity	100.0%; Pred. No. 5.4e+02;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	2 QRSNWP 7
DB	
	515 QRSNWP 520
RESULT 14	
Q9C6J1 ARATH	
ID	Q9C6J1_ARATH' PRELIMINARY; PRT; 788 AA.
AC	Q9C6J1;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Hypothetical protein F8A12.11.
GN	Name=F8A12.11;
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid II; Brassicales; Brassicaceae; Arabidoideae.
OX	NCBI_TaxID=3702;
[1]	
RP	NUCLEOTIDE SEQUENCE.
RA	Liu X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA	Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R.,
RA	Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL	Submitted (JAN-2001) to the ENML/GenBank/DBJ databases.
DR	EMBL; AC079284; AACG50927.1; -; Genomic_DNA.
DR	PIR; H96545; H96545.
DR	GO; GO:0005488; F-binding; IEA.
DR	GO; GO:0007076; P:mitotic chromosome condensation; IEA.
DR	InterPro; IPR011989; ARM-like.
DR	InterPro; IPR000357; HEAT.
DR	Fam; PF02985; HEAT; 2.
KW	Hypothetical protein.
SQ	SEQUENCE 788 AA; 86573 MW; 2D9C051B34F43066 CRC64;
Query Match	76.0%; Score 38; DB 2; Length 788;
Best Local Similarity	62.5%; Pred. No. 6.2e+02;
Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY	1 QORSNWPP 8
DB	:
	462 ENRGNWPP 469
RESULT 15	
Q4SZ58 TEING	
ID	Q4SZ58_TEING PRELIMINARY; PRT; 2135 AA.
AC	Q4SZ58;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)


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RA Mavrod D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Guinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L., III, Thomashow L., Loper J.,
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL: CP000076; AAY94809.1; -; Genomic DNA.
SQ SEQUENCE 112 AA; 12775 MW; 498847F69E9E938 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 112;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
Db 104 QRMNWPP 111

RESULT 17
Q88QRO PSEPK PRELIMINARY; PRT; 112 AA.
AC Q88QRO;
RA 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE HIT family protein.
GN OrderedLocusNames=PP0428;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfle E.K., Scanlan D., Tran K.,
RA Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL: AE016775; AAN66058.1; -; Genomic DNA.
DR HSSP; P80912; 4RHN.
DR TIGR; PP0428; -.
DR InterPro; IPR001310; HIT.
DR Pfam; PF01230; HIT; 1.
DR PIRSF; PIRSF000714; HIT; 1.
DR PRINTS; PR00332; HISTRIAD.
DR PROSITE; PS00892; HIT; 1.
KW Complete proteome.
SQ SEQUENCE 112 AA; 12728 MW; 74F9D250F9C8FAP CRC64;

Query Match 74.0%; Score 37; DB 2; Length 112;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
Db 104 QRMNWPP 111

RESULT 18
Q96CG3 HUMAN PRELIMINARY; PRT; 184 AA.
ID Q96CG3 HUMAN PRELIMINARY;
AC Q96CG3;
, DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE TFAP-interacting protein with a forkhead-associated domain (TIFA)
DE (Putative NPKB activating protein) (Putative MAPK activating protein)
DE (Hypothetical protein tmp_locus_4).
GN Name=TIFA; Synonyms=tifa, tmp_locus_4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1074/jbc.M300720200;
RA Takatuna H., Kato H., Gohda J., Akiyama T., Moriya A., Okamoto Y.,
RA Yamagata Y., Otsuka M., Umezawa K., Samba K., Inoue J.;
RT "Identification of TIFA as an adapter protein that links tumor
RT necrosis factor receptor-associated factor 6 (TRAF6) to interleukin-1
RT (IL-1) receptor-associated kinase-1 (IRAK-1) in IL-1 receptor
RT signaling."
RL J. Biol. Chem. 278:12144-12150(2003).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1038/sj.onc.1206406;
RA Matsuda A., Suzuki Y., Honda G., Muramatsu S., Matsuzaki O.,
RA Nagano Y., Doi T., Shimotohno K., Harada T., Nishida E., Hayashi H.,
RA Sugano S.;
RT "Large-scale identification and characterization of human genes that
RT activate NF-kappaB and MAPK signaling pathways."
RL Oncogene 22:3307-3318(2003).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1073/pnas.242603899;
RA Grewal N., Haglund K.;
RT "The sequence of Homo sapiens BAC clone RP11-73K9."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1073/pnas.242603899;
RA Waterston R.H.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX DOI=10.1073/pnas.242603899;
RA Waterston R.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [8]

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RN NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC014259; AAH14259.1; -; mRNA.
DR EMBL; AB062110; BAB86902.1; -; mRNA.
DR EMBL; AB097011; BAC77364.1; -; mRNA.
DR EMBL; AB097038; BAC77391.1; -; mRNA.
DR EMBL; AC109347; AAY40963.1; -; Genomic DNA.
DR Ensembl; ENSG00000145365; Homo sapiens.
DR InterPro; IPR000253; FHA.
DR Pfam; PF00498; FHA; 1.
DR SMART; SM00240; FHA; 1.
DR PROSITE; PS00006; FHA_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 184 AA; 21445 MW; 2B7FE091A52415B0 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 184;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSNWP 8
DB 150 QENWPP 156

RESULT 19
Q991U7 92ZZZ PRELIMINARY; PRT; 189 AA.
AC Q991U7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS unclassified organism.
OC unclassified; environmental samples.
OX NCBI_TaxID=155900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Stokes H.W., Nield B.S., Mabbutt B.C., Nevalainen H., Holmes A.J.,
RA Gillings M.R.;
RT "Novel and diverse integrin-like gene cassettes are prevalent in
RT natural environments.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349078; AAK28593.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 189 AA; 21176 MW; CID5341F9ADB56BB CRC64;

Query Match 74.0%; Score 37; DB 2; Length 189;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QRSNWP 8
DB 146 QRSNWP 152

RESULT 20
Q8BRN8_MOUSE PRELIMINARY; PRT; 239 AA.
AC Q8BRN8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone:A303039C13 product:hypothetical protein, full insert
DE sequence. (Fragment).
GN Name=Lanc13; Synonyms=6030463G20R1k;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staab F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium.
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa Y., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi S., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda J., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirakata T., Kasukawa T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
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RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sagaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayaishizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR ENMBL; AK043841; BAC31676.1; -; mRNA.
DR DR Ensembl; ENSMUSG0000047344; Mus musculus.
DR MGI; MGI:2443335; Lancel3.
DR MGI; MGI:2443335; Lancel3.
DR InterPro; IPR007822; LANC_like.
DR Pfam; PF05147; LANC_like; 1.
KW Hypothetical protein.
FT NON TR 1
SQ SEQUENCE 239 AA; 27320 MW; B4499C9733CC0759 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 239;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
Db 90 EQNCNWPP 97

RESULT 21
Q84JCO ARATH PRELIMINARY; PRT; 287 AA.
AC Q84JCO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At5g40530.
GN Name=At5g40530;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yanada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayaishizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yanada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayaishizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR ENMBL; BT002940; AA022753.1; -; mRNA.
DR ENMBL; BT004445; AA042439.1; -; mRNA.
DR InterPro; IPR007823; DUF691_mtranefer.
DR Pfam; PF05148; Methyltransf_8; 1.
KW Hypothetical protein.
SQ SEQUENCE 287 AA; 32760 MW; D108B51393E964DE CRC64;

Query Match 74.0%; Score 37; DB 2; Length 287;
Best Local Similarity 85.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWPP 7
Db 112 QQMSNWP 118

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RESULT 22
Q9FM44 ARATH PRELIMINARY; PRT; 310 AA.
AC Q9FM44;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarity to unknown protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:41-54 (1998).
DR ENMBL; AB009052; BAB08523.1; -; Genomic_DNA.
DR InterPro; IPR007823; DUF691_mtransfer.
DR Pfam; PF05148; Methyltransf_8; 1.
SQ SEQUENCE 310 AA; 35647 MW; 51B0C50B38D33324 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 310;
Best Local Similarity 85.7%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWPP 7
Db 112 QQMSNWP 118

RESULT 23
Q6ZV70 HUMAN PRELIMINARY; PRT; 388 AA.
AC Q6ZV70;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein FLJ42925 (Lanc lantibiotic synthetase component
DE C-like 3).
GN Name=LANCL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Maehuo Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Lung and heart;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehyunki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryewinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung and heart;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK124915; BAC05993.1; -; mRNA.
DR EMBL; BC093669; AA093669.1; -; mRNA.
DR EMBL; BC093667; AA093667.1; -; mRNA.
DR InterPro; IPR007822; LANC like.
DR Pfam; PF05147; LANC like; 1.
SQ SEQUENCE 388 AA; 42780 MW; C341A77B5F63AFA6 CRC64;
Query Match 74.0%; Score 37; DB 2; Length 388;
Best Local Similarity 62.5%; Pred. NO. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QQRSNWPP 8
Db 271 EQNCNWPP 278
RESULT 24
O627L7 CAEBR
ID Q627L7 CAEBR, PRELIMINARY; PRT; 419 AA.
AC Q627L7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG00618 (Fragment).
GN Name=CBG00618;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000005; CAB57633.1; -; Genomic DNA.
DR GO; GO:0046677; P:response to antibiotic; IEA.
DR InterPro; IPR001466; Beta lactamase.
DR Pfam; PF001144; Beta-lactamase; 1.
KW Hypothetical protein.1
FT NON_TBR 1
SQ SEQUENCE 419 AA; 48094 MW; 408F3DE8FD34P85 CRC64;
Query Match 74.0%; Score 37; DB 2; Length 419;
Best Local Similarity 71.4%; Pred. NO. 4.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 QQRSNWPP 8
Db 167 QKPNWPP 173

RESULT 25
Q8CD19 MOUSE
ID Q8CD19 MOUSE PRELIMINARY; PRT; 420 AA.
AC Q8CD19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE enriched library, clone:6030463G20 product:hypothetical protein, full
DE insert sequence.
DE Name=Lanc13; Synonym=6030463G20Rik;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyono-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Tanaka S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Kori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031623; BAC27495.1; -, mRNA.
DR Ensembl; ENSMUSG00000047344; Mus musculus.
DR MGI; MGI:2443335; 6030463G20rik.
DR MGI; MGI:2443335; Lancel3.
DR InterPro; IPR007822; LANC like.
DR Pfam; PF05147; LANC_like; 1.
KW Hypothetical protein.
SQ SEQUENCE 420 AA; 46445 MW; 4FFC2598BD7CD708 CRC64;
Query Match 74.0%; Score 37; DB 2; Length 420;
Best Local Similarity 62.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QQRSNWPP 8
Db 271 EQNCNWPP 278
RESULT 26
Q21523 CAEEL
ID Q21523 CAEEL PRELIMINARY; PRT; 429 AA.
AC Q21523;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein M05D6.4.
GN ORFNames=M05D6.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Bristol N2;
RC MEDLINE=95069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.",
RL Science 282:2012-2018(1998).
DR EMBL; Z66523; CAA91413.1; -, Genomic_DNA.
DR PIR; T23734; T23734.
DR Ensembl; M05D6.4; Caenorhabditis elegans.
DR WormBase; WBGene00010877; M05D6.4.
DR WormPep; M05D6.4; CS03502.
DR GO; GO:0046677; P:response to antibiotic; IEA.
DR InterPro; IPR01466; Beta lactamase.
DR InterPro; IPR012338; PBP lptpt fold.
DR Pfam; PF00144; Beta-lactamase1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 429 AA; 49128 MW; 08D762B3144C39E8 CRC64;
Query Match 74.0%; Score 37; DB 2; Length 429;
Best Local Similarity 75.0%; Pred. No. 4.9e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QQRSNWPP 8
Db 176 QQVFNWPP 183
RESULT 27
Q89YTL BACTN
ID Q89YTL BACTN PRELIMINARY; PRT; 524 AA.
AC Q89YTL;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Voltage-gated chloride channel protein.
DR Ordered locus names=BT4650;
GN Bacteroides thetaiotaomicron.
OS Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=VP1-5482 / ATCC 29148;
RC MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RX Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.",
RL Science 299:2074-2076(2003).
DR EMBL; AEO16946; AAO79755.1; -, Genomic DNA.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR001807; Cl-channel_volt.
DR InterPro; IPR006037; TrkAC.
DR Pfam; PF02080; TrkA_C; 1.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
KW Complete proteome.
SQ SEQUENCE 524 AA; 58516 MW; 92F960CF4DD82716 CRC64;
Query Match 74.0%; Score 37; DB 2; Length 524;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 QQRSNWPP 8
Db 483 RDRKNWPP 490
RESULT 28
Q5GB8 EMENI
ID Q5GB8 EMENI PRELIMINARY; PRT; 731 AA.
AC Q5GB8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AN0412.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelheil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,

RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Fero S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer B., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome Sequence of Aspergillus nidulans.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACD01000007; EAA66511.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 731 AA; 81032 MW; 80A499AA3858F87C CRC64;

Query Match 74.0%; Score 37; DB 2; Length 731;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RSNWPP 8
|:||||
Db 440 RTNWPP 445

RESULT 29
Q4IMWS_GIBZE
ID Q4IMWS_GIBZE PRELIMINARY; PRT; 762 AA.
AC Q4IMWS;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=EG01533.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Fero S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer B., Schupback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,

RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACW01000077; EAA68159.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 762 AA; 84643 MW; 4E2FA74798C5F764 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 762;
Best Local Similarity 62.5%; Pred. No. 8.8e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
|:||||
Db 30 QORSNWPP 37

RESULT 30
Q7Q3S0_ANOGA
ID Q7Q3S0_ANOGA PRELIMINARY; PRT; 796 AA.
AC Q7Q3S0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000007067 (fragment).
GN ORFNames=ENSANGG00000005326;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RA The Anopheles gambiae Sequence Committee;
RL "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RA The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABR01008964; EAA12375.2; -; Genomic_DNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 4.
DR PRINTS; PR00320; GPROTEINRPT.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_2.
DR PROSITE; PS00882; WD_REPEATS_2; 2.
DR PROSITE; PS0294; WD_REPEATS_REGION; 2.
KW Repeat; WD repeat.
FT NON TER 796 796
SQ SEQUENCE 796 AA; 88628 MW; 753BAF9863B1F6F1 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 796;
Best Local Similarity 75.0%; Pred. No. 9.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QORSNWPP 8
|:||||
Db 449 QORSNWPP 456

RESULT 31
O28331_ARCFU
ID O28331_ARCFU PRELIMINARY; PRT; 816 AA.
AC O28331;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein AF1948.
GN OrderedLocustNames=AF1948;
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=938475; DOI=10.1038/37052;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M.L., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.R.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,
RA Peterson S.N., Reich C.I., McNeil L.K., Badger J.H., Glodek A.,
RA Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L.A.,
RA Uterback T.R., Cotton M.D., Spriggs T., Artach P., Kaine B.P.,
RA Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C.,
RA Gariand S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O.,
RA Woese C.R., Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE000968; AAB9308.1; -; Genomic_DNA.
DR PIR; C69493; C69493.
DR TIGR; AF1948; -.
DR InterPro; IPR001545; Glyc hormone.
DR PROSITE; PS00261; GLYCO HORMONE BETA.1; UNKNOWN 1.
KW Complete proteome; Glycothermal protein.
SQ SEQUENCE 816 AA; 90267 MW; D5958135239C92FA CRC64;

Query Match 74.0%; Score 37; DB 2; Length 816;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RSNWPP 8
Db 775 RTNWPP 780

RESULT 32
Q5A4M0 CANAL
ID Q5A4M0 CANAL PRELIMINARY; PRT; 2568 AA.
AC Q5A4M0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Potential mitochondrial protein Fmp27.
GN Name=FMP27; ORFNames=CaO19.10926, CaO19.3422;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Izung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AACQ01000065; EAK97678.1; -; Genomic DNA.
DR EMBL; AACQ01000064; EAK97741.1; -; Genomic DNA.
SQ SEQUENCE 2568 AA; 295557 MW; 16E9A1E5C75F1492 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 2568;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RSNWPP 8
Db 2043 KSNWPP 2048

RESULT 33
Q89U49 BRAJA
ID Q89U49 BRAJA PRELIMINARY; PRT; 4108 AA.
AC Q89U49;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bll1570 protein.
GN OrderedLocustNames=bll1570;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Kobata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; BA000040; BAC46835.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 4108 AA; 441546 MW; EB66CA2B5D69A537 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 4108;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RSNWPP 8
Db 3812 RTNWPP 3817

RESULT 34
Q8RY8_ORYSA
ID Q8RY8_ORYSA PRELIMINARY; PRT; 77 AA.
AC Q8RY8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0648C09.12 protein.
GN Name=P0648C09.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Calmodulin mediates the control of a large number of
enzymes by Ca(2+). Among the enzymes to be stimulated by the
calmodulin-Ca(2+) complex are a number of protein kinases and
phosphatases (By similarity).
DR EMBL; AP003922; BAB86223.1; -; Genomic_DNA.

DR Gramene: Q8RYV8: "-
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR InterPro: IPR002048; EF_hand_Ca_bd.
 DR ProDom: PD000012; EF-hand; 1.
 KW Repeat.
 SQ SEQUENCE 77 AA; 8746 MW; B6083B3B72863737 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 77;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 QRSNWP 8
 :||:||||
 DB 43 RRSWPP 49

RESULT 35
 ID Q512M4_MAGGR PRELIMINARY; PRT; 121 AA.
 AC Q512M4;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 CN ORNames=MG06012.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaportha.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nuebaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen T., Allen T., An P., Anderson M., Anderson S.,
 RA Archchi H., Ambreuter J., Bachantung P., Baldwin J., Barry A.,
 RA Bayul T., Blithetrey B., Bloom T., Blye J., Boguelavskiy L.,
 RA Borowsky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gnerre S.,
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagan D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Hoan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kanat A., Kamysseleg M., Karlsson E.,
 RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-Toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabell R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Minova T., Mikkelsen T., Menga V., Moru K.,
 RA Moses J., Mulrain L., Nilson G., Naylor J., Neves C., Nguyen C.,
 RA Nguyen N., Nguyen T., Niscol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'Donnell P., Okawa O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramaamy U., Rameau R., Ray V., Raymond C.,
 RA Ruetan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnaz C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tefaye S., Theodore J., Thoultsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsono N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.
 RT "The genome sequence of Magnaporthe grisea";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACU01000851; EAA52884.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 121 AA; 12736 MW; A796D6B3172B8F53 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 121;
 Best Local Similarity 71.4%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 QRSNWP 8
 :||:||||
 DB 55 RRRNWP 61

RESULT 36
 ID Q9HAG2_HUMAN PRELIMINARY; PRT; 155 AA.
 AC Q9HAG2;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ11699.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole embryo;
 EX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Yamashita H., Hiraoka S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima T., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45 (2004).


```

DR EMBL; AK021761; BAB13897.1; -; mRNA.
DR HSP; P20339; IR20.
DR Ensembl; ENSG00000169236; Homo sapiens.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001806; Ras_trnstrfm.
DR Pfam; PF00071; Ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR GTP-binding; Nucleotide-binding.
KW GTP-binding; Nucleotide-binding.
SQ SEQUENCE 155 AA; 17065 MW; 68FC0D0DE9B842F CRC64;

Query Match 72.0%; Score 36; DB 2; Length 155;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
Db 149 RRSNWP 155
:|:|:|

RESULT 37
Q8WV67_HUMAN
ID Q8WV67_HUMAN PRELIMINARY; PRT; 184 AA.
AC Q8WV67;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE P4748.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Qiu W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Wan D.F.,
RA Gu J.R.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258583; AAG23786.1; -; mRNA.
DR HSP; P32939; IKY3.
DR Ensembl; ENSG00000169236; Homo sapiens.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001806; Ras_trnstrfm.
DR InterPro; IPR005225; Small_GTP.
DR Pfam; PF00071; Ras; 1.
DR PRINTS; PR00449; RASTRNSFRMNG.
DR TIGRFAMs; TIGR00231; small GTP; 1.
DR GTP-binding; Nucleotide-binding.
KW GTP-binding; Nucleotide-binding.
SQ SEQUENCE 184 AA; 20518 MW; 631E895869525760 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 184;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QRSNWP 8
Db 178 RRSNWP 184
:|:|:|

RESULT 38
Q5TQ22_ANOGA
ID Q5TQ22_ANOGA PRELIMINARY; PRT; 219 AA.
AC Q5TQ22;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ENSANGP0000025584.
GN ORFNames=ENSANGG00000018522;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.

OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAA01008960; EAL14071.1; -; Genomic_DNA.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR InterPro; IPR006616; DUF_DM9.
DR SMART; SM00696; DM9; 3.
FT NON TER 1
SQ SEQUENCE 289 AA; 31105 MW; D644C62FB11D2940 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNW 6
Db 145 QORSNW 150
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OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAA01008960; EAL40071.1; -; Genomic_DNA.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR InterPro; IPR006616; DUF_DM9.
DR SMART; SM00696; DM9; 3.
SQ SEQUENCE 219 AA; 23764 MW; 7F871B5850F765E0 CRC64;

```

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Query Match 72.0%; Score 36; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNW 6
Db 146 QORSNW 151
|||||

```

```

RESULT 39
Q7Q5J5_ANOGA
ID Q7Q5J5_ANOGA PRELIMINARY; PRT; 289 AA.
AC Q7Q5J5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000021011 (Fragment).
GN ORFNames=ENSANGG0000018522;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAA01008960; EAL1407.2; -; Genomic_DNA.
DR InterPro; IPR006616; DUF_DM9.
DR SMART; SM00696; DM9; 4.
FT NON TER 1
SQ SEQUENCE 289 AA; 31105 MW; D644C62FB11D2940 CRC64;

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Query Match 72.0%; Score 36; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QORSNW 6
Db 145 QORSNW 150
|||||

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Search completed: December 14, 2005, 07:30:56
Job time : 47.1724 secs

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RESULT 40
QAPCJ6 USTWA PRELIMINARY; PRT; 314 AA.
ID QAPCJ6_
AC QAPCJ6;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=U002167.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Huseby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mienga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigani B.,
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Ustilago maydis."
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; RACP01000079; EAK83289.1; -; Genomic_DNA.
DR InterPro; IPR000379; Ser_estrs.
KW Hydrolase; Hypothetical protein.
SQ SEQUENCE 314 AA; 35311 MW; ADCDB8A62FE8808 CRC64;
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Query Match          72.0%; Score 36; DB 2; Length 314;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQRSNWPP 8
   ||| |||
DB 242 QQRKNFPP 249
```

THE UNIVERSITY OF CHICAGO

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: December 14, 2005, 07:31:09 ; Search time 78.1101 Seconds
(without alignments)
669.389 Million cell updates/sec

Title: US-10-720-323-7

Perfect score: 623

Sequence: 1 QVQLVESGGGVQPGSRRL.....ARGSYAFDIWGQGMVTIVSS 119

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:*

1: Geneseqp1980a:*

2: Geneseqp1990a:*

3: Geneseqp2000a:*

4: Geneseqp2001a:*

5: Geneseqp2002a:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004a:*

9: Geneseqp2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	119	5 AAU76333	AAU76333 Human ant
2	550	88.3	519	5 AAU81993	AAU81993 Human sec
3	549	88.1	123	6 ADA89270	ADA89270 Human ant
4	546.5	87.7	223	2 AAY08598	AAY08598 Anti-huma
5	543.5	87.2	223	8 ADL70773	ADL70773 Anti-TNFA
6	543	87.2	119	2 AAR95216	AAR95216 Human foe
7	542.5	87.1	249	5 ABP45098	ABP45098 Human hly
8	542.5	87.1	249	7 ADG95925	ADG95925 Single ch
9	542	87.0	119	6 AAE32095	AAE32095 Human VEG
10	541.5	86.9	128	6 ABR55797	ABR55797 Heavy cha
11	539.5	86.6	119	8 ADP47222	ADP47222 Human pho
12	539	86.5	119	9 AEB27733	AEB27733 Prostate
13	539	86.5	245	9 AEB27753	AEB27753 Anti-pros
14	538.5	86.4	119	8 ADP47106	ADP47106 Human pho
15	538	86.4	121	7 ADP03962	ADP03962 Murine-ex
16	537.5	86.3	120	4 AAU02501	AAU02501 Anti-adip
17	537.5	86.3	121	8 ADP47221	ADP47221 Human pho
18	537.5	86.3	141	9 ADP67314	ADP67314 Amino aci
19	536	86.0	118	8 ADP82561	ADP82561 Anti-IL-2
20	536	86.0	242	8 ADS82563	ADS82563 Anti-IL-2
21	535.5	86.0	120	6 ADA89174	ADA89174 Human ant
22	535.5	86.0	124	8 ADP22136	ADP22136 Human ant
23	535	85.9	128	8 ADP46947	ADP46947 Murine he
24	535	85.9	451	3 AAY93734	AAY93734 The heavy

25	535	85.9	451	6 AAE35889	AAE35889 Human 11.
26	534.5	85.8	116	7 ADC60983	ADC60983 Human ant
27	534.5	85.8	135	7 ADC61048	ADC61048 Human ant
28	534	85.7	127	9 ADZ70856	ADZ70856 Human Ig
29	534	85.7	127	9 AEB28928	AEB28928 Human ant
30	532.5	85.5	116	8 ADS84380	ADS84380 Human ant
31	532.5	85.5	116	8 ADR68522	ADR68522 Anti-EPO-
32	532	85.4	117	8 ADI22096	ADI22096 Anti-plat
33	532	85.4	123	8 ADS84372	ADS84372 Human ant
34	532	85.4	123	8 ADR68514	ADR68514 Anti-EPO-
35	531	85.2	117	8 ADI22095	ADI22095 Anti-plat
36	530.5	85.2	143	3 AAY82629	AAY82629 Human PTH
37	530	85.1	117	8 ADI22094	ADI22094 Anti-plat
38	530	85.1	117	8 ADO36345	ADO36345 Intracell
39	530	85.1	119	4 AAB67516	AAB67516 Heavy cha
40	530	85.1	119	7 ADL91318	ADL91318 VH chain
41	530	85.1	120	2 AAR52064	AAR52064 Heavy cha
42	530	85.1	123	8 ADR72700	ADR72700 Human mon
43	530	85.1	123	8 ADR72704	ADR72704 Human mon
44	530	85.1	123	8 ADR72698	ADR72698 Human mon
45	530	85.1	472	8 ADR72764	ADR72764 Human mon

ALIGNMENTS

RESULT 1

AAU76333

ID AAU76333 standard; peptide; 119 AA.

AC AAU76333;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human anti-dual integrin antibody complete variable region #1.

XX

KW Human; antibody; dual integrin; HC CDR; variable region; LC CDR;

KW medical device; immune related disease; rheumatoid arthritis;

KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;

KW sickle cell anemia; diabetes; cardiovascular disease; arteriosclerosis;

KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;

KW infectious disease; pneumonia; leprosy; malaria; malignant disease;

KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;

KW neurological disease; multiple sclerosis; Parkinson's disease;

KW Alzheimer's disease; Creutzfeldt-Jakob disease.

XX

OS Homo sapiens.

XX

FN WO200212501-A2.

XX

PD 14-FEB-2002.

XX

PF 07-AUG-2001; 2001WO-US024784.

XX

PR 07-AUG-2000; 2000US-0223363P.

XX

PR 01-AUG-2001; 2001US-00920267.

XX

PA (CENZ) CENTOCOR INC.

XX

PI Giles-Komar J, Heavner G, Snyder L, Trikha M;

XX

DR WPI; 2002-217193/27.

XX

PT Novel isolated mammalian anti-dual integrin antibody, useful for

XX

PT diagnosing or treating dual integrin related condition such as rheumatoid

XX

PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

XX

PS Claim 1; Page 134; 144pp; English.

XX

CC The invention relates to an isolated mammalian anti-dual integrin

XX

CC antibody having at least one of the human heavy chain or light chain

XX

CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also

CC included are the nucleic acids encoding the CDRs, a vector comprising the

CC nucleic acids, a host cell comprising the vector, an anti-idiotype
 CC antibody that binds to the anti-dual integrin, a medical device comprising
 CC the antibody suitable for administration by parenteral, subcutaneous,
 CC intramuscular, intravenous, intrarticular, intrabronchial,
 CC intracapsular, intracavitary, intracavitary, intracavitary,
 CC intracerebellar, or other routes as given in specification. The antibody
 CC is useful for diagnosing or treating a dual integrin related condition in
 CC an animal for example, immune related disease such as rheumatoid
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
 CC sickle cell anaemia, diabetes, cardiovascular disease such as
 CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
 CC myocardial infarction, infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma, multiple myeloma; neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
 CC Creutzfeldt-Jakob disease and many other diseases given in the
 CC specification. The present sequence is an anti-dual integrin human
 CC variable region containing at least one of the six CDRs listed above
 CC (AAU76327-AAU76332)

XX Sequence 119 AA;

Query Match 100.0%; Score 623; DB 5; Length 119;
 Best Local Similarity 100.0%; Pred. No. 9.1e-50;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISFDGSKYY 60
 Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISFDGSKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYICAREAGSYAFDIWGQGTMTVYSS 119
 Db 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYICAREAGSYAFDIWGQGTMTVYSS 119

RESULT 2

AAU81993
 ID AAU81993 standard; protein; 519 AA.

XX AAU81993;

XX 09-APR-2002 (first entry)

XX Human secreted protein SECP19.

XX Human; SECP; antiinflammatory; cytostatic; cardiant; immunosuppressive;
 XX antiviral; anti-HIV; antiarthritic; antirheumatic;
 XX muscular active general; anticonvulsant; nootropic; neuroprotective;
 XX antiallergic; hypotensive; cardiovascular disorder; atherosclerosis;
 XX hypertension; myocardial infarction; autoimmune disorder;
 XX inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy;
 XX rheumatoid arthritis; cell proliferative disorder; cancer;
 XX developmental disorder; Duchenne muscular dystrophy;
 XX neurological disorder; epilepsy; Alzheimer's disease.

XX Homo sapiens.

XX WO200198353-A2.

XX 27-DEC-2001.

XX 20-JUN-2001; 2001WO-US019862.

XX 20-JUN-2000; 2000US-0212890P.

XX 23-JUN-2000; 2000US-0213466P.

XX 27-JUN-2000; 2000US-0214601P.

XX 31-JUL-2000; 2000US-0223727P.

XX 08-SEP-2000; 2000US-0231435P.

XX 15-SEP-2000; 2000US-0232889P.

XX (INCY-) INCYTE GENOMICS INC.

PI Hillman JL, Tang YT, Yue H, Elliott VS, Tribouley CM, Lee EA;
 PI Ramkumar J, Lal P, Xu Y, Warren BA, Hafalia AJA, Baughn MR;
 PI Azimzai Y, Batra S, Burford N, Yao MG, Nguyen DB, Lu DAM, Walia NK;
 PI Gandhi AR, Au-Young J, Patterson C;
 XX WPI; 2002-090431/12.
 DR N-PSDB; ABK28652.

XX Forty four human secreted proteins (referred to as SECP-1 to SECP-44),
 PT useful in the diagnosis, treatment and prevention of cardiovascular (e.g.
 PT atherosclerosis), autoimmune/inflammatory (e.g. allergies) and cell
 PT proliferative disorders.

XX Claim 1; Page 142-143; 195pp; English.

XX The invention relates to forty four human secreted proteins (referred to
 CC as SECP-1 to SECP-44) and the nucleic acids encoding them. Also included
 CC are a host cell transformed with the nucleic acid, a transgenic animal
 CC comprising the nucleic acid, an anti-SECP antibody, use of the SECP
 CC proteins in isolating agonists and antagonists of SECP activity and a
 CC method of isolating compounds which alter the expression of the SECP
 CC nucleic acid. The SECP polynucleotides and polypeptides are useful in the
 CC diagnosis, treatment and prevention of cardiovascular (e.g.
 CC atherosclerosis, hypertension, myocardial infarction),
 CC autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS),
 CC allergies, rheumatoid arthritis), cell proliferative (e.g. cancer),
 CC developmental (e.g. Duchenne and Becker muscular dystrophy), and
 CC neurological (e.g. epilepsy, Alzheimer's disease) disorders. Numerous
 CC other examples of each disorder are given in the specification. The
 CC present sequence represents a SECP protein

XX Sequence 519 AA;

Query Match 88.3%; Score 550; DB 5; Length 519;

Best Local Similarity 87.0%; Pred. No. 2.3e-42;

Matches 107; Conservative 3; Mismatches 9; Indels 4; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISFDGSKYY 60

Db 20 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISFDGSKYY 79

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYICAREAGS----YAFDIWGQGTMTV 116

Db 80 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYICAREAGSGPDTLVAFDIWGQGTMTV 139

Qy 117 VSS 119

Db 140 VSS 142

RESULT 3

ADA89270

ID ADA89270 standard; protein; 123 AA.

XX ADA89270;

XX 20-NOV-2003 (first entry)

XX Human antibody 3G3 heavy chain amino acid sequence SEQ ID NO:114.

XX immunoglobulin; Ig; heavy chain variable domain;
 XX light chain variable domain; major histocompatibility complex; MHC;
 XX gp100; MUC1; TAX; hTERT; cytostatic; gene therapy; cancerous disorder;
 XX cancer.

XX Synthetic.

XX Homo sapiens.

XX WO2003070752-A2.

XX 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005128.

XX PF

PA (BIOR-) BIOREXIS PHARM CORP.
XX Prior CP, Turner AJ, Sadeghi H;
XX WPI; 2004-239175/22.
XX
XX Novel library containing several fusion proteins each of which comprises
PT first transferrin polypeptide fused to at least one second peptide,
PT useful for screening for transferrin fusion protein having the particular
PT activity.
XX
XX Example 8; SEQ ID NO 46; 243pp; English.
XX
XX The present invention relates to a library (I) of modified fusion
CC proteins of transferrin (Tf) and therapeutic proteins with increased
CC serum half-life or serum stability. Preferred fusion proteins include
CC those modified so that the Tf moiety exhibits no or reduced
CC glycosylation, iron binding and/or Tf receptor binding. The transferrin
CC fusion proteins are useful for treating, preventing or ameliorating
CC disorders or diseases of endocrine system, nervous system, immune system,
CC respiratory system, cardiovascular system, diseases and/or disorders
CC relating to cell proliferation, and/or diseases or disorders relating to
CC blood. The modified fusion proteins are useful in diagnosis, prognosis,
CC prevention and/or treatment of autoimmune disorders, diseases and
CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia
CC and thrombocytopenia); allergic reactions such as allergic asthma,
CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
CC eczema; inflammatory conditions e.g., inflammation associated with
CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel
CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The
CC fusion protein is also useful as an adjuvant to enhance antibacterial or
CC antifungal immune responses, antiparasitic immune responses, etc. The
CC fusion protein is also useful for treating monoclonal gammopathy of
CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,
CC adult respiratory distress syndrome, for stimulating wound repair, for
CC preventing or treating infections of joints, bones, skin, etc. The fusion
CC protein is also useful for treating or preventing thrombosis, myocardial
CC infarction, cancers, thrombocytopenia, sickle cell anaemia,
CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf
CC and a specific example of a SCA that can be fused to Tf is anti-tumour
CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence
CC from an anti-TNFalpha antibody.
XX
SQ Sequence 223 AA;

Query Match 87.2%; Score 543.5; DB 8; Length 223;
Best Local Similarity 87.4%; Pred. No. 3.8e-42;
Matches 104; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGRRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAISFDGSKNY 60
Db 1 QVQLVESGGGVQPGRRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAISFDGSKNY 60

Qy 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREAGSVAFDIWGQGTWVTVSS 119
Db 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAKDS-GDLAFDIWGQGTWVTVSS 118

RESULT 6
ID AAR95216 standard; protein; 119 AA.
XX AAR95216;
AC AAR95216;
XX 16-DEC-1996 (first entry)
XX Human foetal immunoglobulin 56P1'CL variable heavy chain.
XX

KW Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
KW detection; imaging; immunotoxin; targeting; assay; immunoassay;
KW Lewis(Y) carbohydrate antigen.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 31..35
FT /label= CDR 1.
FT Domain 50..56
FT /label= CDR 2.
FT Domain 99..108
FT /label= CDR 3.
XX
XX WO9613594-A1.
XX
XX 09-MAY-1996.
XX
XX 26-OCT-1995; 95WO-US013811.
XX
XX 28-OCT-1994; 94US-00331396.
XX 28-OCT-1994; 94US-00331397.
XX 28-OCT-1994; 94US-00331398.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;
PI Fitzgerald D, Brinkmann U, Pai L;
XX WPI; 1996-251462/25.
XX
XX Single chain fusion proteins and antibodies - useful to diagnose and
PT treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.
XX
XX Example 13; Fig 11A; 116pp; English.
XX
XX A novel recombinant DNA molecule which encodes a single chain fusion
CC protein or antibody comprising the Fv region of both the light and heavy
CC chains of an antibody (Ab) fused together, and an effector molecule,
CC where the fusion protein or Ab has the binding specificity of monoclonal
CC Ab (Mab) B1, B3 or B5, can be used for the production of such fusion
CC proteins or antibodies. The fusion proteins can be used in compositions
CC as an immunotoxin to inhibit tumour cell growth. The single chain
CC antibody can be used to detect the presence or absence of cells bearing a
CC Lewis(Y) carbohydrate antigen in a patient. The antibodies are also
CC useful as multiple targeting moieties, providing at least 2 kinds of
CC biological activity. They can also be used in diagnostic assays and for
CC the imaging of tumours when attached to a radiolabel and for the
CC pathological diagnosis of tumours. Humanised antibodies are less
CC immunogenic than the mouse Mabs B1, B3 and B5, making them more suitable
CC for long term treatment
XX
SQ Sequence 119 AA;

Query Match 87.2%; Score 543; DB 2; Length 119;
Best Local Similarity 85.7%; Pred. No. 2.2e-42;
Matches 102; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQPGRRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAISFDGSKNY 60
Db 1 QVELVESGGGVQPGRRSLRLSCAASGFTFSRYAMHWVRQAPGKLEWVAISYDGSNKY 60

Qy 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREAGSVAFDIWGQGTWVTVSS 119
Db 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARRSARTYFYDWGQGTWVTVSS 119

RESULT 7
ID ABP45098 standard; protein; 249 AA.
XX ABP45098;
AC ABP45098;
XX

19-AUG-2002 (first entry)
Human Blys binding scFv SEQ ID 1109.
Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
Homo sapiens.
WO200202641-A1.
10-JAN-2002.
15-JUN-2001; 2001WO-US019110.
16-JUN-2000; 2000US-0212210P.
17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
(HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
WPI; 2002-114799/15.
Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.
Claim 1; Page 1726-1727; 3148pp; English.
This invention describes novel antibodies that immunospecifically bind to B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention.
Sequence 249 AA;
Query Match 87.1%; Score 542.5; DB 5; Length 249;
Best Local Similarity 85.7%; Pred. No. 5.3e-42;
Matches 108; Conservative 4; Mismatches 7; Indels 7; Gaps 2;
Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHWVRQAPGKLEWAVISFDGSKYY 60
Dy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHWVRQAPGKLEWAVISFDGSKYY 60
Qy 61 VDSYKGRFTISRDNSENTLYIQVNIQLRAEDTAVYVCAREA-----RGSY--AFDIWGQGT 113
Dy 61 VDSYKGRFTISRDNSENTLYIQVNIQLRAEDTAVYVCARASYDILTGYKGAFDIWGQGT 120
Qy 114 MVTYSS 119
Dy 121 MVTYSS 126

RESULT 8
ADG95925
ID ADG95925 standard; protein; 249 AA.
AC ADG95925;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SeqID 1109.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator (Blys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1109; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (Blys). The Blys gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey Blys. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of Blys or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antirheumatic, antiallergic and neuroprotective, antiinflammatory, antiasthmatic, antiallergic and cytostatic. This polypeptide sequence is a single chain antibody that binds Blys of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
Sequence 249 AA;
Query Match 87.1%; Score 542.5; DB 7; Length 249;
Best Local Similarity 85.7%; Pred. No. 5.3e-42;
Matches 108; Conservative 4; Mismatches 7; Indels 7; Gaps 2;
Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHWVRQAPGKLEWAVISFDGSKYY 60
Dy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHWVRQAPGKLEWAVISFDGSKYY 60

```

QY 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVVYCAREAA-----RGSY--AFDIMGQGT 113
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVVYCAREASYDILTGYYKGAFDIMGQGT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 114 MVTVSS 119
Db 121 MVTVSS 126
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
AAE32095
ID AAE32095 standard; protein; 119 AA.
XX
AC AAE32095;
XX
XX
DT 24-MAR-2003 (first entry)
XX
DE Human VEGF-2 hybridoma antibody #1.
XX
XX Human; vascular endothelial growth factor; VEGF-2; inflammatory disease;
KW proliferative disorder; tumour; breast; cancer; brain; prostate; colon;
KW lymphangioma; infection; Kaposi's sarcoma; psoriasis; immunosuppressive;
KW rheumatoid arthritis; diabetic retinopathy; gene therapy; antimicrobial;
KW cytostatic; ophthalmological; antibody; autoimmune disease.
XX
OS Homo sapiens.
XX
PN W0200283849-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US011404.
XX
PR 13-APR-2001; 2001US-0283391P.
PR 07-SEP-2001; 2001US-0317600P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Albert VR, Ruben SM, Wager RE;
XX
XX WPI; 2003-093007/08.
DR N-PSDB; AAD49586.
XX
XX New vascular endothelial growth factor (VEGF) - 2 antibodies, for
PT treating, preventing or ameliorating a disease or disorder, such as
PT inflammatory diseases, proliferative disorders, autoimmune disorders or
PT diabetic retinopathy.
XX
PS Disclosure; Page 394; 399pp; English.
XX
XX The invention relates to vascular endothelial growth factor (VEGF)-2
CC antibodies. VEGF-2 antibodies are useful for treating, preventing or
CC ameliorating a disease or disorder, such as inflammatory diseases or
CC disorders, proliferative disorders, tumours, tumour metastasis, breast
CC cancer, brain cancer, prostate cancer, colon cancer, lymphangioma, an
CC infectious disease, Kaposi's sarcoma, an autoimmune disease, rheumatoid
CC arthritis, psoriasis, diabetic retinopathy, a disease or disorder
CC associated with aberrant VEGF-2 (receptor) expression, or a disease or
CC disorder associated with the lack of VEGF-2 (receptor) function. The
CC antibody is also useful for detecting, diagnosing, prognosing, or
CC monitoring cancers and other hyperproliferative disorders. VEGF-2 is also
CC used in gene therapy. The present sequence is human VEGF-2 hybridoma
CC antibody
XX
SQ Sequence 119 AA;
    Query Match 87.0%; Score 542; DB 6; Length 119;
    Best Local Similarity 86.6%; Pred. No. 2.7e-42;
    Matches 103; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVQLVSGGGVYVQPSRRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVTSFGSNKYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLVSGGGVYVQPSRRRLSCAASGFTFSRYGMHWRQAPGKGLEWVAVTSFGSNKYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIMGQGTMTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVVYCARGDVGSGCFDYGQGLTVTVSS 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
ABR55797
ID ABR55797 standard; protein; 128 AA.
XX
XX ABR55797;
AC ABR55797;
XX
XX 02-SEP-2003 (first entry)
XX
DE Heavy chain variable region of anti-Ang-2 antibody 555 HC.
XX
XX Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;
KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;
KW angiogenesis; antibody.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Region 26..36
FT /note= "complementarity determining region (CDR) 1"
FT Region 50..66
FT /note= "complementarity determining region (CDR) 2"
FT Region 96..118
FT /note= "complementarity determining region (CDR) 3"
XX
XX W02003030833-A2.
PN
XX
XX 17-APR-2003.
PD
XX
XX 11-OCT-2002; 2002WO-US032613.
PF
XX
XX 11-OCT-2001; 2001US-0328604P.
PR
XX 10-OCT-2002; 2002US-00269805.
PR
XX
XX (AMGE-) AMGEN INC.
PA
XX
XX Oliner JD;
PI
XX
XX WPI; 2003-504963/47.
DR
XX
XX New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful
PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,
PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.
XX
XX Claim 1; Page 92; 161pp; English.
XX
XX The invention relates to a specific binding agent, which comprises at
CC least one peptide selected from any of 62 peptides (ABR55769-830) or its
CC fragment. The binding agents are antibodies that recognize and bind to
CC angiotensin-2 (Ang-2). The specific binding agent, particularly the
CC antibody, is useful for inhibiting undesired angiogenesis, treating
CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-
CC 2 activity, modulating vascular permeability or plasma leakage, or
CC treating a disease (e.g. ocular neovascular disease, obesity,
CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,
CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic
CC disease, bone-related disease, or psoriasis) in a mammal. The present
CC sequence represents a heavy chain variable region of an anti-Ang-2
CC antibody
XX
SQ Sequence 128 AA;
    Query Match 86.9%; Score 541.5; DB 6; Length 128;
    Best Local Similarity 82.8%; Pred. No. 3.3e-42;
    Matches 106; Conservative 3; Mismatches 10; Indels 9; Gaps 1;

QY 1 QVQLVSGGGVYVQPSRRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVTSFGSNKYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db      1 QVQLQESGGGVVQPGSRSLRLSCAASGFTFSYAMHWVRQAPGKGLWVAIVISYDGSNKYY 60
QY      61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSY-----APDIWGQ 111
Db      61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSY-----APDIWGQ 120
QY      112 GTMTVTSS 119
Db      121 GTMTVTSS 128

RESULT 11
ID      ADP47222 standard; protein; 119 AA.
XX
AC      ADP47222;
XX
DT      09-SEP-2004 (first entry)
XX
DE      Human phospholipase A2-specific monoclonal antibody heavy chain #20.
XX
KW      human; monoclonal antibody; phospholipase A2; PLA2;
KW      inflammatory disorder; degenerative disorder;
KW      joint inflammatory reaction; skin inflammatory reaction;
KW      blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
KW      Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
XX
OS      Homo sapiens.
XX
PN      WO2004050850-A2.
XX
PD      17-JUN-2004.
XX
PF      02-DEC-2003; 2003WO-US038234.
XX
PR      02-DEC-2002; 2002US-0430724P.
XX
PA      (ABGE-) AGENIX INC.
PA      (LEXI-) LEXICON GENETICS INC.
XX
PI      Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Feng X;
PI      Jia X, Nocerini MR;
XX
WPI: 2004-461119/43.
XX
New human monoclonal antibody that binds to phospholipase A2 (PLA2),
XX      useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
XX      asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX
PS      Example 5; SEQ ID NO 137; 128pp; English.
XX
The invention comprises a human monoclonal antibody that binds to
XX      phospholipase A2 (PLA2). The monoclonal antibody of the invention is
XX      useful in the preparation of a medicament for the treatment of
XX      inflammatory and degenerative disorders stemming from inflammatory
XX      reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
XX      asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
XX      amino acid sequence represents the heavy chain from a monoclonal antibody
XX      that is specific for the human phospholipase A2 (PLA2) enzyme.
XX
SQ      Sequence 119 AA;
XX
Query Match      86.6%; Score 539.5; DB 8; Length 119;
Best Local Similarity 88.2%; Pred. No. 4.6e-42;
Matches 105; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
QY      1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSRYTMHWVRQAPGKGLWVAIVISYDGSNKYY 60
Db      1 QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKGLWVAIVISYDGSNKYY 60
QY      61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQTMVTSS 119
Db      61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQTMVTSS 118
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RESULT 12
ID      AEB27733 standard; protein; 119 AA.
XX
AC      AEB27733;
XX
DT      22-SEP-2005 (first entry)
XX
DE      Prostate cancer antibody OA12 heavy chain variable region SEQ ID NO 5.
XX
KW      cytostatic; antibody therapy; pharmaceutical; cancer; metastasis;
KW      solid tumor; prostate tumor; neoplasm; heavy chain variable region.
XX
OS      Homo sapiens.
XX
Key      Location/Qualifiers
FH      Region 1..30
FT      /note= "Framework 1"
FT      /note= "CDR1"
FT      /note= "CDR1"
FT      /note= "Framework 2"
FT      /note= "CDR2"
FT      /note= "CDR2"
FT      /note= "Framework 3"
FT      /note= "CDR3"
FT      /note= "CDR3"
FT      /note= "Framework 4"
XX
WO2005062977-A2.
XX
14-JUL-2005.
XX
21-DEC-2004; 2004WO-US043574.
XX
23-DEC-2003; 2003US-0532433P.
XX      (REGC ) UNIV CALIFORNIA.
XX
Liu B, Marks JD;
XX
WPI: 2005-522452/53.
XX
Novel antibody that specifically binds and is internalized into prostate
XX      cancer cell, useful for inhibiting growth or proliferation of prostate
XX      cancer cell and for detecting prostate cancer cell.
XX
Disclosure; SEQ ID NO 5; 77pp; English.
XX
The invention describes an antibody (I) that specifically binds and is
XX      internalized into a prostate cancer cell, comprising an antibody that
XX      specifically binds an epitope that is specifically bound by an antibody
XX      chosen from A33 (SEQ ID No. 22), M10A12 (SEQ ID No. 23), M9A4 (SEQ ID No.
XX      24), OA12 (SEQ ID No. 25), M11G12 (SEQ ID No. 26), M11F12 (SEQ ID No.
XX      27), and C10 (SEQ ID No. 28). Also described are: a chimeric molecule
XX      (II), comprising an effector attached to (I); a pharmaceutical
XX      formulation (III) comprising an excipient and (I) or (II); detecting (M1)
XX      a prostate cancer cell, comprising contacting the prostate cancer cell
XX      with (II) attached to an epitope tag, contacting (II) with a chelate
XX      comprising a detectable group, where the chelate binds to the epitope tag
XX      therefore associating the detectable group with the chelate and detecting
XX      the detectable group; a nucleic acid (IV) comprising a nucleic acid that
XX      encodes (I); an expression vector (V) comprising (IV); a cell comprising
XX      (V); and a kit (VI) comprising a container containing (I), (I) and a
XX      chimeric molecule (II) are useful for inhibiting the growth or
XX      proliferation of a prostate cancer cell, which involves contacting the
XX      cell with (I), or with (II) attached to a cytotoxin or radionuclide. The
XX      cell is a metastatic cell or solid tumor cell. (II) is useful for
XX      detecting a prostate cancer cell, which involves contacting the prostate
```

CC cancer cell with (II) attached to a detectable label and detecting the
 CC presence or absence of the detectable label. This is the amino acid
 CC sequence of an anti-prostate cancer-antibody heavy chain variable region.
 XX
 SQ Sequence 119 AA;

Query Match 86.5%; Score 539; DB 9; Length 119;
 Best Local Similarity 85.7%; Pred. No. 5.1e-42;
 Matches 102; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 QVQLVESGGGVQPGRRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVISFGSNKYY 60
 Db 1 QVQLQESGGGVQPGRRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAVIWDGSKYY 60
 Qy 61 VDSYKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREARGSVAFDIWGOGTMTVTSS 119
 Db 61 ADSYKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARDRYGDLFDYWGOGTMTVTSS 119

RESULT 13
 AEB27753
 ID AEB27753 standard; protein; 245 AA.
 XX
 AC AEB27753;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Anti-prostate cancer-antibody OA12 SEQ ID NO 25.
 XX
 KW cytosstatic; antibody therapy; pharmaceutical; cancer; metastasis;
 KW solid tumor; prostate tumor; neoplasm; antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO2005062977-A2.
 XX
 PD 14-JUL-2005.
 XX
 PF 21-DEC-2004; 2004WO-US043574.
 XX
 PR 23-DEC-2003; 2003US-0532433P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Liu B, Marks JD;
 XX
 DR WPI; 2005-522452/53.
 XX
 PT Novel antibody that specifically binds and is internalized into prostate
 PT cancer cell, useful for inhibiting growth or proliferation of prostate
 PT cancer cell and for detecting prostate cancer cell.
 XX
 PS Claim 1; SEQ ID NO 25; 77pp; English.

XX The invention describes an antibody (I) that specifically binds and is
 CC internalized into a prostate cancer cell, comprising an antibody that
 CC specifically binds an epitope that is specifically bound by an antibody
 CC chosen from A33 (SEQ ID No. 22), M10A12 (SEQ ID No. 23), M9E4 (SEQ ID No.
 CC 24), OA12 (SEQ ID No. 25), M1G12 (SEQ ID No. 26), M1F12 (SEQ ID No.
 CC 27), and C10 (SEQ ID No. 28). Also described are: a chimeric molecule
 CC (II), comprising an effector attached to (I); a pharmaceutical
 CC formulation (III) comprising an excipient and (I) or (II); detecting (M1)
 CC a prostate cancer cell, comprising contacting the prostate cancer cell
 CC with (II) attached to an epitope tag, contacting (II) with a chelate
 CC comprising a detectable group, where the chelate binds to the epitope tag
 CC therefore associating the detectable group with the chelate and detecting
 CC the detectable group; a nucleic acid (IV) comprising a nucleic acid that
 CC encodes (I); an expression vector (V) comprising (IV); a cell comprising
 CC (V); and a kit (VI) comprising a container containing (I), (II) and a
 CC chimeric molecule (II) are useful for inhibiting the growth or
 CC proliferation of a prostate cancer cell, which involves contacting the
 CC cell with (I), or with (II) attached to a cytotoxin or radionuclide. The
 CC cell is a metastatic cell or solid tumor cell. (II) is useful for

CC detecting a prostate cancer cell, which involves contacting the prostate
 CC cancer cell with (II) attached to a detectable label and detecting the
 CC presence or absence of the detectable label. This is the amino acid
 CC sequence of anti-prostate cancer-antibody OA12.
 XX
 SQ Sequence 245 AA;

Query Match 86.5%; Score 539; DB 9; Length 245;
 Best Local Similarity 85.7%; Pred. No. 1.1e-41;
 Matches 102; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Qy 1 QVQLVESGGGVQPGRRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVISFGSNKYY 60
 Db 1 QVQLQESGGGVQPGRRSLRLSCAASGFTFSYDMHWVRQAPGKGLEWVAVIWDGSKYY 60
 Qy 61 VDSYKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREARGSVAFDIWGOGTMTVTSS 119
 Db 61 ADSYKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARDRYGDLFDYWGOGTMTVTSS 119

RESULT 14
 ADP47106
 ID ADP47106 standard; protein; 119 AA.
 XX
 AC ADP47106;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human phospholipase A2-specific monoclonal antibody heavy chain #10.
 XX
 KW human; monoclonal antibody; phospholipase A2; PLA2;
 KW inflammatory disorder; degenerative disorder;
 KW joint inflammatory reaction; skin inflammatory reaction;
 KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
 KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain.
 XX
 OS Homo sapiens.
 XX
 PN WO2004050850-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038234.
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 XX
 PA (ABGE-) ABGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Landes GM, Haak-Frendescho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX
 DR WPI; 2004-461119/43.
 XX
 PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX
 PS Claim 1; SEQ ID NO 21; 128pp; English.
 XX
 CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents the heavy chain from a monoclonal antibody
 CC that is specific for the human phospholipase A2 (PLA2) enzyme.
 XX
 SQ Sequence 119 AA;

Query Match 86.4%; Score 538.5; DB 8; Length 119;
 Best Local Similarity 88.2%; Pred. No. 5.7e-42;

Matches 105; Conservative 4; Mismatches 9; Indels 1; Gaps 1;	
Qy	1 QVQLVSGGGVVPQGRSRLSCAASGFTFSRYTHMHWVRQAPGKGLEWVAVISFDGSNKYY 60
Db	1 QVQLVSGGGVVPQGRSRLSCAASGFTFSRYTHMHWVRQAPGKGLEWVAVISFDGSNKYY 60
Qy	61 VDSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCAREAGSYAFDIWGQGTMTVTS 119
Db	61 ADSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCARR-DWNYAFDIWGQGTMTVTS 118

RESULT 15

ID ADP03962 standard; protein; 121 AA.

AC ADP03962;

DT 29-JUL-2004 (first entry)

DE Murine-expressed anti-human CA IX monoclonal antibody VH protein SEQ 132.

XX monoclonal antibody; carbonic anhydrase IX; CA IX tumour antigen;
XX cytotatic; colorectal neoplasm; renal cell carcinoma;
XX cervical intraepithelial squamous neoplasia;
XX cervical intraepithelial glandular neoplasia; oesophageal; breast cancer;
XX gene therapy; murine; mouse; human; heavy chain variable domain.
XX Unidentified.

OS WO2003048328-A2.

XX 12-JUN-2003.

XX 02-DEC-2002; 2002WO-US038550.

XX 03-DEC-2001; 2001US-0337275P.

XX (ABGE-) ABGENIX INC.

XX Gudas J, Foltz I, Handa M, Gallo M;

XX WPI; 2003-523295/49.

XX New anti-CA IX monoclonal antibody, useful for treating a tumor e.g.;
XX colorectal neoplasms, colorectal tumors, cervical carcinoma, cervical
XX intraepithelial squamous and glandular neoplasia or esophageal tumors.

XX Example 2; SEQ ID NO 132; 89pp; English.

XX The invention relates to a novel isolated monoclonal antibody (mAb)
XX comprising a heavy chain polypeptide and light chain polypeptide having a
XX sequence chosen from one of 53 fully defined amino acid sequences given
XX in the specification, where the antibody specifically binds carbonic
XX anhydrase IX (CA IX) tumour antigen. The antibody of the invention
XX demonstrates cytostatic activity and may be useful for treating a tumour,
XX such as colorectal neoplasm, renal cell carcinoma, cervical carcinoma,
XX cervical intraepithelial squamous and glandular neoplasia, oesophageal
XX tumour or breast cancer, possibly via gene therapy. The current sequence
XX is that of a murine-expressed anti-human CA IX monoclonal antibody VH
XX (heavy chain variable domain) protein of the invention. The protein was
XX generated via the introduction of the human CA IX protein into a
XX transgenic mouse strain.

XX Sequence 121 AA;

Query Match 86.4%; Score 538; DB 7; Length 121;
Best Local Similarity 86.0%; Pred. No. 6.5e-42;
Matches 104; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy	1 QVQLVSGGGVVPQGRSRLSCAASGFTFSRYTHMHWVRQAPGKGLEWVAVISFDGSNKYY 60
Db	1 QVQLVSGGGVVPQGRSRLSCAASGFTFSRYTHMHWVRQAPGKGLEWVAVISFDGSNKYY 60

Qy 61 VDSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCAR--BARGSYAFDIWGQGTMTVTS 118
Db 61 ADSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCARITWVRGYGMDVWGQGTMTVTS 120
Qy 119 S 119
Db 121 S 121
Search completed: December 14, 2005, 07:40:51
Job time : 79.1101 secs

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:38:04 ; Search time 24.1145 Seconds
(without alignments)
407.987 Million cell updates/sec

Title: US-10-720-323-7

Perfect score: 623

Sequence: 1 QVQLVESGGGVQPSRRL.....ARGSYAFDIWGQTMVTVSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB pep:*

2: /cgn2_6/ptodata/1/iaa/6 COMB pep:*

3: /cgn2_6/ptodata/1/iaa/H COMB pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS COMB pep:*

5: /cgn2_6/ptodata/1/iaa/RE COMB pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1 pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	543	87.2	115	2	US-09-269-332-89
2	543	87.2	119	1	US-08-331-398A-46
3	543	87.2	119	1	US-08-331-397B-46
4	543	87.2	119	1	US-08-759-804A-46
5	543	87.2	119	2	US-09-227-693-46
6	535	85.9	451	2	US-09-472-087-70
7	530	85.1	120	1	US-07-942-245-35
8	526.5	84.5	120	2	US-10-330-613A-29
9	524.5	84.2	124	2	US-09-424-840B-16
10	521.5	83.7	248	2	US-09-315-926A-80
11	518	83.1	125	2	US-09-240-274-8
12	518	83.1	125	2	US-09-240-274-20
13	518	83.1	125	2	US-09-240-274-21
14	518	83.1	125	2	US-09-240-274-22
15	518	83.1	125	2	US-09-848-798-8
16	518	83.1	125	2	US-09-848-798-20
17	518	83.1	125	2	US-09-848-798-21
18	518	83.1	125	2	US-09-848-798-22
19	517	83.0	225	2	US-09-456-090A-60
20	517	83.0	225	2	US-09-456-090A-92
21	517	83.0	225	2	US-09-453-234-60
22	517	83.0	225	2	US-09-453-234-92
23	516	82.8	126	2	US-09-424-840B-22
24	515.5	82.7	126	2	US-09-240-274-152
25	515.5	82.7	126	2	US-09-848-798-152
26	515	82.7	125	2	US-09-240-274-24
27	515	82.7	125	2	US-09-848-798-24

ALIGNMENTS

RESULT 1

US-09-269-332-89
; Sequence 89, Application US/09269332
; Patent No. 6903194

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: WAKAHARA, YUJI

; APPLICANT: YABUTA, NAOHITO

; TITLE OF INVENTION: ANTIBODY AGAINST HUMAN PARATHORMONE RELATED PEPTIDES
; FILE REFERENCE: 04853-0033
; CURRENT APPLICATION NUMBER: US/09/269,332

; CURRENT FILING DATE: 1999-03-25

; PRIOR APPLICATION NUMBER: PCT/JP97/03382

; PRIOR FILING DATE: 1997-09-24

; PRIOR APPLICATION NUMBER: JP 255196/1996

; PRIOR FILING DATE: 1996-09-26

; PRIOR APPLICATION NUMBER: JP 214168/1997

; PRIOR FILING DATE: 1997-07-24

; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 89

; LENGTH: 115

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-269-332-89

Query Match 87.2%; Score 543; DB 2; Length 115;

Best Local Similarity 87.4%; Pred. No. 5.9e-49;

Matches 104; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

Qy 1 QVQLVESGGGVQPSRRLSCAASGTFSSYTHHWYRQAPGKGLWAVISFDGSNKYY 60

Db 1 QVQLVESGGGVQPSRRLSCAASGTFSSYTHHWYRQAPGKGLWAVISFDGSNKYY 60

Qy 61 VDSVKGRFTISRDNSNTLYQVNIILRAEDTAVYYCAREAGSYAFDIWGQTMVTVSS 119

Db 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADTAVYYCARESGDY----WGQTLTVTSS 115

RESULT 2

US-08-331-398A-46

; Sequence 46, Application US/08331398A

; Patent No. 5608039

; GENERAL INFORMATION:

; APPLICANT: Pastan, Ira

; APPLICANT: Willingham, Mark

; APPLICANT: Fitzgerald, David

; APPLICANT: Brinkmann, Ulrich

; APPLICANT: Fai, Lee

; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins

```
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note="Human fetal immunoglobulin
; OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
;
; US-08-331-398A-46
;
; Query Match 87.2%; Score 543; DB 1; Length 119;
; Best Local Similarity 85.7%; Pred. No. 6.2e-49;
; Matches 102; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
;
; Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAISFDGSKYY 60
; Db 1 QVELVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAISFDGSKYY 60
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; Qy 61 VDSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS 119
; Db 61 ADSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS 119
;
; RESULT 3
; US-08-331-397B-46
; Sequence 46, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
;
; Qy 61 VDSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS 119
; Db 61 ADSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS 119
;
; RESULT 4
; US-08-759-804A-46
; Sequence 46, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note="Human fetal immunoglobulin
; OTHER INFORMATION: 56P1'CL Variable Heavy chain (V-H)"
;
; US-08-331-397B-46
;
; Query Match 87.2%; Score 543; DB 1; Length 119;
; Best Local Similarity 85.7%; Pred. No. 6.2e-49;
; Matches 102; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
;
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; Db 1 QVELVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAISFDGSKYY 60
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; Qy 61 VDSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS 119
; Db 61 ADSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS 119
;
; RESULT 4
; US-08-759-804A-46
; Sequence 46, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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US-09-472-087-70

Query Match 85.9%; Score 535; DB 2; Length 451;
Best Local Similarity 82.4%; Pred. No. 2e-47;
Matches 103; Conservative 6; Mismatches 10; Indels 6; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60
Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAREAR-----YAFDIWGQGT 114
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARDPRGATLYYYGMDVWGQGT 120

Qy 115 TVSS 119
Db 121 TVSS 125

RESULT 7

US-07-942-245-35
; Sequence 35, Application US/07942245
; Patent No. 5639641
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Jan T.
; APPLICANT: SEARLE, Stephen M.J.
; APPLICANT: REES, Anthony R.
; APPLICANT: ROGUSKA, Michael A.
; APPLICANT: GUILD, Braydon C.
; TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 522
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zimm, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: HP 9000/700 Workstation
; OPERATING SYSTEM: UNIX
; SOFTWARE: In house
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942.245
; FILING DATE: 09-SEP-1992
; CLASSIFICATION: 530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-942-245-35

Query Match 85.1%; Score 530; DB 1; Length 120;
Best Local Similarity 85.0%; Pred. No. 1.4e-47;
Matches 102; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60
Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAREAR--GSYAFDIWGQGTMTVS 118
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARDKDWGALFDYWGQGTMTVS 120

RESULT 8

US-10-330-613A-29
; Sequence 29, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
; APPLICANT: Gudus, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: AGENIX 022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-330-613A-29

Query Match 84.5%; Score 526.5; DB 2; Length 120;
Best Local Similarity 84.2%; Pred. No. 3.2e-47;
Matches 101; Conservative 4; Mismatches 12; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60
Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAREAR---SYAFDIWGQGTMTV 117
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARISFGVVVDYGMVDVWGQGTMTV 120

RESULT 9

US-09-424-840B-16
; Sequence 16, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-16

Query Match 84.2%; Score 524.5; DB 2; Length 124;
Best Local Similarity 81.5%; Pred. No. 5.4e-47;
Matches 101; Conservative 9; Mismatches 9; Indels 5; Gaps 2;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60
Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKLEWVAVISFDGSKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAREAR--GSYA----FDIWGQGTMTV 115
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAKDGSGSYARFDGMDVWGQGTMTV 120

Qy 116 TVSS 119
Db 121 TVSS 124

RESULT 10
US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlingen, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80

Query Match 83.7%; Score 521.5; DB 2; Length 248;
Best Local Similarity 84.2%; Pred. No. 2.5e-46;
Matches 101; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVQAQPGKGLEWVAVISFDGSNKYY 60
Db 23 QVQLVQSGGGVVQPGSRRLSCAASGFTFSRYTHMHWVQAQPGKGLEWVAVISFDGSNKYY 82

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREAGSYA-FDIWGQGTMTVTVSS 119
Db 83 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARGITVTSRFDYWGQGTTLTVTVSS 142

RESULT 11
US-09-240-274-8
; Sequence 8, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D01
US-09-240-274-8

Query Match 83.1%; Score 518; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 2.6e-46;
Matches 100; Conservative 7; Mismatches 12; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVQAQPGKGLEWVAVISFDGSNKYY 60
Db 1 EVQLLESGGGVVQPGSRRLSCVWSGFTFNYYGMHWVQAQPGKGLEWVAVISFDGSNKYY 60

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARE-----ARGSYAFDIWGQGTM 114
Db 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARENQIKLWSRYLYFDYWGQGTTL 120

QY 115 VTVSS 119
Db 121 VTVSS 125

RESULT 12
US-09-240-274-20
; Sequence 20, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D15
US-09-240-274-20

Query Match 83.1%; Score 518; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 2.6e-46;
Matches 100; Conservative 7; Mismatches 12; Indels 6; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVQAQPGKGLEWVAVISFDGSNKYY 60
Db 1 EVQLLESGGGVVQPGSRRLSCVWSGFTFNYYGMHWVQAQPGKGLEWVAVISFDGSNKYY 60

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARE-----ARGSYAFDIWGQGTM 114
Db 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARENQIKLWSRYLYFDYWGQGTTL 120

QY 115 VTVSS 119
Db 121 VTVSS 125

RESULT 13
US-09-240-274-21
; Sequence 21, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 21
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D16
US-09-240-274-21

Query Match      83.1%; Score 518; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 2.6e-46;
Matches 100; Conservative 7; Mismatches 12; Indels 6; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVISFDGSNKYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGVVQPGSRSLRLSCVSGFTFNNGHWHVRQAPGKGLEWVAVIWFPGSNKY 60

Qy 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARE-----ARGSYAFDIWGQGT 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARENQIKLWSRYLYYFDYWGQGT 120

Qy 115 VTSS 119
   |||||
Db 121 VTSS 125

RESULT 14
US-09-240-274-22
; Sequence 22, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D17
US-09-240-274-22

Query Match      83.1%; Score 518; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 2.6e-46;
Matches 100; Conservative 7; Mismatches 12; Indels 6; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVISFDGSNKYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLLESGGGVVQPGSRSLRLSCVSGFTFNNGHWHVRQAPGKGLEWVAVIWFPGSNKY 60

Qy 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARE-----ARGSYAFDIWGQGT 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARENQIKLWSRYLYYFDYWGQGT 120

Qy 115 VTSS 119
   |||||
Db 121 VTSS 125

RESULT 15
US-09-848-798-8
; Sequence 8, Application US/09848798
; Patent No. 6858719
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D01
US-09-848-798-8

Query Match      83.1%; Score 518; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 2.6e-46;
Matches 100; Conservative 7; Mismatches 12; Indels 6; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVISFDGSNKYY 60
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Db 1 EVQLLESGGGVVQPGSRSLRLSCVSGFTFNNGHWHVRQAPGKGLEWVAVIWFPGSNKY 60

Qy 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARE-----ARGSYAFDIWGQGT 114
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Db 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARENQIKLWSRYLYYFDYWGQGT 120

Qy 115 VTSS 119
   |||||
Db 121 VTSS 125

Search completed: December 14, 2005, 07:45:45
Job time : 25.1145 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:38:24 ; Search time 68.1498 Seconds
(without alignments)
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Title: US-10-720-323-7
Perfect score: 623
Sequence: 1 QVQLVESGGGVVQPSRRL.....ARGSYAFDIWGQGTWTVSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	623	100.0	119	3	US-09-920-267C-7
2	623	100.0	119	4	US-10-720-323-7
3	550	88.3	519	4	US-10-312-354-19
4	549	88.1	123	4	US-10-371-942-114
5	543	87.2	115	6	US-11-047-996-89
6	542.5	87.1	249	3	US-09-880-748-1109
7	542.5	87.1	249	4	US-10-293-418-1109
8	542	87.0	119	4	US-10-120-377-76
9	542	87.0	119	5	US-10-980-815-76
10	542	87.0	119	5	US-10-992-196-76
11	541.5	86.9	128	4	US-10-269-805-29
12	539.5	86.6	119	5	US-10-726-332-137
13	539	86.5	119	6	US-11-021-438-5
14	539	86.5	245	6	US-11-021-438-25
15	539	86.5	245	6	US-11-021-438-27
16	538.5	86.4	119	5	US-10-726-332-21
17	538	86.4	121	4	US-10-309-762-132
18	537.5	86.3	121	5	US-10-726-332-136
19	537.5	86.3	141	5	US-10-858-855-11
20	536	86.0	118	5	US-10-798-380-19
21	536	86.0	242	5	US-10-798-380-21
22	535.5	86.0	120	4	US-10-371-942-18
23	535.5	86.0	124	5	US-10-727-155-42
24	535	85.9	123	4	US-10-292-088-115
25	535	85.9	128	5	US-10-725-962-3
26	535	85.9	451	4	US-10-153-382-17
27	535	85.9	451	5	US-10-612-497-70

28	535	85.9	451	5	US-10-776-649-70
29	535	85.9	451	6	US-11-085-368-17
30	534.5	85.8	116	4	US-10-309-764-10
31	534.5	85.8	135	4	US-10-309-764-75
32	534	85.7	127	5	US-10-706-689-22
33	534	85.7	127	5	US-10-988-360-22
34	532.5	85.5	116	4	US-10-269-711-19
35	532.5	85.5	116	4	US-10-684-109-19
36	532	85.4	117	6	US-11-021-715-59
37	532	85.4	123	4	US-10-269-711-11
38	532	85.4	123	4	US-10-269-711-23
39	532	85.4	123	4	US-10-269-711-27
40	532	85.4	123	4	US-10-269-711-31
41	532	85.4	123	4	US-10-269-711-35
42	532	85.4	123	4	US-10-684-109-11
43	531	85.2	117	6	US-11-021-715-58
44	530	85.1	117	6	US-11-021-715-57
45	530	85.1	119	3	US-09-948-939-23

ALIGNMENTS

RESULT 1

US-09-920-267C-7
; Sequence 7, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-7

Query Match	100.0%	Score 623;	DB 3;	Length 119;
Best Local Similarity	100.0%	Pred. No.: 2e-49;		
Matches 119;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVQLVESGGGVVQPSRRLSCAASGFTFSRYTHHWVRQAPGKGLVAVISFDGSNKYY	60	
Db	1	QVQLVESGGGVVQPSRRLSCAASGFTFSRYTHHWVRQAPGKGLVAVISFDGSNKYY	60	
QY	61	VDSVKGRFTISRDNSNTLYIQVNIILRAEDTAVYYCAEARGSYAFDIWGQGTWTVSS	119	
Db	61	VDSVKGRFTISRDNSNTLYIQVNIILRAEDTAVYYCAEARGSYAFDIWGQGTWTVSS	119	

RESULT 2

US-10-720-323-7
; Sequence 7, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323

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; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-7

Query Match      100.0%; Score 623; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 2e-49;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKGLEWVAVISPDGSNKYY 60
Db      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKGLEWVAVISPDGSNKYY 60

Qy      61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREARGSYAFDINGQGTMTVSS 119
Db      61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREARGSYAFDINGQGTMTVSS 119

RESULT 3
US-10-312-354-19
; Sequence 19, Application US/10312354
; Publication No. US20040101930A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; JACKSON, Jennifer L.;
; APPLICANT: TANG, Y. Tom; YUB, Henry;
; APPLICANT: ELLIOTT, Vicki S.; TRIBOULEY, Catherine M.;
; APPLICANT: LEE, Ernestine A.; RAMKUMAR, Jayalaxmi;
; APPLICANT: LAL, Preeti G.; XU, Yuming;
; APPLICANT: WARREN, Bridget A.; HAFALIA, April J. A.;
; APPLICANT: BAUGHN, Marian R.; AZIMZAI, Yalda;
; APPLICANT: BATRA, Sajeev; BURFORD, Neil;
; APPLICANT: YAO, Monique G.; NGUYEN, Dannel B.;
; APPLICANT: LU, Dyung Aina M.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Aneena R.; AU-YOUNG, Janice;
; APPLICANT: ARVIZU, Chandra S.
; TITLE OF INVENTION: SECRETED PROTEINS
; FILE REFERENCE: PI-0133 USN
; CURRENT APPLICATION NUMBER: US/10/312,354
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: US 01/19862
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/212,890
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US 60/213,466
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,601
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/222,372
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/231,435
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,889
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3506590CD1
US-10-312-354-19

Query Match      88.3%; Score 550; DB 4; Length 519;
Best Local Similarity 87.0%; Pred. No. 4.3e-42;
Matches 107; Conservative 3; Mismatches 9; Indels 4; Gaps 1;

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Qy      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKGLEWVAVISPDGSNKYY 60
Db      20 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKGLEWVAVISPDGSNKYY 79

Qy      61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREARGSYAFDINGQGTMTV 116
Db      80 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARAGEGSPDTLVAFDINGQGTMTV 139

Qy      117 VSS 119
Db      140 VSS 142

RESULT 4
US-10-371-942-114
; Sequence 114, Application US/10371942
; Publication No. US20030223994A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: MHC-PEPTIDE COMPLEX BINDING LIGANDS
; FILE REFERENCE: 10280-034001
; CURRENT APPLICATION NUMBER: US/10/371,942
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,994
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-371-942-114

Query Match      88.1%; Score 549; DB 4; Length 123;
Best Local Similarity 87.0%; Pred. No. 1.3e-42;
Matches 107; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

Qy      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKGLEWVAVISPDGSNKYY 60
Db      1 QVQLVDSGGGVQPGSRRLSCAASGFTFSRYTHHWVROAPGKGLEWVAVISPDGSNKYY 60

Qy      61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCAREAR----GSYAFDINGQGTMTV 116
Db      61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARELRFLWSDDAFDINGQGTMTV 120

Qy      117 VSS 119
Db      121 VSS 123

RESULT 5
US-11-047-996-89
; Sequence 89, Application US/11047996
; Publication No. US20050136057A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: WAKAHARA, YUJI
; APPLICANT: YABUTA, NAOHRO
; TITLE OF INVENTION: ANTIBODY AGAINST HUMAN PARATHORMONE RELATED PEPTIDES
; FILE REFERENCE: 04853-0033
; CURRENT APPLICATION NUMBER: US/11/047,996
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US/09/269,332
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03382
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: JP 255196/1996
; PRIOR FILING DATE: 1996-09-26
; PRIOR APPLICATION NUMBER: JP 214168/1997
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 113

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; SOFTWARE: PatentIn Ver. 2.11
; SEQ ID NO 89
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-047-996-89

Query Match      87.2%; Score 543; DB 6; Length 115;
Best Local Similarity 87.4%; Pred. No. 4.2e-42;
Matches 104; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 1 QQLVESGGVVQPGSRRLSCAASGFTFSRYTMHWVQAQPGKLEWVAVISFDGSKNY 60
    |||||
Db 1 QQLVESGGVVQPGSRRLSCAASGFTFSRYTMHWVQAQPGKLEWVAVISFDGSKNY 60
    |||||

QY 61 VDSVKGRTISRDNSENTLYLQVNIILRAEDTAVVYCAREAGSYAFDIWGQGTMTVSS 119
    |||||
Db 61 ADSVKGRTISRDNSENTLYLQVNIILRAEDTAVVYCAREAGSYAFDIWGQGTMTVSS 115

RESULT 6
US-09-880-748-1109
; Sequence 1109, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1109
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1109

Query Match      87.1%; Score 542.5; DB 3; Length 249;
Best Local Similarity 85.7%; Pred. No. 1e-41;
Matches 108; Conservative 4; Mismatches 7; Indels 7; Gaps 2;

QY 1 QQLVESGGVVQPGSRRLSCAASGFTFSRYTMHWVQAQPGKLEWVAVISFDGSKNY 60
    |||||
Db 1 QQLVESGGVVQPGSRRLSCAASGFTFSRYTMHWVQAQPGKLEWVAVISFDGSKNY 60
    |||||

QY 61 VDSVKGRTISRDNSENTLYLQVNIILRAEDTAVVYCAREAGSYAFDIWGQGTMTVSS 113
    |||||
Db 61 VDSVKGRTISRDNSENTLYLQVNIILRAEDTAVVYCAREAGSYAFDIWGQGTMTVSS 120

QY 114 MVTVSS 119
    |||||
Db 121 MVTVSS 126

RESULT 7
US-10-293-418-1109
; Sequence 1109, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
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Db          |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   61 ADSVKGRFTISRDNKNTLYLQWNSRAEDTAVVYCARDGFGSGCFDYGWGQGLTVTVSS 119

RESULT 9
US-10-980-815-76
; Sequence 76, Application US/10980815
; Publication No. US20050059117A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P8
; CURRENT APPLICATION NUMBER: US/10/980,815
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/10/120,377
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/283,391
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/317,600
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-815-76

Query Match      87.0%; Score 542; DB 5; Length 119;
Best Local Similarity 86.6%; Pred. No. 5.3e-42;
Matches 103; Conservative 6; Mismatches 10; Indels 0; Gaps

Qy    1 QVLVESGGGVQPGRSRRRLSCAASGFTFSRYTMHWVROAPKGLEWVAIVSFDGSNKYY 60
Db    1 QVLVESGGGVQPGRSLRLSCAASGFTFSRYGMHWVROAPKGLEWVAIIYDGSKNYY 60

Qy    61 VDSYKGRFTISRDNSENTLYLQWNLRAEDTAVVYCCAREAGSYAFDIWGQGTMTVTSS 119
Db    61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAVVYCARDGFGSGCFDYGWGQGLTVTVSS 119

RESULT 10
US-10-992-196-76
; Sequence 76, Application US/10992196
; Publication No. US20050192429A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig, et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PF112P8P1
; CURRENT APPLICATION NUMBER: US/10/992,196
; CURRENT FILING DATE: 2004-11-19
; PRIOR APPLICATION NUMBER: 60/523,661
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/283,391
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/317,600
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 10/120,377
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 76
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-196-76

Query Match      87.0%; Score 542; DB 5; Length 119;
Best Local Similarity 86.6%; Pred. No. 5.3e-42;
Matches 103; Conservative 6; Mismatches 10; Indels 0; Gaps

Qy    1 QVLVESGGGVQPGRSRRRLSCAASGFTFSRYTMHWVROAPKGLEWVAIVSFDGSNKYY 60
Db    1 QVLVESGGGVQPGRSLRLSCAASGFTFSRYGMHWVROAPKGLEWVAIIYDGSKNYY 60
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STP 9-13
11-10-11

Result No.	Score	Query Match	Length	DB	ID	Description	
1	542.5	87.1	249	7	US-11-054-515-1109	Sequence 1109, Ap	
2	530	85.1	117	7	US-11-127-677-9	Sequence 9, Appli	
3	529.5	85.0	247	7	US-11-054-515-924	Sequence 924, App	
4	528	84.8	117	7	US-11-093-274-19	Sequence 19, Appl	
5	526.5	84.5	477	7	US-11-000-463-395	Sequence 395, App	
6	525.5	84.3	249	7	US-11-054-515-512	Sequence 512, App	
7	524.5	84.2	248	7	US-11-054-515-1890	Sequence 1890, Ap	
8	524.5	84.2	252	7	US-11-054-515-1627	Sequence 1627, Ap	
9	524.5	84.2	254	7	US-11-054-515-983	Sequence 983, App	
10	521	83.6	252	7	US-11-054-515-1731	Sequence 1731, Ap	
11	520.5	83.5	124	7	US-11-040-159-14	Sequence 14, Appl	
12	520.5	83.5	252	7	US-11-054-515-1519	Sequence 1519, Ap	
13	519	83.3	117	7	US-11-127-677-18	Sequence 18, Appl	
14	518	83.1	119	7	US-11-127-677-21	Sequence 21, Appl	
15	517.5	83.1	244	7	US-11-054-515-1933	Sequence 1933, Ap	
16	517	83.0	248	7	US-11-054-515-1004	Sequence 1004, Ap	
17	516.5	82.9	116	7	US-11-093-274-20	Sequence 20, Appl	
18	516.5	82.9	254	7	US-11-054-515-981	Sequence 981, App	
19	516.5	82.9	254	7	US-11-054-515-1759	Sequence 1759, Ap	
20	516	82.8	241	7	US-11-054-515-2055	Sequence 2055, Ap	
21	516	82.8	242	7	US-11-054-515-1394	Sequence 1394, Ap	
22	515	82.7	258	7	US-11-054-515-1421	Sequence 1421, Ap	
23	514.5	82.6	249	7	US-11-054-515-397	Sequence 397, App	
24	514.5	82.6	249	7	US-11-054-515-1102	Sequence 1102, Ap	
25	514.5	82.6	249	7	US-11-054-515-1115	Sequence 1115, Ap	

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Db      61 VDSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCARASYDILTGYKGAFDIMGQGT 120
Qy      114 MVTVSS 119
Db      121 MVTVSS 126

RESULT 2
US-11-127-677-9
; Sequence 9, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2462
; CURRENT APPLICATION NUMBER: US/11/127,677
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: PCT/GB03/04942
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: GB 0226729.2
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-9

Query Match      85.1%; Score 530; DB 7; Length 117;
Best Local Similarity 85.7%; Pred. No. 3.5e-36;
Matches 102; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

Qy      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSDGSKYY 60
Db      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSDGSKYY 60

Qy      61 VDSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCARAGSYAFDIWGQGTMTVTVSS 119
Db      61 ADSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCAR--GDGNYDYWGQGTMTVTVSS 117

RESULT 3
US-11-054-515-924
; Sequence 924, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248

Db      61 VDSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCARASYDILTGYKGAFDIMGQGT 120
Qy      114 MVTVSS 119
Db      121 MVTVSS 126

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 924
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-924

Query Match      85.0%; Score 529.5; DB 7; Length 247;
Best Local Similarity 83.1%; Pred. No. 7.3e-36;
Matches 103; Conservative 5; Mismatches 11; Indels 5; Gaps 1;

Qy      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSDGSKYY 60
Db      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSDGSKYY 60

Qy      61 VDSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCARAGSYAFDIWGQGTMTVTVSS 115
Db      61 ADSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCARPSYDILTGLTYLYFDYWGQGTTLV 120

Qy      116 TVSS 119
Db      121 TVSS 124

RESULT 4
US-11-093-274-19
; Sequence 19, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-19

Query Match      84.8%; Score 528; DB 7; Length 117;
Best Local Similarity 86.6%; Pred. No. 5.1e-36;
Matches 103; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

Qy      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSDGSKYY 60
Db      1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSDGSKYY 60

Qy      61 VDSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCARAGSYAFDIWGQGTMTVTVSS 119
Db      61 ADSVKGRFTISRDNSENKNTLYLQMSLRAEDTAVVYCARD--WGRAFDIWGQGTMTVTVSS 117

RESULT 5
US-11-000-463-395
; Sequence 395, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
```

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; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785C1F4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-395

Query Match      84.5%; Score 526.5; DB 7; Length 477;
Best Local Similarity 79.7%; Pred. No. 2.2e-35;
Matches 102; Conservative 5; Mismatches 12; Indels 9; Gaps 1;

Qy 1 QVQLVESGGGVVQGRSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSFDGSNKYY 60
Db 20 QVQLVESGGGVVQGRSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVAIVSFDGSNKYY 79
Qy 61 VDSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCAREG-----SYAFDIWGQ 111
Db 80 ADSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCAREGRWRYRTTITGYYFDYWGQ 139
Qy 112 GTMTVTSS 119
Db 140 GTLVTVSS 147

RESULT 6
US-11-054-515-512
; Sequence 512, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1890
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1890

Query Match      84.2%; Score 524.5; DB 7; Length 248;
Best Local Similarity 83.6%; Pred. No. 1.8e-35;

; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 512
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-512

Query Match      84.3%; Score 525.5; DB 7; Length 249;
Best Local Similarity 80.2%; Pred. No. 1.5e-35;
Matches 101; Conservative 6; Mismatches 12; Indels 7; Gaps 1;

Qy 1 QVQLVESGGGVVQGRSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAIVSFDGSNKYY 60
Db 1 QVQLVESGGGVVQGRSLRLSCAASGFTFSRYGMHWVRQAPGKGLEWVAIVSFDGSNKYY 60
Qy 61 VDSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCARE-----ARGSYAFDIWGQ 113
Db 61 ADSVKGRTTISRDNSENTLYLQVNLRAEDTAVYYCAKGYDILTGYSYGMVWGQ 120
Qy 114 MVTVSS 119
Db 121 MVTVSS 126

RESULT 7
US-11-054-515-1890
; Sequence 1890, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1890
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1890

Query Match      84.2%; Score 524.5; DB 7; Length 248;
Best Local Similarity 83.6%; Pred. No. 1.8e-35;
```

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Matches 102; Conservative 7; Mismatches 10; Indels 3; Gaps 1;
Qy 1 QVQLVSGGQVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISPDGSNKYY 60
Db 1 QMQLVQSGGGVQPGSRSLRSLCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSNKYY 60
Qy 61 VDSVKGRFTISRDNSENKNTLYLQVNLRAEDTAVYYCAR---EARGSYAFDIWGQGTMTV 117
Db 61 ADSVKGRFTISRDNSENKNTLYLQVNLRAEDTAVYYCARYYYHSSGSDAFDIWGQGTMTV 120
Qy 118 SS 119
Db 121 PS 122

RESULT 8
US-11-054-515-1627
; Sequence 1627, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1627
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1627

Query Match 84.2%; Score 524.5; DB 7; Length 252;
Best Local Similarity 81.0%; Pred. No. 1.8e-35;
Matches 102; Conservative 5; Mismatches 12; Indels 7; Gaps 1;
Qy 1 QVQLVSGGQVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISPDGSNKYY 60
Db 1 QVQLVQSGGGVQPGSRSLRSLCAASGFTFSYGMHWVRQAPGKLEWVAVISYDGSNKYY 60
Qy 61 VDSVKGRFTISRDNSENKNTLYLQVNLRAEDTAVYYCAR---SYAFDIWGQGT 113
Db 61 ADSVKGRFTISRDNSENKNTLYLQVNLRAEDTAVYYCARGSDDIITGYKYFYFDWGQGT 120
Qy 114 MVTSS 119
Db 121 LVTSS 126

RESULT 9
US-11-054-515-983
; Sequence 983, Application US/11054515

```

```

; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 983
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-983

Query Match 84.2%; Score 524.5; DB 7; Length 254;
Best Local Similarity 81.2%; Pred. No. 1.9e-35;
Matches 104; Conservative 4; Mismatches 11; Indels 9; Gaps 2;
Qy 1 QVQLVSGGGVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISPDGSNKYY 60
Db 1 QVQLQSGGGVQPGSRSLRSLCAASGFTFSYAMHWVRQAPGKLEWVAVISYDGSNKYY 60
Qy 61 VDSVKGRFTISRDNSENKNTLYLQVNLRAEDTAVYYCARE-----ARGSYA---FDIWGQ 111
Db 61 ADSVKGRFTISRDNSENKNTLYLQVNLRAEDTAVYYCARESGFYDILTYGYPGYFDYWGK 120
Qy 112 GTWTVSS 119
Db 121 GTWTVSS 128

RESULT 10
US-11-054-515-1731
; Sequence 1731, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748

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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1731
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1731

Query Match      83.6%; Score 521; DB 7; Length 252;
Best Local Similarity 78.3%; Pred. No. 3.5e-35;
Matches 101; Conservative 7; Mismatches 11; Indels 10; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPKGLWVAVISFDGSNKYY 60
Db 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPKGLWVAVISFDGSNKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAREAG-----SYAFDIWGQTM 110
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARN-RGDIYYDYTYAMDYWGQSTG 119

Qy 111 QGTWTVSS 119
Db 121 RGLTVTVSS 129

RESULT 11
US-11-040-159-14
; Sequence 14, Application US/11040159
; Publication No. US2005025552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehreen, Kenneth
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey T.
; APPLICANT: KaloBios, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; FILE REFERENCE: Binding Determinants
; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:V-region of
; OTHER INFORMATION: anti-PcrV antibody P6 VH
US-11-040-159-14

Query Match      83.5%; Score 520.5; DB 7; Length 124;
Best Local Similarity 82.4%; Pred. No. 2.1e-35;
Matches 103; Conservative 5; Mismatches 10; Indels 7; Gaps 2;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPKGLWVAVISFDGSNKYY 60
Db 1 EVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPKGLWVAVISFDGSNKYY 60

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Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAREAG-----SYAFDIWGQTM 114
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARN-RGDIYYDYTYAMDYWGQSTG 119

Qy 115 TVSS 119
Db 120 TVSS 124

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RESULT 12

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US-11-054-515-1519
; Sequence 1519, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1519
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1519

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```

Query Match      83.5%; Score 520.5; DB 7; Length 252;
Best Local Similarity 83.1%; Pred. No. 3.8e-35;
Matches 103; Conservative 4; Mismatches 12; Indels 5; Gaps 2;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPKGLWVAVISFDGSNKYY 60
Db 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPKGLWVAVISFDGSNKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARE----ARGSY-APDIWGQTMV 115
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAKRYDILTGYGGFDYWGQTMV 120

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```

Qy 116 TVSS 119
Db 121 TVSS 124

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RESULT 13

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US-11-127-677-18
; Sequence 18, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: Rabbitts, Terence H
; APPLICANT: Tanaka, Tomoyuki

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:33:29 ; Search time 18.8722 Seconds
(without alignments)
606.700 Million cell updates/sec

Title: US-10-720-323-7
Perfect score: 623
Sequence: 1 QQLVESGGGVVQPGSRRL.....ARGSYAFDIWGQTMVTSS 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	558	89.6	119	2 F36005	Ig heavy chain V r
2	543	87.2	134	2 S31679	Ig heavy chain V r
3	541.5	86.9	118	2 S31116	Ig heavy chain - h
4	537.5	86.3	122	2 S36005	Ig heavy chain V r
5	534	85.7	121	2 G36005	Ig heavy chain V r
6	528	84.8	132	2 S31603	Ig heavy chain V r
7	527.5	84.7	137	2 S31701	Ig heavy chain V r
8	520	83.5	121	2 S19666	Ig heavy chain V r
9	517.5	83.1	114	2 S46390	Ig heavy chain V r
10	517.5	83.1	122	2 S31117	Ig heavy chain - h
11	517.5	83.1	128	2 S48797	Ig heavy chain V r
12	517.5	83.1	139	2 S31674	Ig heavy chain V r
13	517	83.0	111	2 PH1645	Ig heavy chain V-I
14	516	82.8	133	2 A49028	Ig heavy chain V r
15	514.5	82.6	140	2 S70442	Ig heavy chain pre
16	513	82.3	123	2 S38493	Ig heavy chain - h
17	511.5	82.1	120	2 S31112	Ig heavy chain - h
18	511	82.0	130	2 S31601	Ig heavy chain V r
19	509.5	81.8	114	2 S46392	Ig heavy chain V r
20	509.5	81.8	133	2 S31510	Ig heavy chain - h
21	508	81.5	135	2 S31598	Ig heavy chain V r
22	505	81.1	111	2 PH1643	Ig heavy chain V r
23	504.5	81.0	151	2 A60943	Ig heavy chain pre
24	503.5	80.8	122	1 M3HUM	Ig heavy chain V-I
25	503	80.7	130	2 PL0098	Ig heavy chain pre
26	498	79.9	109	2 PH1644	Ig heavy chain V r
27	497	79.8	139	2 I37781	Ig variable region
28	495.5	79.5	108	2 PH1642	Ig heavy chain V r
29	494.5	79.4	136	2 S31587	Ig heavy chain V r

30	494	79.3	109	2 PH1646	Ig heavy chain V r
31	492.5	79.1	118	2 S31677	Ig heavy chain V r
32	492.5	79.1	120	2 S44111	Ig heavy chain V-D
33	491	78.8	119	2 S31107	Ig heavy chain - h
34	489.5	78.6	114	2 S46391	Ig heavy chain V r
35	488	78.3	117	2 S78486	Ig heavy chain V r
36	487.5	78.3	147	2 I37780	Ig variable region
37	485.5	77.9	118	2 PH1662	Ig heavy chain V r
38	484	77.7	119	1 GHUNI	Ig heavy chain V-I
39	481.5	77.3	128	2 S31595	Ig heavy chain V r
40	480	77.0	119	2 S36005	Ig heavy chain V r
41	480	77.0	119	2 S31108	Ig heavy chain - h
42	480	77.0	127	2 S38489	Ig heavy chain - h
43	480	77.0	138	2 S31666	Ig heavy chain V r
44	477	76.6	113	2 S38490	Ig heavy chain - h
45	476.5	76.5	118	2 PH1660	Ig heavy chain V r

ALIGNMENTS

RESULT 1

F36005
Ig heavy chain V region (M49) - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C:Accession: F36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2111773
A:Accession: F36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026
C:Genetics:
A:Gene: GDB:IGH@; IGHDY1
A:Cross-references: GDB:118731; OMIM:146910
A:Map position: 14q32.33-14q32.33
A:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	89.6%	Score 558;	DB 2;	Length 119;
Best Local Similarity	89.1%	Pred. No. 4.8e-46;		
Matches 106;	Conservative 5;	Mismatches 8;	Indels 0;	Gaps 0;
QY	1	QQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVQAPGKGLEWVAVISFDGSNKYY	60	
Db	1	QQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVQAPGKGLEWVAVISFDGSNKYY	60	
QY	61	VDSVKGRFTISRDNSNTLYLQVNILRAEDTAVYVCAREAGSYAFDIWGQTMVTSS	119	
Db	61	ADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYVCARDKASDAFDIWGQTMVTSS	119	

RESULT 2

S31679
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31679
R:Cuisinier, A.M.; Gauthier, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31679
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-134 <CUI>
A:Cross-references: UNIPARC:UPI0000116475; EMBL:Z14203; NID:G30965; PIDN:CAA78572.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 543; DB 2; Length 134;
Best Local Similarity 87.4%; Pred. No. 1.4e-44;
Matches 104; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 60
|||
Db 20 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 79
|||
Qy 61 VDSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVYSS 119
|||
Db 80 ADSVKGRFTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVYSS 134
|||

RESULT 3

S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voosen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.9%; Score 541.5; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 1.7e-44;
Matches 105; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 60
|||
Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 60
|||
Qy 61 VDSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTVYSS 119
|||
Db 61 ADSVKGRFTISRDNSENNTLYLQVNLRAEDTAVYYCATDYG-KGAAFDIWGQGTMTVYSS 118
|||

RESULT 4

E36005
Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
C;Accession: E36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
A;Cross-references: UNIPARC:UPI0000176C30; GB:M34030
C;Genetics:
A;Gene: GDB:IGH@; IGHDI1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.3%; Score 537.5; DB 2; Length 122;

Best Local Similarity 84.4%; Pred. No. 4.3e-44;
Matches 103; Conservative 5; Mismatches 11; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 60
|||
Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 60
|||
Qy 61 VDSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTV 117
|||
Db 61 ADSVKGRFTISRDNSENNTLYLQVNLRAEDTAVYYCARDHRSSSWYGYMDVWGQGTMTV 120
|||
Qy 118 SS 119
||
Db 121 SS 122

RESULT 5

G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C2C; GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDI1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 534; DB 2; Length 121;
Best Local Similarity 85.1%; Pred. No. 9.2e-44;
Matches 103; Conservative 6; Mismatches 10; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 60
|||
Db 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTMHWVRQAPGKLEWVAVISFDGSKYY 60
|||
Qy 61 VDSVKGRTISRDNSENNTLYLQVNLRAEDTAVYYCAREARGSYAFDIWGQGTMTV 118
|||
Db 61 ADSVKGRFTISRDNSENNTLYLQVNLRAEDTAVYYCARDHRSSSWYGYMDVWGQGTMTV 120
|||

RESULT 6

S31603
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31603
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31603
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <CUI>
A;Cross-references: UNIPARC:UPI0000116455; EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F:30-113/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 528; DB 2; Length 132;
Best Local Similarity 85.7%; Pred. No. 3.8e-43;
Matches 102; Conservative 6; Mismatches 9; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60
DB 16 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 75

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQGTMTVTS 119
DB 76 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQGTMTVTS 132

RESULT 7
S31701
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31701
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the submitted to the EMBL Data Library, June 1992
A:Reference number: S31585
A:Accession: S31701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CUI>
A:Cross-references: UNIPARC:UPI000011645D; EMBL:Z14177; NID:g31020; PIDN:CAA78546.1; PID submitted to the EMBL Data Library, June 1992
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 84.7%; Score 527.5; DB 2; Length 137;
Best Local Similarity 86.6%; Pred. No. 4.4e-43;
Matches 103; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60
DB 20 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 79

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQGTMTVTS 119
DB 80 PDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQGTMTVTS 137

RESULT 8
S19666
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Mark, J.D.; Hoogenboom, H.R.; Bonnett, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.Mol. Biol. 222, 581-597, 1991
A:Title: By-passing immunization. Human antibodies from V-gene libraries displayed on phage particles by phage immunization. Human antibodies from V-gene libraries displayed on phage particles by phage immunization.
A:Reference number: S19663; MUID:92085276; PMID:1748994
A:Accession: S19666
A:Molecule type: mRNA
A:Residues: 1-121 <MAR>
A:Cross-references: UNIPARC:UPI0000115FE5; EMBL:X61646; NID:g37688; PIDN:CAA43827.1; PID submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 520; DB 2; Length 121;
Best Local Similarity 83.5%; Pred. No. 2e-42;
Matches 101; Conservative 7; Mismatches 11; Indels 2; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60
DB 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARE--ARGSYAFDIWGQGTMTVTS 118
DB 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARE--ARGSYAFDIWGQGTMTVTS 120

QY 119 S 119
DB 121 S 121

RESULT 9
S46390
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46390
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: UNIPARC:UPI000011663F; EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PID submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 517.5; DB 2; Length 114;
Best Local Similarity 84.0%; Pred. No. 3.2e-42;
Matches 100; Conservative 6; Mismatches 8; Indels 5; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60
DB 1 EVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQGTMTVTS 119
DB 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCAREAGSYAFDIWGQGTMTVTS 114

RESULT 10
S31117
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complementing regions in the human heavy chain variable region.
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 517.5; DB 2; Length 122;
Best Local Similarity 83.6%; Pred. No. 3.4e-42;
Matches 102; Conservative 8; Mismatches 9; Indels 3; Gaps 2;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60
DB 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHMHWVRQAPGKLEWVAIVFDGSNKYY 60

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARE--ARGSYA-FDIWGQGTMTV 117
DB 61 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVVYCARE--ARGSYA-FDIWGQGTMTV 120

Qy 118 SS 119
||
Db 121 SS 122

RESULT 11

S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C:Accession: S48797; S26893
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <MAH>
A:Cross-references: UNIPARC:UPI0000116700; EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PI
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: UNIPARC:UPI0000038183; EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 517.5; DB 2; Length 128;
Best Local Similarity 79.7%; Pred. No. 3.6e-42;
Matches 102; Conservative 7; Mismatches 10; Indels 9; Gaps 2;

Qy 1 QVQLVESGGGVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISFDGSKNYK 60
|||
Db 1 QVQLVESGGGVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISFDGSKNYK 60
|||

Qy 61 VDSVKGRFTISRDNSNTLYIQVNIILRAEDTAVYYCAREAGSYAFDIWGQTMVTSS 111
|||
Db 61 ADSVKGRFTISRDNSKNTLYIQMNSLRAEDTAVYYCARDNYDSDSGYYYYGVDVWGQ 120
|||

Qy 112 GTMTVSS 119
|||
Db 121 GTTVTSS 128
|||

RESULT 12

S31674
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31674
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31674
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CUI>
A:Cross-references: UNIPARC:UPI0000116476; EMBL:Z14204; NID:G30967; PIDN:CAA78573.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 83.1%; Score 517.5; DB 2; Length 139;
Best Local Similarity 84.2%; Pred. No. 3.9e-42;
Matches 101; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISFDGSKNYK 60
|||
Db 1 QVQLVESGGGVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISFDGSKNYK 60
|||

Db 20 QVQLVESGGGVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISYDGSNKYY 79
|||

Qy 61 VDSVKGRFTISRDNSNTLYIQVNIILRAEDTAVYYCAREAGSYA-PDIWGQTMVTSS 119
|||
Db 80 ADSVKGRFTISRDNSKNTLYIQMNSLRAEDTAVYYCAKAGLGFNWFDPWGQGLTVTSS 139
|||

RESULT 13

PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C:Accession: PH1645
R:Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1645
A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:QBWUK1; UNIPARC:UPI0000176B7B
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 517; DB 2; Length 111;
Best Local Similarity 85.6%; Pred. No. 3.5e-42;
Matches 95; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 9 GGVVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISFDGSKNYVDVSVKGRF 68
|||
Db 1 GGVVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISFDGSKNYADSVKGRF 60
|||

Qy 69 TISRDNSNTLYIQVNIILRAEDTAVYYCAREAGSYAFDIWGQTMVTSS 119
|||
Db 61 TISRDNSKNTLYIQMNSLRAEDTAVYYCARDRGAWTFDLWGRGLTVTSS 111
|||

RESULT 14

A49028
Ig heavy chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49028
R:Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuur
Eur. J. Immunol. 21, 2355-2363, 1991
A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A:Reference number: A49028; MUID:92008140; PMID:1915549
A:Accession: A49028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-133 <TIM>
A:Cross-references: UNIPARC:UPI0000113P2C; GB:S64471; NID:G236904; PIDN:AAB20011.1; PID:
A:Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A:Note: sequence extracted from NCBI backbone (NCBIN:64471, NCBIIP:64470)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 516; DB 2; Length 133;
Best Local Similarity 82.1%; Pred. No. 5.2e-42;
Matches 101; Conservative 6; Mismatches 12; Indels 4; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISFDGSKNYK 60
|||
Db 1 QVQLVESGGGVQPGSRRLSCLASGGFTFSRYTHMHWVRQAPGKLEWVAVISYDGSNKYY 60
|||

Qy 61 VDSVKGRFTISRDNSNTLYIQVNIILRAEDTAVYYCAREAGSYA----FDIWGQTMVT 116
|||
Db 61 ADSVKGRFTISRDNSKNTLYIQMNSLRAEDTAVYYCARDRELTIAAGNFYDWGQGLTAT 120
|||

Qy 117 VSS 119
|||

Db 121 VSS 123

RESULT 15

S70442

Ig heavy chain precursor V region (mu) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 31-Dec-2004

C:Accession: S70442

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A:Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fe

A:Reference number: S70442; MUID:93024508; PMID:1383695

A:Accession: S70442

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176EB7

C:Superfamily: immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 514.5; DB 2; Length 140;

Beat Local Similarity 83.3%; Pred. NO. 7.7e-42;

Matches 100; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

QY 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPGKGLEWVAVISFDGSNKYY 60

Db |||||

QY 20 QVQLVESGGGVVQPGSURLSCAASGFTFSNYGMHWVRQAPGKGLEWVAFIYDGSNKYY 79

Db |||||

QY 61 VDSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARE-ARGSYAFDIWGQGTMTVTVSS 119

Db |||||

QY 80 ADSVKGRFTISRDNSENTLYLQVNLRAEDTAVYYCARDHIVGATYFDYWGQGTMTVTVSS 139

Search completed: December 14, 2005, 07:44:53

Job time : 18.8722 secs

11-13-1911

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:32:04 ; Search time 101.176 Seconds
(without alignment)
829.818 Million cell updates/sec

Title: US-10-720-323-7

Perfect score: 623

Sequence: 1 QVQLVSGGGVQVQGRSRL.....ARGSYAFDIWQGTMTVTSS 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	539.5	86.6	613	Q8WUK1_HUMAN	Q8wuk1 homo sapien
2	508	81.5	116	Q9UL93_HUMAN	Q9ul93 homo sapien
3	504	80.9	240	Q65ZC9_HUMAN	Q65zc9 homo sapien
4	503.5	80.8	122	HV3G_HUMAN	P01768 homo sapien
5	495	79.5	113	Q9UL90_HUMAN	Q9ul90 homo sapien
6	487.5	78.3	122	Q9UL84_HUMAN	Q9ul84 homo sapien
7	484	77.7	119	HV3I_HUMAN	P01770 homo sapien
8	479.5	77.0	469	Q569F4_HUMAN	Q569f4 homo sapien
9	479.5	77.0	475	Q5EFES_HUMAN	Q5efes homo sapien
10	475	76.2	470	Q6PJA4_HUMAN	Q6pja4 homo sapien
11	474	76.1	519	Q6N092_HUMAN	Q6n092 homo sapien
12	473	75.9	121	Q9UL71_HUMAN	Q9ul71 homo sapien
13	473	75.9	478	Q6P181_HUMAN	Q6p181 homo sapien
14	471.5	75.7	544	Q6PJ95_HUMAN	Q6pj95 homo sapien
15	471	75.6	121	HV3J_HUMAN	P01771 homo sapien
16	466.5	74.9	147	Q9Y509_HUMAN	Q9y509 homo sapien
17	466.5	74.9	573	Q8WU38_HUMAN	Q8wu38 homo sapien
18	465.5	74.7	122	HV3H_HUMAN	P01769 homo sapien
19	463.5	74.4	118	Q9UL91_HUMAN	Q9ul91 homo sapien
20	463	74.3	597	Q96BB9_HUMAN	Q96bb9 homo sapien
21	461.5	74.1	467	Q4VBH1_RAT	Q4vbh1 rattus norv
22	459	73.7	472	Q6N089_HUMAN	Q6n089 homo sapien
23	454.5	73.0	126	HV3K_HUMAN	P01772 homo sapien
24	450.5	72.3	118	Q9UL72_HUMAN	Q9ul72 homo sapien
25	450	72.2	464	Q6MZU6_HUMAN	Q6mzu6 homo sapien
26	447	71.7	493	Q6GMX2_HUMAN	Q6gmx2 homo sapien
27	446.5	71.7	606	Q6GMY2_HUMAN	Q6gmy2 homo sapien
28	444.5	71.3	465	Q6P6C4_HUMAN	Q6p6c4 homo sapien
29	443	71.1	479	Q5PQK9_RAT	Q5pqk9 rattus norv
30	441.5	70.9	461	Q5M7V3_RAT	Q5m7v3 rattus norv
31	440	70.6	493	Q8NC16_HUMAN	Q8nc16 homo sapien

RESULT 1

ID	Q8WUK1_HUMAN	PRELIMINARY;	PRT;	613	AA.
AC	Q8WUK1;				
DT	01-MAR-2002	(TrEMBLrel. 20, Created)			
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	IGHM protein.				
GN	Name=IGHM;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Primary B-Cells.				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,				
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Primary B-Cells;				
RG	NIH MGC Project;				
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RX	PubMed=2117273;				
RA	Schroeder H.W., Jr, Wang J.Y.;				
RT	"Preferential utilization of conserved immunoglobulin heavy chain				
RT	variable gene segments during human fetal life."				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).				
RN	[4]				
RP	NUCLEOTIDE SEQUENCE.				
RX	PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;				
RA	Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;				

ALIGNMENTS

RT "IGM kappa/lambda EBV human B cell clone: an early step of
RT differentiation of fetal B cells or a distinct B lineage?";
RL Mol. Immunol. 29:1363-1373(1992).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
RT complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT immunoglobulin heavy chain rearrangements";
RL Eur. J. Immunol. 22:247-251(1992).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1904154;
RA Neale G.A., Kitchingman G.R.;
RT "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT chain enhancer region contain a non-translatable exon and are
RT extremely heterogeneous at the 5' end.";
RL Nucleic Acids Res. 19:2427-2433(1991).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2840480; DOI=10.1084/jem.168.1.229;
RA Bird J., Galili N., Link M., Stites D., Sklar J.;
RT "Continuing rearrangement but absence of somatic hypermutation in
RT immunoglobulin genes of human B cell precursor leukemia.";
RL J. Exp. Med. 168:229-245(1988).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RA Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RT "Early human IgH gene assembly in Epstein-Barr virus-transformed fetal
RT B cell lines. Preferential utilization of the most JH-proximal D
RT segment (DQ52) and two unusual VH-related rearrangements.";
RL J. Exp. Med. 169:1391-1403(1989).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germline-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336(1993).
DR EMBL; BC020240; AAH20240.1; -; mRNA.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSP; P01861; IADQ.
DR SMR; Q8WUK1; 20-242.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 613 AA; 67296 MW; 60C7F5950671E315 CRC64;

Query Match 86.6%; Score 539.5; DB 2; Length 613;
Best Local Similarity 86.7%; Pred. No. 3.8e-48;
Matches 104; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 QVQVSEGGGVQPGRSRLSCAASGFTFSRYTHHWVRQAPGKLEWAVISFDGSKYY 60
Db 20 QVQVSEGGGVQPGRSRLSCAASGFTFSRYTHHWVRQAPGKLEWAVISFDGSKYY 79
Qy 61 VDSVKGRFTISRDNSENNTLYQVNIIRAEDTAVYYCARE-ARGSYAFDIWGQGTMTVSS 119
Db 80 ADSVKGRFTISRDNSENNTLYQVNIIRAEDTAVYYCAKDWSEGVETFDIWGQGTMTVSS 139
RESULT 2
Q9UL93_HUMAN
ID Q9UL93_HUMAN PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA Hillson J.L., Karr N.S., Opplinger I.R., Mannik M., Sasso E.H.;
RT "The structural basis of germline-encoded VH3 immunoglobulin binding
RT to staphylococcal protein A.";
RL J. Exp. Med. 178:331-336(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2840480;
RA Bird J., Galili N., Link M., Stites D., Sklar J.;
RT "Continuing rearrangement but absence of somatic hypermutation in
RT immunoglobulin genes of human B cell precursor leukemia.";
RL J. Exp. Med. 168:229-245(1988).
DR EMBL; AF035021; AAD56257.1; -; mRNA.
DR PIR; PH1644; PH1644.
DR PIR; PL0120; PL0120.
DR HSP; P01772; 2PB4.
DR SMR; Q9UL93; 1-116.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;
Query Match 81.5%; Score 508; DB 2; Length 116;
Best Local Similarity 83.1%; Pred. No. 1.2e-45;
Matches 98; Conservative 5; Mismatches 13; Indels 2; Gaps 1;
Qy 2 VOLVESGGVVQPGRSRLSCAASGFTFSRYTHHWVRQAPGKLEWAVISFDGSKYY 61
Db 1 VOLVESGGVVQPGRSRLSCAASGFTFSRYTHHWVRQAPGKLEWAVISFDGSKYY 60
Qy 62 DSVKGRFTISRDNSENNTLYQVNIIRAEDTAVYYCAREARGSYAFDIWGQGTMTVSS 119
Db 61 DSVKGRFTISRDNSENNTLYQVNIIRAEDTAVYYCA--GGGLGLGYWGQGTMTVSS 116
RESULT 3
Q652C9_HUMAN

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ID Q65ZC9 HUMAN PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=SCFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C16/7;
RA MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1 240
FT SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 80.9%; Score 504; DB 2; Length 240;
Best Local Similarity 82.4%; Pred. No. 7.2e-45;
Matches 98; Conservative 8; Mismatches 11; Indels 2; Gaps 1;

Qy 1 QVQLVSGGTVGPGSRRLSCAASGFTFSRYTHMVRQAPKGLWVAVISFDGSKNY 60
Db 1 QVQLVSGGTVGPGSLRLSCAASGFTFSYGMHVRQAPKGLWVAVISYDGSKNY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCAREAGSVAFDIWGQGTWTV 119
Db 61 ADSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARDWGDG--LDPWGKGLTVTV 117

RESULT 4
HV3G HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain:
location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCCELLANEOUS; This mu chain was isolated from the plasma of a
patient with macrolobulinemia.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
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DR PIR; A02051; M3HUAM.
DR HSSP; P01772; 2FB4.
DR SMR; P01768; 2-122.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyridoxine carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 112
FT NON_TER 122 122
FT SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 80.8%; Score 503.5; DB 1; Length 122;
Best Local Similarity 77.0%; Pred. No. 3.7e-45;
Matches 94; Conservative 14; Mismatches 11; Indels 3; Gaps 2;

Qy 1 QVQLVSGGTVGPGSRRLSCAASGFTFSRYTHMVRQAPKGLWVAVISFDGSKNY 60
Db 1 QVQLVSGGTVGPGSLRLSCAASGFTFSYGMHVRQAPKGLWVAVISYBGBKYY 60

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARE--ARGSY-AFDIWGQGTWTV 117
Db 61 ABSVKGRTISRDNSENTLYLQVNLRAEDTAVYYCARDRLPLYGBYAFNMGQGLTVTV 120

Qy 118 SS 119
Db 121 SS 122

RESULT 5
Q9UL90 HUMAN PRELIMINARY; PRT; 113 AA.
ID Q9UL90;
AC Q9UL90;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE MYosin-reactive immunoglobulin heavy chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1730252;
RA Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
Schuurman R.K.;
RT "Restricted utilization of germ-line VH3 genes and short diverse third
complementarity-determining regions (CDR3) in human fetal B lymphocyte
immunoglobulin heavy chain rearrangements.";
RL Eur. J. Immunol. 22:247-251(1992).
DR EMBL; AF035024; AAD56260.1; -; mRNA.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR SMR; Q9UL90; 1-113.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match
Best Local Similarity 79.5%; Score 495; DB 2; Length 113;
Matches 95; Conservative 8; Mismatches 10; Indels 6; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLRSLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISFDGSKNY 60
Db 1 EVQLVESGGGVQPGGSLRLSLSCAASGFTFSYGHVHWVRQAPGKLEWVAIFRDGSKNY 60

Qy 61 VDSVKGRTISRDNSENNTLYQVNLRAEDTAVYVCAREAGSVAFDIWGQGTMTVYSS 119
Db 61 ADSVKGRTISRDNSENNTLYQVNLRAEDTAVYVCAREAGSVAFDIWGQGTMTVYSS 119

RESULT 6
Q9UL84_HUMAN
ID Q9UL84_HUMAN PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56286.1; -; mRNA.
DR HSP; P01772; 2FB4.
DR SMR; Q9UL84; 1-122.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match
Best Local Similarity 78.3%; Score 487.5; DB 2; Length 122;
Matches 95; Conservative 8; Mismatches 16; Indels 3; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLRSLSCAASGFTFSRYTHHWVRQAPGKLEWVAVISFDGSKNY 60
Db 1 EVQLVESGGGVQPGGSLRLSLSCAASGFTFSYGHVHWVRQAPGKLEWVAISNDGSKNY 60

Qy 61 VDSVKGRTISRDNSENNTLYQVNLRAEDTAVYVCAREAGSVAFDIWGQGTMTV 117
Db 61 ADSVKGRTISRDNSENNTLYQVNLRAEDTAVYVCAREAGSVAFDIWGQGTMTV 120

Qy 118 SS 119
Db 121 SS 122

RESULT 7
HV31_HUMAN
ID HV31_HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77070289; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT characterization of the protein, the L- and H-chains, the cyanogen
RT bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC -I- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC protein.
CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A91668; GIHUNI.
CC HSP; P01772; 2FB4.
CC SMR; P01770; 1-119.
CC GO; GO:0005576; Extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG-LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyridoxone carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 1 1 Pyridoxone carboxylic acid.
FT DISULFID 22 95
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13243 MW; C96935A65E5E165B CRC64;

Query Match
Best Local Similarity 77.7%; Score 484; DB 1; Length 119;
Matches 91; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QVQLVESGGGVQPGSRRLRSLSCAASGFTFSRYTHHWVRQAPGKLEWVAISFDGSKNY 60
Db 1 QVQLVQSGGGVQPGSRRLRSLSCAASGFTFSRYTHHWVRQAPGKLEWVAISYBGBKH 60

Qy 61 VDSVKGRTISRDNSENNTLYQVNLRAEDTAVYVCAREAGSVAFDIWGQGTMTVYSS 119
Db 61 ADSVNGRTISRDNSENNTLYQVNLRAEDTAVYVCAREAGSVAFDIWGQGTMTVYSS 119

RESULT 8
Q569F4_HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q569F4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
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DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IGHG1 protein.
CN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC092518; AAB2518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 77.0%; Score 479.5; DB 2; Length 469;
Best Local Similarity 76.2%; Pred. No. 6.1e-42;
Matches 93; Conservative 11; Mismatches 13; Indels 5; Gaps 2;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPCKGLEWVAIVSFDGSNKKY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVQLVESGGGVVQPGSRLSCTASGFTFKYAMHWVRQAPKAGLEWVAIVSYDGRNIQ 79

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYVCAREAGSYA---FDIWGGTWT 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ADSVKGRTISRDNSENKSLYLQVNLRAEDTALYCA--TRGGYSTAGFDYWGQTLTV 137

Qy 118 SS 119
||
Db 138 SS 139

RESULT 9
Q5FEF5 HUMAN PRELIMINARY; PRT; 475 AA.
AC Q5FEF5
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Anti-Rhd monoclonal T125 gammaal heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Gaucher C., Klein P., Bellard R.;

RT "Sequence determination of the recombinant human anti-Rhd monoclonal
antibody T125.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY894992; AAW82028.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CI-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW SIGNAL.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammaal heavy
chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 77.0%; Score 479.5; DB 2; Length 475;
Best Local Similarity 74.6%; Pred. No. 6.2e-42;
Matches 94; Conservative 20; Mismatches 5; Indels 7; Gaps 1;

Qy 1 QVQLVESGGGVVQPGSRRLSCAASGFTFSRYTHHWVRQAPCKGLEWVAIVSFDGSNKKY 60
Db 20 QVQLVESGGGVVQPGSRLSCTASGFTFKYAMHWVRQAPKAGLEWVAIVSYDGRNIQ 79

Qy 61 VDSVKGRTISRDNSENTLYLQVNLRAEDTAVYVCAREAGSYA---AFDIWGQGT 113
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ADSVKGRTISRDNSENQDTLYLQVNLRAEDTAVYVCARPVRSRWLQGLGDAFHWGQGT 139

Qy 114 MVTVSS 119
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Db 140 MVTVSS 145

RESULT 10
Q6PJA4 HUMAN PRELIMINARY; PRT; 470 AA.
ID Q6PJA4 HUMAN PRELIMINARY;
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
CN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC092518; AAB2518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;
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Search completed: December 14, 2005, 07:44:11
Job time : 102.176 secs

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Qy 61 VDSVKGRFTISRNSENTLYLQVNLRAEDTAVYYCAREAGSYA-----FDINGQGT 113
Db 80 AASVKGRTISRDNKNTLSLQMSLRVEDTAVYYCAKQDKPWSNSWFLTNFDSWGRGT 139
Qy 114 MVTVSS 119
Db 140 LVTVSS 145
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RESULT 15
HV3J_HUMAN STANDARD; PRT; 121 AA.
AC P01771;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region HIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79124695; PubMed=420800;
RA Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT "Amino acid sequence of the VH region of human myeloma
  cryoimmunoglobulin IGG Hil.";
RL Biochemistry 18:553-560(1979).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
  protein.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A02054; G1HUHL.
DR HSP; P01772; 2FB4.
DR SMR; P01771; 2-121.
DR GO; GO:000576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 121 Pyrrolidone carboxylic acid.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EF5DAB CRC64;
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Query Match 75.6%; Score 471; DB 1; Length 121;
Best Local Similarity 73.6%; Pred. No. 1e-41;
Matches 89; Conservative 14; Mismatches 16; Indels 2; Gaps 1;

Qy 1 QVQLVESGGGVQPGSRRLSCAASGFTFSRYTHVWRQAFKGLWVAVISPDGSNKYY 60
Db 1 QVQLVQAGGVDVQGRSLRLSCIASGFTFSNYGMHWVRQAFKGLWVAVIWNYSRTYY 60

Qy 61 VDSVKGRFTISRNSENTLYLQVNLRAEDTAVYYCAR--EARGSYAFDIWGQGTMTVVS 118
Db 61 GDSVKGRTISRDNKRTLYMZNLSRTEDTAVYYCARDPDIILAFSPDYWGQGLVTVS 120

Qy 119 S 119
Db 121 S 121
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OM protein - protein search, using sw model
Run on: December 14, 2005, 07:38:04 ; Search time 21.8855 Seconds
(without alignments)
407.987 Million cell updates/sec

Title: US-10-720-323-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWPFFTFGPGTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PTCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529.5	93.7	224	2	US-09-456-090A-46
2	529.5	93.7	224	2	US-09-453-234-46
3	528.5	93.5	107	2	US-09-434-870-2
4	524.5	92.8	224	2	US-09-456-090A-82
5	524.5	92.8	224	2	US-09-456-090A-88
6	524.5	92.8	224	2	US-09-456-090A-90
7	524.5	92.8	224	2	US-09-453-234-82
8	524.5	92.8	224	2	US-09-453-234-88
9	524.5	92.8	224	2	US-09-453-234-90
10	523.5	92.7	224	2	US-09-456-090A-36
11	523.5	92.7	224	2	US-09-453-234-36
12	520.5	92.1	224	2	US-09-456-090A-84
13	520.5	92.1	224	2	US-09-453-234-84
14	515.5	91.2	107	2	US-09-438-954-40
15	499.5	88.4	226	2	US-09-456-090A-38
16	499.5	88.4	226	2	US-09-453-234-38
17	497.5	88.1	234	2	US-09-848-832-4
18	495	87.6	117	2	US-09-203-768A-4
19	493	87.3	95	2	US-10-194-975-86
20	493	87.3	115	1	US-08-053-131-179
21	493	87.3	115	1	US-08-096-762-179
22	493	87.3	115	2	US-09-042-353-42
23	493	87.3	115	2	US-08-758-417A-307
24	492	87.1	105	2	US-08-635-109-6
25	492	87.1	105	2	US-08-844-215-9
26	491.5	87.0	226	2	US-09-456-090A-72
27	491.5	87.0	226	2	US-09-453-234-72

28	485.5	85.9	226	2	US-09-456-090A-42	Sequence 42, Appl
29	485.5	85.9	226	2	US-09-453-234-42	Sequence 42, Appl
30	480	85.0	110	2	US-09-025-769B-30	Sequence 30, Appl
31	480	85.0	110	2	US-09-025-769B-47	Sequence 47, Appl
32	480	85.0	110	2	US-09-490-070A-30	Sequence 30, Appl
33	480	85.0	110	2	US-09-490-070A-47	Sequence 47, Appl
34	480	85.0	110	2	US-09-490-153-30	Sequence 30, Appl
35	480	85.0	110	2	US-09-490-153-47	Sequence 47, Appl
36	480	85.0	110	2	US-09-490-324-30	Sequence 30, Appl
37	480	85.0	110	2	US-09-490-324-47	Sequence 47, Appl
38	479.5	84.9	226	2	US-09-456-090A-50	Sequence 50, Appl
39	479.5	84.9	226	2	US-09-456-090A-86	Sequence 86, Appl
40	479.5	84.9	226	2	US-09-453-234-50	Sequence 50, Appl
41	479.5	84.9	226	2	US-09-453-234-86	Sequence 86, Appl
42	478.5	84.7	226	2	US-09-456-090A-74	Sequence 74, Appl
43	478.5	84.7	226	2	US-09-453-234-74	Sequence 74, Appl
44	477.5	84.5	234	2	US-09-472-087-17	Sequence 17, Appl
45	477.5	84.5	234	2	US-09-472-087-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-09-456-090A-46
; Sequence 46, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: MI-10L
US-09-456-090A-46

Query Match	93.7%	Score 529.5;	DB 2;	Length 224;
Best Local Similarity	94.4%	Pred. No. 5.5e-43;		
Matches 102;	Conservative 4;	Mismatches 1;	Indels 1;	Gaps 1;
QY	1	EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIYDASNRATGIPA	60	
Db	1	DVMTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGQAPRLIYDASNRATGIPA	60	
QY	61	RFSGSGSGTDFTLTISLPEDEFAVYYCQRNWPFFTFGPGTKVDIK	108	
Db	61	RFSGSGSGTDFTLTISLPEDEFAVYYCQRNWPFFTFGPGTKVDIK	107	

RESULT 2
US-09-453-234-46
; Sequence 46, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01

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; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-10L
US-09-453-234-46

Query Match      93.7%; Score 529.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 5.5e-43;
Matches 102; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 DVNMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRSNWPPFTFGPGTKVDIK 108
Db 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRSNWPP-PTFGGGTKVEIK 107

RESULT 3
US-09-434-870-2
; Sequence 2, Application US/09434870
; Patent No. 6849425
; GENERAL INFORMATION:
; APPLICANT: Huse, William
; APPLICANT: Watkins, Jeffery
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AMB-06352
; CURRENT APPLICATION NUMBER: US/09/434,870
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/159,689
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-434-870-2

Query Match      93.5%; Score 528.5; DB 2; Length 107;
Best Local Similarity 96.3%; Pred. No. 3.1e-43;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRSNWPPFTFGPGTKVDIK 108
Db 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRSNW-PLTFGGGTKVEIK 107

RESULT 4
US-09-456-090A-82
; Sequence 82, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-456-090A-82

Query Match      92.8%; Score 524.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 1.7e-42;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRSNWPPFTFGPGTKVDIK 108
Db 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRTNMPR-TFGGGTKVEIK 107

RESULT 5
US-09-456-090A-88
; Sequence 88, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-456-090A-88

Query Match      92.8%; Score 524.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 1.7e-42;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRSNWPPFTFGPGTKVDIK 108
Db 61 RFGSGSGTDTLTITISLSEPEDFAVYVCOQRTNMPR-TFGGGTKVEIK 107

RESULT 6
US-09-456-090A-90
; Sequence 90, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match          92.8%; Score 524.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 1.7e-42;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 107

RESULT 7
US-09-453-234-82
; Sequence 82, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 82
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31L
US-09-453-234-82

Query Match          92.8%; Score 524.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 1.7e-42;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 107

RESULT 8
US-09-453-234-88
; Sequence 88, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; FILE REFERENCE: 020015-000200US
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US

; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-456-090A-90

Query Match          92.8%; Score 524.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 1.7e-42;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 107

RESULT 9
US-09-453-234-90
; Sequence 90, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 90
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-35L
US-09-453-234-90

Query Match          92.8%; Score 524.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 1.7e-42;
Matches 103; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAHYQKPGQAPRLIIYDASNRTGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPCTKVDIK 107

RESULT 10
US-09-456-090A-36
; Sequence 36, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; FILE REFERENCE: 020015-000200US
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
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; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M1-1L
US-09-456-090A-36

Query Match 92.7%; Score 523.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 2.1e-42;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Qy 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGGTVKDIK 108
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPR-TFGGTVKVEIK 107

RESULT 11
US-09-453-234-36
; Sequence 36, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453.234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 224
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-453-234-36

Query Match 92.7%; Score 523.5; DB 2; Length 224;
Best Local Similarity 95.4%; Pred. No. 2.1e-42;
Matches 103; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Qy 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGGTVKDIK 108
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPR-TFGGTVKVEIK 107

RESULT 12
US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS

; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PR1
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-456-090A-84

Query Match 92.1%; Score 520.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 4e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Qy 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGGTVKDIK 108
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRNNW-PLTFGGGTVKVEIK 107

RESULT 13
US-09-453-234-84
; Sequence 84, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453.234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; LENGTH: 224
; TYPE: PR1
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-32L
US-09-453-234-84

Query Match 92.1%; Score 520.5; DB 2; Length 224;
Best Local Similarity 94.4%; Pred. No. 4e-42;
Matches 102; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAAYQKPGQAPRLLIYDASNRATGIPA 60
Qy 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPFTFGGTVKDIK 108
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRNNW-PLTFGGGTVKVEIK 107

RESULT 14
US-09-438-954-40
; Sequence 40, Application US/09438954
; Patent No. 6458934
; GENERAL INFORMATION:
; APPLICANT: HONG, Hyo Jeong
; APPLICANT: PARK, Sung Sup
; APPLICANT: KANG, Young Jun
; APPLICANT: KANG, Chang-Yuil


```
; APPLICANT: YOON, Sung Kwan
; TITLE OF INVENTION: HUMANIZED ANTIBODY SPECIFIC FOR HUMAN 4-1BB AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION COMPRISING SAME
; FILE REFERENCE: 1303-124P
; CURRENT APPLICATION NUMBER: US/09/438,954
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Variable
; OTHER INFORMATION: region of light chain of human antibody (X82934)
US-09-438-954-40
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Query Match          91.2%; Score 515.5; DB 2; Length 107;
Best Local Similarity 91.7%; Pred. No. 5,3e-42;
Matches 99; Conservative 5; Mismatches 3; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLIYDASNRRATGIPA 60
Db 1 DVMTQSPATLSVSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLIYDASNRRATGIPA 60

Qy 61 RFSGSGGTFTLTLSISLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 RFSGSGGTFTLTLSISLEPEDFAVYYC-QRSNWPPFTFGPGTKVKEIK 107
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RESULT 15

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US-09-456-090A-38
; Sequence 38, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3L
US-09-456-090A-38
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Query Match          88.4%; Score 499.5; DB 2; Length 226;
Best Local Similarity 90.8%; Pred. No. 4e-40;
Matches 99; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPKQAPRLIYDASNRRATGIP 59
Db 1 EIVMTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLIYDASNRRATGIP 60

Qy 60 ARFSGSGGTFTLTLSISLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 DRFSGSGGTFTLTISRLEPEDFAVYYCQQYGSPPFTFGPGTKVDIK 109
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Search completed: December 14, 2005, 07:45:45
Job time : 21.8855 secs

(Signature)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:38:24 ; Search time 61.8502 Seconds
(without alignments)
729.594 Million cell updates/sec

Title: US-10-720-323-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPKTKVDIK 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	100.0	108	3	US-09-920-267C-8
2	565	100.0	108	4	US-10-305-347A-8
3	565	100.0	108	4	US-10-720-323-8
4	565	100.0	108	5	US-10-954-900A-8
5	547	96.8	108	6	US-11-009-731-90
6	547	96.8	109	4	US-10-408-901-24
7	547	96.8	215	4	US-10-408-901-48
8	546	96.6	128	4	US-10-656-769-12
9	546	96.6	130	4	US-10-394-71B-16
10	546	96.6	235	4	US-10-656-769-38
11	544	96.3	108	4	US-10-173-551-9
12	542	95.9	108	5	US-10-886-838-4
13	542	95.9	109	4	US-10-408-901-8
14	542	95.9	215	4	US-10-408-901-32
15	541	95.8	108	6	US-11-021-715-101
16	540	95.6	108	6	US-11-009-731-85
17	540	95.6	108	6	US-11-102-403-9
18	540	95.6	108	6	US-11-102-403-11
19	540	95.6	109	4	US-10-408-901-16
20	540	95.6	109	4	US-10-408-901-28
21	540	95.6	215	4	US-10-408-901-40
22	540	95.6	215	4	US-10-408-901-52
23	537.5	95.1	129	4	US-10-478-056-19
24	535.5	94.8	107	4	US-10-251-085B-142
25	535.5	94.8	107	4	US-10-737-252-142
26	535.5	94.8	236	5	US-10-961-567A-6
27	535	94.7	251	3	US-09-880-748-1049

28	535	94.7	251	4	US-10-293-418-1049
29	530.5	93.9	107	5	US-10-891-658-91
30	530	93.8	108	5	US-10-886-838-2
31	530	93.8	108	6	US-11-009-731-92
32	529.5	93.7	107	3	US-09-791-153A-69
33	529.5	93.7	224	3	US-09-453-234-46
34	529	93.6	130	4	US-10-443-466A-25
35	528.5	93.5	107	3	US-09-791-153A-71
36	528.5	93.5	107	3	US-09-982-464-2
37	528.5	93.5	107	4	US-10-697-399-2
38	528.5	93.5	107	5	US-10-697-400-2
39	528.5	93.5	107	5	US-10-911-838-14
40	528.5	93.5	107	6	US-10-911-838-21
41	528.5	93.5	107	6	US-11-102-403-3
42	528.5	93.5	128	4	US-10-478-056-31
43	528.5	93.5	139	4	US-10-687-799-55
44	528	93.5	106	6	US-11-021-715-99
45	526.5	93.2	107	6	US-11-021-715-98

ALIGNMENTS

RESULT 1
US-09-920-267C-8
; Sequence 8, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-8

Query Match	100.0%	Score 565;	DB 3;	Length 108;
Best Local Similarity	100.0%	Pred. No. 2.4e-41;	Mismatches 0;	Indels 0; Gaps 0;
Matches 108;	Conservative 0;			
QY	1	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKGQAPRLIYDASNRATGIPA 60		
Db	1	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKGQAPRLIYDASNRATGIPA 60		
QY	61	RFSGSGSGTDTLTLSLEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108		
Db	61	RFSGSGSGTDTLTLSLEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108		

RESULT 2
US-10-305-347A-8
; Sequence 8, Application US/10305347A
; Publication No. US20030143603A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Bernie Scallon
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN5005
; CURRENT APPLICATION NUMBER: US/10/305,347A
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.0

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; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-305-347A-8

Query Match      100.0%; Score 565; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKDIK 108
Db 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKDIK 108

RESULT 3
US-10-720-323-8
; Sequence 8, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10720.323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-8

Query Match      100.0%; Score 565; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKDIK 108
Db 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKDIK 108

RESULT 4
US-10-954-900A-8
; Sequence 8, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallon
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954.900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR APPLICATION NUMBER: 60/223,360
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; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 8
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-8

Query Match      100.0%; Score 565; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.4e-41;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKDIK 108
Db 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKDIK 108

RESULT 5
US-11-009-731-90
; Sequence 90, Application US/11009731
; Publication No. US20050191293A1
; GENERAL INFORMATION:
; APPLICANT: DESHPANDE, Shirkant
; APPLICANT: HUANG, Haichun
; APPLICANT: SRINIVASAN, Mohan
; APPLICANT: CARDARELLI, Josephine M.
; APPLICANT: WANG, Changyu
; APPLICANT: PASSMORE, David
; APPLICANT: RANGAN, Vangipuram
; APPLICANT: LANE, Thomas E.
; APPLICANT: KEIRSTEAD, Hans S.
; APPLICANT: LIU, Michael T.
; TITLE OF INVENTION: IP-10 ANTIBODIES AND THEIR USES
; FILE REFERENCE: MXI-312
; CURRENT APPLICATION NUMBER: US/11/009,731
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: 60/529180
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-009-731-90

Query Match      96.8%; Score 547; DB 6; Length 108;
Best Local Similarity 96.3%; Pred. No. 8.5e-40;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKDIK 108
Db 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRSNWPPPTFGGTVKLEIK 108

RESULT 6
US-10-408-901-24
; Sequence 24, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
```

```
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: Inhibitors
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-24

Query Match          96.8%; Score 547; DB 4; Length 109;
Best Local Similarity 96.3%; Pred. No. 8.6e-40;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 60

QY 61 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108

RESULT 7
US-10-408-901-48
; Sequence 48, Application US/10408901
; Publication No. US20040023131A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; FILE REFERENCE: Inhibitors
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-48

Query Match          96.8%; Score 547; DB 4; Length 215;
Best Local Similarity 96.3%; Pred. No. 1.7e-39;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 60

QY 61 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108

RESULT 8
US-10-656-769-12
; Sequence 12, Application US/10656769
; Publication No. US2004009712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
```

```
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
; FILE REFERENCE: 01.1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-12

Query Match          96.6%; Score 546; DB 4; Length 128;
Best Local Similarity 97.2%; Pred. No. 1.2e-39;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 80

QY 61 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 81 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 128

RESULT 9
US-10-394-471B-16
; Sequence 16, Application US/10394471B
; Publication No. US20040185047A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill; Carton, Jill; Scallon, Bernard J.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0202
; CURRENT APPLICATION NUMBER: US/10/394,471B
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,903
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 16
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-471B-16

Query Match          96.6%; Score 546; DB 4; Length 130;
Best Local Similarity 97.2%; Pred. No. 1.3e-39;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYDASNRATGIPA 80

QY 61 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 81 RPSGSGSGTDFTLTITSSLEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 128

RESULT 10
US-10-656-769-38
; Sequence 38, Application US/10656769
; Publication No. US2004009712A1
; GENERAL INFORMATION:
; APPLICANT: Varnum, Brian
; APPLICANT: Witte, Alison
; APPLICANT: Vezina, Chris
; APPLICANT: Wong, Lu Min
; APPLICANT: Qian, Xueming
; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
```

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; FILE REFERENCE: 01,1554
; CURRENT APPLICATION NUMBER: US/10/656,769
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769--38

Query Match          96.6%; Score 546; DB 4; Length 235;
Best Local Similarity 97.2%; Pred. No. 2.2e-39;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 80

Qy 61 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
Db 81 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKVEIK 128

RESULT 11
US-10-173-551-9
; Sequence 9, Application US/10173551
; Publication No. US20030232387A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Chafen
; TITLE OF INVENTION: Antibodies that bind alphaE Integrin
; FILE REFERENCE: 1655-2025-000
; CURRENT APPLICATION NUMBER: US/10/173,551
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (24)...(34)
; OTHER INFORMATION: CDR1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (50)...(56)
; OTHER INFORMATION: CDR2
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)...(98)
; OTHER INFORMATION: CDR3
US-10-173-551-9

Query Match          96.3%; Score 544; DB 4; Length 108;
Best Local Similarity 97.2%; Pred. No. 1.6e-39;
Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKVEIK 108

RESULT 12
US-10-886-838-4
; Sequence 4, Application US/10886838
; Publication No. US20050008642A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
```

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; TITLE OF INVENTION: Antibodies against insulin-like growth factor I receptor and uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 21695
; CURRENT APPLICATION NUMBER: US/10/886,838
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: EP 03015526
; PRIOR FILING DATE: 2003-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-886-838-4

Query Match          95.9%; Score 542; DB 5; Length 108;
Best Local Similarity 96.3%; Pred. No. 2.3e-39;
Matches 104; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKVEIK 108

RESULT 13
US-10-408-901-8
; Sequence 8, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MEHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-8

Query Match          95.9%; Score 542; DB 4; Length 109;
Best Local Similarity 94.4%; Pred. No. 2.3e-39;
Matches 102; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVNSYLAWFQQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEDPEDFAVYYCQQRSNWPPFTFGGTKLEIK 108

RESULT 14
US-10-408-901-32
; Sequence 32, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
```

! APPLICANT: Sullivan, John
! APPLICANT: Medlock, Eugene
! APPLICANT: Martin, Francis
! TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
! TITLE OF INVENTION: Inhibitors
! FILE REFERENCE: MBHB 01-1145-A
! CURRENT APPLICATION NUMBER: US/10/408,901
! CURRENT FILING DATE: 2003-04-07
! NUMBER OF SEQ ID NOS: 76
! SOFTWARE: PatentIn version 3.0
! SEQ ID NO 32
! LENGTH: 215
! TYPE: PRT
! ORGANISM: Homo sapiens
US-10-408-901-32

Query Match 95.9%; Score 542; DB 4; Length 215;
Best Local Similarity 94.4%; Pred. No. 4.5e-39;
Matches 102; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Qy 61 RFSGSGGTDFLTITISLPEDEFAVYQCQRSNWPPFTFGPCTKVDIK 108
Db 61 RFSGSGGTDFLTITISLPEDEFAVYQCQRSNWPPFTFGGQTKLEIK 108

RESULT 15
US-11-021-715-101
! Sequence 101, Application US/11021715
! Publication No. US20050208596A1
! GENERAL INFORMATION:
! APPLICANT: Siegel, Donald L.
! TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
! TITLE OF INVENTION: AUTOANTIBODIES AND INHIBITORS THEREOF
! FILE REFERENCE: 053893-5050
! CURRENT APPLICATION NUMBER: US/11/021,715
! CURRENT FILING DATE: 2004-12-23
! PRIOR APPLICATION NUMBER: PCT/US03/21304
! PRIOR FILING DATE: 2003-07-03
! PRIOR APPLICATION NUMBER: 60/394,352
! PRIOR FILING DATE: 2002-07-03
! PRIOR APPLICATION NUMBER: 60/411,694
! PRIOR FILING DATE: 2002-09-18
! NUMBER OF SEQ ID NOS: 153
! SOFTWARE: PatentIn version 3.2
! SEQ ID NO 101
! LENGTH: 108
! TYPE: PRT
! ORGANISM: Homo sapiens
US-11-021-715-101

Query Match 95.8%; Score 541; DB 6; Length 108;
Best Local Similarity 95.4%; Pred. No. 2.8e-39;
Matches 103; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Qy 61 RFSGSGGTDFLTITISLPEDEFAVYQCQRSNWPPFTFGPCTKVDIK 108
Db 61 RFSGSGGTDFLTITISLPEDEFAVYQCQRSNWPPFTFGGQTRLEIK 108

Search completed: December 14, 2005, 07:48:01
Job time : 61.8502 secs

1. 2. 3. 4. 5. 6. 7. 8. 9. 10.

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:41:05 ; Search time 5.23348 Seconds
(without alignments)
138.965 Million cell updates/sec

Title: US-10-720-323-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QORSNWPFPTFGPGTKVDIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cn2.6/ctodata/1/pubpaa/US06_NEW_PUB.pcp.*
3: /cn2.6/ctodata/1/pubpaa/US07_NEW_PUB.pcp.*
4: /cn2.6/ctodata/1/pubpaa/US08_NEW_PUB.pcp.*
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6: /cn2.6/ctodata/1/pubpaa/US10_NEW_PUB.pcp.*
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545	96.5	108	7	US-11-093-274-23
2	537.5	95.1	129	6	US-10-721-763-19
3	536.5	95.0	107	7	US-11-093-274-24
4	535	94.7	251	7	US-11-054-515-1049
5	534	94.5	108	7	US-11-093-274-22
6	528.5	93.5	129	6	US-10-721-763-31
7	526.5	93.2	129	6	US-10-721-763-23
8	493.5	87.3	107	7	US-11-040-159-17
9	493	87.3	95	7	US-11-054-669-86
10	493	87.3	95	7	US-11-084-554-138
11	486	86.0	94	7	US-11-093-274-33
12	477	84.4	95	7	US-11-054-669-87
13	477	84.4	95	7	US-11-084-554-131
14	469.5	83.1	131	6	US-10-721-763-27
15	469	83.0	307	7	US-11-000-463-332
16	469	83.0	312	7	US-11-000-463-334
17	468	82.8	251	7	US-11-054-515-1238
18	466	82.5	384	7	US-11-000-463-804
19	466	82.5	384	7	US-11-000-463-805
20	466	82.5	384	7	US-11-000-463-806
21	465	82.3	247	7	US-11-000-463-807
22	465	82.3	247	7	US-11-056-825-8
23	465	82.3	249	7	US-11-056-825-4
24	463.5	82.0	246	7	US-11-054-515-1268
25	462.5	81.9	250	7	US-11-054-515-1952

ALIGNMENTS

RESULT 1

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US-11-093-274-23
; Sequence 23, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,747
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-23

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Query Match 96.5%; Score 545; DB 7; Length 108;
Best Local Similarity 96.3%; Pred. No. 8.8e-32;
Matches 104: Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy	1 EIVLTQPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTGIPA 60
D_B	1 EIVLTQPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIIYDASNRTGIPA 60

QY	61	R	F	S	G	S	G	T	D	F	T	L	T	I	S	L	E	P	E	D	F	A	V	Y	C	Q	R	S	N	W	P	P	T	F	G	P	G	T	K	V	D	I	K	108
Dp	61	R	F	S	G	S	G	T	D	F	T	L	T	I	S	L	E	P	E	D	F	A	V	Y	C	Q	R	S	N	W	P	P	T	F	G	P	G	T	K	V	E	I	K	108

RESINT 2

US/10-721-763-19
; Sequence 19, Application US/10721.763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721.763
; PRIOR FILING DATE: 2003-11-26
; CURRENT APPLICATION NUMBER: JP2001-150213

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; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-19

Query Match          95.1%; Score 537.5; DB 6; Length 129;
Best Local Similarity 97.2%; Pred. No. 3.3e-31;
Matches 105; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 80

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 81 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNW-PLTFGPGTKVDIK 127

RESULT 3
US-11-093-274-24
; Sequence 24, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-24

Query Match          95.0%; Score 536.5; DB 7; Length 107;
Best Local Similarity 97.2%; Pred. No. 3.3e-31;
Matches 105; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPP-TFGGQTKVEIK 107

RESULT 4
US-11-054-515-1049
; Sequence 1049, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23F3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
```

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; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1049
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1049

Query Match          94.7%; Score 535; DB 7; Length 251;
Best Local Similarity 96.3%; Pred. No. 7.9e-31;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 143 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 202

Qy 61 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPGTKVDIK 108
Db 203 RFGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFLTGGGQTKVEIK 250

RESULT 5
US-11-093-274-22
; Sequence 22, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-22

Query Match          94.5%; Score 534; DB 7; Length 108;
Best Local Similarity 93.5%; Pred. No. 5e-31;
Matches 101; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
```



```
Query Match      87.3%; Score 493; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 95
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 95

RESULT 10
US-11-084-554-138
; Sequence 138, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ARGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-138

Query Match      87.3%; Score 493; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 95
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 95

RESULT 11
US-11-093-274-33
; Sequence 33, Application US/11093274
; Publication No. US20050260608A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
.
```

```
US-11-093-274-33
Query Match      86.0%; Score 486; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 8.3e-28;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNW 94
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNW 94

RESULT 12
US-11-054-669-87
; Sequence 87, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-87

Query Match      84.4%; Score 477; DB 7; Length 95;
Best Local Similarity 97.9%; Pred. No. 3.4e-27;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNW 94
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNW 94

RESULT 13
US-11-084-554-131
; Sequence 131, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ARGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
.
```

US-11-084-554-131

Query Match 84.4%; Score 477; DB 7; Length 95;
Best Local Similarity 97.9%; Pred. No. 3.4e-27;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNW 94
Db 61 RFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNW 94

RESULT 14

US-10-721-763-27
; Sequence 27, Application US/10721763
; Publication No. US20050249729A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: ANTI TRAIL-R ANTIBODY
; FILE REFERENCE: PH-1573-PCT
; CURRENT APPLICATION NUMBER: US/10/721,763
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: JP2001-150213
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP2001-243040
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: JP2001-314489
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 27
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-721-763-27

Query Match 83.1%; Score 469.5; DB 6; Length 131;
Best Local Similarity 86.2%; Pred. No. 1.4e-26;
Matches 94; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQKPGQAPRLLIYDASNRATGIP 59
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIP 80

Qy 60 ARFSGSGSGTDFTLTISLSLEPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 108
Db 81 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGSGLYTFGGGKLEIK 129

RESULT 15

US-11-000-463-332
; Sequence 332, Application US/110000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radóje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265

; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-332

Query Match 83.0%; Score 469; DB 7; Length 307;
Best Local Similarity 88.1%; Pred. No. 2.8e-26;
Matches 96; Conservative 2; Mismatches 9; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQKPGQAPRLLIYDASNRATGIP 59
Db 150 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIP 209

Qy 60 ARFSGSGSGTDFTLTISRLEPEDFAVYYCQQRSNWPPPTFGPGTKVDIK 108
Db 210 DRFSGSGSGTDFTLTISRLEPEDFAVYYCQQTGRIPP-TFGGKVEIK 257

Search completed: December 14, 2005, 07:48:18
Job time : 5.23348 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:33:29 : Search time 17.1278 Seconds
(without alignments)
606.700 Million cell updates/sec

Title: US-10-720-323-8
Perfect score: 565
Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRSNWPPFTFGPTKVDIK 108

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	534	94.5	114	2 S54905	Ig kappa chain V r
2	530.5	93.9	111	2 S23628	Ig kappa chain V r
3	525.5	93.0	144	2 PL0106	Ig kappa chain pre
4	523.5	92.7	128	2 A56701	Ig kappa chain V r
5	518.5	91.8	108	2 G44151	Ig kappa chain V r
6	514.5	91.1	128	2 S40345	Ig kappa chain V-J
7	513.5	90.9	129	2 S29627	Ig kappa chain V r
8	503.5	89.1	128	2 S40379	Ig kappa chain V r
9	500.5	88.6	107	2 S57444	Ig kappa chain V-J
10	494.5	87.5	125	2 S40344	Ig kappa chain V-J
11	493	87.3	115	1 K3HUVG	Ig kappa chain pre
12	479.5	84.9	106	2 PC4282	Ig kappa chain (an
13	478.5	84.7	114	2 S46375	Ig kappa chain V-J
14	478	84.6	215	2 J50244	Ig kappa chain NIG
15	477	84.4	117	2 S11697	Ig kappa chain pre
16	476.5	84.3	115	2 S40362	Ig kappa chain - h
17	473.5	83.8	107	2 S34005	Ig kappa chain V r
18	473.5	83.8	129	2 S40325	Ig kappa chain - h
19	470	83.2	129	2 S40363	Ig kappa chain - h
20	468.5	82.9	128	2 S40343	Ig kappa chain V-J
21	466	82.5	109	2 A30608	Ig kappa chain V-I
22	465	82.3	116	2 B26555	Ig kappa chain V-I
23	465	82.3	130	2 S40360	Ig kappa chain - h
24	465	82.3	215	2 J50242	Ig kappa chain NIG
25	464	82.1	109	2 H30601	Ig kappa chain V-I
26	464	82.1	109	2 B30601	Ig kappa chain V-I
27	464	82.1	109	2 PH0963	Ig kappa chain V r
28	462	81.8	92	2 S37506	Ig kappa chain V r
29	462	81.8	108	2 C30608	Ig kappa chain V-I

30	462	81.8	109	2 G30607	Ig kappa chain V-I
31	462	81.8	109	2 F30607	Ig kappa chain V-I
32	461.5	81.7	108	2 E30609	Ig kappa chain V-I
33	461	81.6	92	2 S37516	Ig kappa chain V r
34	461	81.6	109	2 C30601	Ig kappa chain V-I
35	461	81.6	109	2 D30601	Ig kappa chain V-I
36	460	81.4	128	2 S20636	Ig kappa chain V r
37	460	81.4	129	1 K3HURA	Ig kappa chain pre
38	459	81.2	109	1 K3HUPM	Ig kappa chain V-I
39	459	81.2	129	1 K3HURH	Ig kappa chain pre
40	458	81.1	109	2 G30601	Ig kappa chain V-I
41	458	81.1	129	2 S46369	Ig light chain var
42	458	81.1	131	2 S40328	Ig kappa chain - h
43	458	81.1	134	2 S38643	Ig kappa chain V r
44	454	80.4	108	2 B30608	Ig kappa chain V-I
45	454	80.4	109	1 K3HUSI	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S54905

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S54905

R:Esposito, G.; Traboni, C.

A:Description: Cloning and sequencing of cDNA coding for the variable domains of a human

A:Reference number: S54905

A:Accession: S54905

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-114 <ESP>

A:Cross-references: UNIPARC:UPI000011620A; EMBL:X82934; NID:g809554; PIDN:CAA58108.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 94.5%; Score 534; DB 2; Length 114;

Best Local Similarity 93.5%; Pred. No. 4.5e-39;

Matches 101; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIYDASNRATGIPA 60

Db 1 DVMTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIYDASRRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWPPFTFGPTKVDIK 108

Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWPPFTFGGTRKVEIK 108

RESULT 2

S23628

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S23628

R:Olee, T.; Lu, E.W.; Huang, D.P.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23628

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-111 <OLE>

A:Cross-references: UNIPARC:UPI0000115F96; EMBL:X59705; NID:g34022; PIDN:CAA42226.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 530.5; DB 2; Length 111;

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Best Local Similarity 96.3%; Pred. No. 8.7e-39;
Matches 104; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPPFTFGPGTKVDIK 108
Db 61 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNW-PWTFGGGTKVEIK 107

RESULT 3
G4106
Ig kappa chain precursor V-J-C region (LSI) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: P0106
J:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma sec
A:Reference number: P0106; MUID:8923583; PMID:2541221
A:Accession: P0106
A:Molecule type: mRNA
A:Residues: 1-144 <SIL>
A:Cross-references: UNIPARC:UPI00001767A2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 93.0%; Score 525.5; DB 2; Length 144;
Best Local Similarity 95.4%; Pred. No. 3e-38;
Matches 103; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPPFTFGPGTKVDIK 108
Db 81 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNW-PLTFGGGTKVEIK 127

RESULT 4
A56701
Ig kappa chain V region precursor (HuA) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are nea
A:Reference number: A56701; MUID:95279371; PMID:7759488
A:Accession: A56701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
A:Cross-references: UNIPARC:UPI0000113B26; GB:L41174; NID:9762823; PIDN:AAA64877.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 523.5; DB 2; Length 128;
Best Local Similarity 95.4%; Pred. No. 4e-38;
Matches 103; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
```

```
Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPPFTFGPGTKVDIK 108
Db 81 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPR-SFGQGTKEIK 127

RESULT 5
G44151
Ig kappa chain V region (JM-10) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C:Accession: G44151
R:Zbbedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; DeGraw, J.; Pys
Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A:Reference number: A44151; MUID:92228746; PMID:1373487
A:Accession: G44151
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-108 <ZEB>
A:Cross-references: UNIPARC:UPI00001139AC; GB:M88317; NID:8183968; PIDN:AAA35975.1; PID:
A:Note: nucleotide translation not given
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-89/Domain: immunoglobulin homology <IMM>

Query Match 91.8%; Score 518.5; DB 2; Length 108;
Best Local Similarity 96.2%; Pred. No. 9e-38;
Matches 101; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 4 LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPARFS 63
Db 3 LTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPARFS 62

Qy 64 GSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPPFTFGPGTKVDIK 108
Db 63 GSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPP-SFGGGTKVEIK 106

RESULT 6
S40345
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40345
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40345
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: UNIPARC:UPI000011615F; EMBL:X72455; NID:9441378; PIDN:CAA51123.1; PI:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 91.1%; Score 514.5; DB 2; Length 128;
Best Local Similarity 91.7%; Pred. No. 2.3e-37;
Matches 100; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 17 EIVLTQSPATLSLSPGERATLSCRASQSVRIYLAWYQKPGQAPRLIIYDAINRATGIPA 76

Qy 61 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPP-FTFGPGTKVDIK 108
Db 77 RFSGSGSGTDFTLTISLSEPEDEFAVYVYCOQRSNWPPPTLTFGGGTKVEIK 125
```


A;Note: the sequence was determined from the germline gene

C;Genetics:
A;Gene: GDB:IGKV3
A;Cross-references: GDB:136266
A;Map position: 2p12-2p11
A;Introns: 17/1
C;Comment: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V-III region (Vg) #status predicted <NAT>
F;21-43/Region: framework 1
F;36-110/Domain: immunoglobulin homology <IMW>
F;44-54/Region: complementarity-determining 1
F;55-69/Region: framework 2
F;70-76/Region: complementarity-determining 2
F;77-108/Region: framework 3
F;109-115/Region: complementarity-determining 3
F;43-108/disulfide bonds: #status predicted

Query Match 87.3%; Score 493; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 21 EVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 80

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 95
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWP 115

RESULT 12

IG kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: PC4282; PC4284
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A;Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin
A;Reference number: PC4279; MUID:97236289; PMID:9125110
A;Accession: PC4282
A;Molecule type: protein
A;Residues: 1-106 <SUZ>
A;Cross-references: UNIPARC:UPI0000176E92
A;Note: E-42
A;Accession: PC4284
A;Molecule type: protein
A;Residues: 1-106 <SU2>
A;Cross-references: UNIPARC:UPI0000176E92
A;Note: E-56
C;Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjoe
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;14-88/Domain: immunoglobulin homology <IMW>

Query Match 84.9%; Score 479.5; DB 2; Length 106;
Best Local Similarity 86.8%; Pred. No. 1.9e-34;
Matches 92; Conservative 8; Mismatches 5; Indels 1; Gaps 1;

Qy 3 VLTSQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPARF 62
Db 1 VLTSQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDISKRATGIPAKF 60

Qy 63 SGSGSGTDFTLTISLSEPEDFAVYQCQRSNWPPTFGPGTKVDIK 108
Db 61 SGSGSGTDFTLTISLSEPEDFAVYCCQRASW-PLTFGGGTVKEIK 105

RESULT 13

, S46375

IG kappa chain V-J region (T33-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46375; S38648
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46375
A;Molecule type: mRNA
A;Residues: 1-114 <BEN>
A;Cross-references: UNIPARC:UPI00001165A8; EMBL:Z27176; NID:G415967; PIDN:CAA81700.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;20-95/Domain: immunoglobulin homology <IMW>

Query Match 84.7%; Score 478.5; DB 2; Length 114;
Best Local Similarity 86.2%; Pred. No. 2.5e-34;
Matches 94; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQKPGQAPRLIIYDASNRATGIP 59
Db 5 EIVLTQSPATLSLSPGERATLSCRASQSISSSYLAWYQKPGQAPRLIIYGASSRATGIP 64

Qy 60 ARFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWPPTFGPGTKVDIK 108
Db 65 DRFSGSGSGTDFTLTISLSEPEDFAVYCCQYSGSPPTFGQGTKEIK 113

RESULT 14

IG kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Ta
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
A;Cross-references: UNIPARC:UPI0000176982
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMW>

Query Match 84.6%; Score 478; DB 2; Length 215;
Best Local Similarity 85.2%; Pred. No. 5.1e-34;
Matches 92; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
Db 1 EVVLTQSPATLSVSPGERATLSCRASQSVHSNLAWYQKPGQAPRLIIYRASTRATGIPA 60

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNWPPTFGPGTKVDIK 108
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYCCQYNTWPPLTFGGGTVKEIK 108

RESULT 15

IG kappa chain precursor V-III region - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
R;Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A;Title: A large section of the gene locus encoding human immunoglobulin variable region
A;Reference number: S11697; MUID:85264787; PMID:3927006
A;Accession: S11697
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <PEC>

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYCCQYNTWPPLTFGGGTVKEIK 108
Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYCCQYNTWPPLTFGGGTVKEIK 108

A;Cross-references: UNIPARC:UPI0000115841; EMBL:X17264; NID:q37898; PIDN:CRA35168.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
C;Genetics: 17/1

A;introns: 17/1
C;superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 477; DB 2; Length 115;
Best Local Similarity 97.9%; Pred. No. 3.4e-34;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLIIYDASNRATGIPA 60
|||
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQOKPGQAPRLIIYDASNRATGIPA 80
|||

Qy 61 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNW 94
|||
Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYQCQRSNW 114
|||

Search completed: December 14, 2005, 07:44:53
Job time : 17.1278 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:32:04 ; Search time 91.8238 Seconds
(without alignment)
829.818 Million cell updates/sec

Title: US-10-720-323-8

Perfect score: 565

Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWPFFTFPGTKVDIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	493	87.3	115	1 KV31_HUMAN	P04433 homo sapien
2	485.5	85.9	108	2 Q9UL83_HUMAN	Q9ul83 homo sapien
3	480	85.0	129	1 KV3H_HUMAN	P04207 homo sapien
4	474	83.9	109	2 Q9UL85_HUMAN	Q9ul85 homo sapien
5	460	81.4	129	1 KV3L_HUMAN	P18135 homo sapien
6	459	81.2	109	1 KV3F_HUMAN	P01624 homo sapien
7	459	81.2	129	1 KV3M_HUMAN	P18136 homo sapien
8	455	80.5	109	2 Q9UL78_HUMAN	Q9ul78 homo sapien
9	454	80.4	109	1 KV3B_HUMAN	P01620 homo sapien
10	454	80.4	109	1 KV3D_HUMAN	P01622 homo sapien
11	454	80.4	109	2 Q9UL86_HUMAN	Q9ul86 homo sapien
12	453.5	80.3	236	2 Q6PIL8_HUMAN	Q6pil8 homo sapien
13	453	80.2	235	2 Q6PIF2_HUMAN	Q6pif2 homo sapien
14	448	79.3	109	1 KV3E_HUMAN	P01623 homo sapien
15	448	79.3	235	2 Q6GMW0_HUMAN	Q6gmw0 homo sapien
16	444.5	78.7	236	2 Q6P5S8_HUMAN	Q6p5s8 homo sapien
17	437.5	77.4	128	1 KV3K_HUMAN	P06311 homo sapien
18	435	77.0	108	1 KV3A_HUMAN	P06319 homo sapien
19	431	76.3	235	2 Q6GMV9_HUMAN	Q6gmv9 homo sapien
20	429	75.9	109	1 KV3J_HUMAN	P04206 homo sapien
21	420.5	74.4	116	1 KV3J_HUMAN	P04434 homo sapien
22	417.5	73.9	100	1 KV3C_HUMAN	P01621 homo sapien
23	417.5	73.9	236	2 Q6GMX8_HUMAN	Q6gmx8 homo sapien
24	410.5	72.7	108	1 KV1M_HUMAN	P01605 homo sapien
25	404	71.5	107	1 KV1D_HUMAN	P01596 homo sapien
26	402.5	71.2	236	2 Q6PIH7_HUMAN	Q6pih7 homo sapien
27	399.5	70.7	108	2 Q9UL79_HUMAN	Q9ul79 homo sapien
28	398	70.4	107	2 Q96SA9_HUMAN	Q96sa9 homo sapien
29	396.5	70.2	108	2 Q9UL77_HUMAN	Q9ul77 homo sapien
30	392.5	69.5	244	2 Q65ZC8_HUMAN	Q65zc8 homo sapien
31	391.5	69.3	108	1 KV1H_HUMAN	P01600 homo sapien

32	391	69.2	107	2 Q9UL81_HUMAN	Q9ul81 homo sapien
33	388.5	68.8	108	1 KV1V_HUMAN	P04430 homo sapien
34	388.5	68.8	234	2 Q569I9_HUMAN	Q569i9 homo sapien
35	388.5	68.8	240	2 Q65ZC9_HUMAN	Q65zc9 homo sapien
36	387.5	68.6	111	1 KV3M_MOUSE	P01665 mus musculus
37	386.5	68.4	236	2 Q6GMW1_HUMAN	Q6gmw1 homo sapien
38	385.5	68.2	108	2 Q9UL70_HUMAN	Q9ul70 homo sapien
39	384.5	68.1	108	1 KV1L_HUMAN	P01604 homo sapien
40	383.5	67.9	111	1 KV3O_MOUSE	P01667 mus musculus
41	383.5	67.9	134	1 KV4C_HUMAN	P06314 homo sapien
42	382.5	67.7	236	2 Q6PIT5_HUMAN	Q6pit5 homo sapien
43	381.5	67.5	108	1 KV1K_HUMAN	P01603 homo sapien
44	380.5	67.3	108	1 KV1E_HUMAN	P01597 homo sapien
45	380.5	67.3	108	1 KV1P_HUMAN	P01608 homo sapien

ALIGNMENTS

RESULT 1

KV31_HUMAN
ID KV31_HUMAN STANDARD; PRT; 115 AA.
AC P04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region VG precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated within the VK locus".
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL; X01668; ; NOT_ANNOTATED_CDS; Genomic_DNA.
CC PIR; A01900; K3HUVG.
CC HSSP; P01625; 1EEQ.
CC SMR; P04433; 21-115.
CC GO; GO:0005576; C:extracellular region; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; IG_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin domain; Immunoglobulin V region; Signal.
CC SIGNAL 1 20
FT CHAIN 21 >115
FT REGION 21 43
FT REGION 44 54
FT REGION 55 69
FT REGION 70 76
FT REGION 77 108
FT REGION 109 115
FT DISULFID 43 108
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 87.3%; Score 493; DB 1; Length 115;
Best Local Similarity 100.0%; Pred.No. 2.9e-43; Indels 0; Gaps 0;
Matches 95; Conservative 0; Mismatches 0;


```
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -; mRNA.
DR PIR; D30609; D30609.
DR HSSP; P01625; 1EK3.
DR SMR; Q9UL85; 1-109.
DR InterPro; IPR007110; Ig-like.
DR SMART; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 109 109
FT SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
SQ QUERY Match 83.9%; Score 474; DB 2; Length 109;
Best Local Similarity 83.3%; Pred. No. 2.6e-41;
Matches 90; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRTATGIPA 60
DB 1 EIVLTQSPATLSVSPGERATLSCWASQISNNLAWYQKPGQAPRLIIYGASTATGIPA 60
QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCOQRSNWPPFTFGGCTKVDIK 108
DB 61 RFSGSGSGTEFTLTISLSQSDFAIYHCQYNSWPLPFTGGGTRKVEIK 108
RESULT 5
KV3L_HUMAN
ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; P10022; K3HUHA.
DR HSSP; P01625; 1EEQ.
DR SMR; P18135; 21-129.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0006955; P:immune response; NAS.
```

```
DR InterPro; IPR007110; Ig-like.
DR SMART; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HAH.
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 JKL segment.
FT DISULFID 43 109 By similarity.
FT NON_TER 129 129
FT SEQUENCE 129 AA; 14073 MW; D3C529272774D0 CRC64;
SQ QUERY Match 81.4%; Score 460; DB 1; Length 129;
Best Local Similarity 87.2%; Pred. No. 8.9e-40;
Matches 95; Conservative 2; Mismatches 10; Indels 2; Gaps 2;
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRTATGIP 59
DB 21 EIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYGASSRATGIP 80
QY 60 ARFGSGSGTDFTLTISLSEPEDFAVYYCOQRSNWPPFTFGGCTKVDIK 108
DB 81 DRFGSGSGTDFTLTISRLEPEDFAVYYCOQYGT-SPRTFGGCTKVEIK 128
RESULT 6
KV3F_HUMAN
ID KV3F_HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -!- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
CC globulin activity.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR; A01897; K3HUPM.
DR HSSP; P01625; 1LVE.
DR SMR; P01624; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
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FT NON TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match
Best Local Similarity 81.2%; Score 459; DB 1; Length 109;
Matches 90; Conservative 9; Mismatches 8; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRSQSVSSSYLAWYQQKPKGAPRLIIYDASNRATGIP 59
Db 1 EIVMTQSPVTLSPGERATLSCRSQSVSSSYLAWYQQKPKGAPRLIIYGASTRATGIP 60

Qy 60 ARFSGSGSGDTFTLTISLSPEDFVAVYCCQQRNWPFFTFPGTKVDIK 108
Db 61 ARFSGSGSGTEFTLTISLQSEDFAVYCCQYNNWPP-TEGQGRVBEIK 108

RESULT 7
KV3W_HUMAN
ID KV3W_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
antibodies expressed in patients with chronic lymphocytic
leukemia.
-----
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use as long as its content is in no way modified and this statement is not
removed.
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DR PIR; FLO021; K3HUHI.
DR HSSP; P01625; 1EEQ.
DR SMR; P18136; 21-129.
DR Ensembl; ENSG00000169769; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1_.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 Ig kappa chain V-III region HIC.
FT REGION 21 43 Framework-1.
FT REGION 44 55 Complementarity-determining-1.
FT REGION 56 70 Framework-2.
FT REGION 71 77 Complementarity-determining-2.
FT REGION 78 109 Framework-3.
FT REGION 110 118 Complementarity-determining-3.
FT REGION 119 129 JK1 segment.
FT DISULFID 43 109 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14071 MW; 7395528EA2BB74D6 CRC64;

Query Match
81.2%; Score 459; DB 1; Length 129;

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Best Local Similarity 86.2%; Pred. No. 1.1e-39;
Matches 94; Conservative 4; Mismatches 9; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRSQSVSSSYLAWYQQKPKGAPRLIIYDASNRATGIP 59
Db 21 EIVLTQSPATLSLSPGERATLSCRSQSVSSSYLAWYQQKPKGAPRLIIYGASRAATGIP 80

Qy 60 ARFSGSGSGDTFTLTISLSPEDFVAVYCCQQRNWPFFTFPGTKVDIK 108
Db 81 DRFSGSGSGDTFTLTISRLPEXDFVAVYCCQYGS-SPWTFGQGTKEIK 128

RESULT 8
Q9UL78_HUMAN
ID Q9UL78_HUMAN PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.;
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1373487;
RA Zebede S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT "Human combinatorial antibody libraries to hepatitis B surface
antigen.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=8436174;
RA Wagner S.D., Luzzatto L.;
RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
distributed over a large portion of the V kappa locus and do not show
somatic mutation.";
RL Eur. J. Immunol. 23:391-397(1993).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1552291;
RA Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
RT "Evidence for somatic selection of natural autoantibodies.";
RL J. Exp. Med. 175:983-991(1992).
DR EMBL; AF035036; AAD56272.1; -; mRNA.
DR PIR; A30601; A30601.
DR PIR; A30608; A30608.
DR PIR; B30601; B30601.
DR PIR; B30607; B30607.
DR PIR; C30601; C30601.
DR PIR; C30607; C30607.
DR PIR; C30608; C30608.
DR PIR; D30601; D30601.
DR PIR; D30607; D30607.
DR PIR; D30608; D30608.
DR PIR; F30607; F30607.
DR PIR; F30608; F30608.
DR PIR; G30601; G30601.
DR PIR; G30608; G30608.
DR PIR; H30607; H30607.
DR PIR; H30608; H30608.

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DR PIR: H44151; H44151.
DR PIR: I30601; I30601.
DR PIR: PH0963; PH0963.
DR PIR: PH0964; PH0964.
DR PIR: PH0965; PH0965.
DR PIR: S33988; S33988.
DR PIR: S34096; S34096.
DR HSSP: P01625; 1EX3.
DR SMR: Q9UL78; 1-109.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 80.5%; Score 455; DB 2; Length 109;
Best Local Similarity 86.2%; Pred. No. 2.4e-39;
Matches 94; Conservative 3; Mismatches 10; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPKGQAPRLIYDASNRATGIP 59
Db 1 EIVLTQSPGTLTLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLIYDASNRATGIP 60

Qy 60 ARFSGSGGTFTLTISLSEPEDFAVYCCQQRNSWPPPTFGPGTKVDIK 108
Db 61 DRFSGSGGTFTLTISRLEPEDCAVYCCQYGS-SPLTFGGGTKEIK 108

RESULT 9
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region SIg.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC Globulin activity.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: A01892; K3HUSI.
DR HSSP: P01625; 1LVE.
DR SMR: P01620; 1-109.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 80.5%; Score 455; DB 2; Length 109;
Best Local Similarity 86.2%; Pred. No. 2.4e-39;
Matches 94; Conservative 3; Mismatches 10; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPKGQAPRLIYDASNRATGIP 59
Db 1 EIVLTQSPGTLTLSPGERATLSCRASQSVSSSYLAWYQQKPKGQAPRLIYDASNRATGIP 60

Qy 60 ARFSGSGGTFTLTISLSEPEDFAVYCCQQRNSWPPPTFGPGTKVDIK 108
Db 61 DRFSGSGGTFTLTISRLEPEDCAVYCCQYGS-SPLTFGGGTKEIK 108

RESULT 9
KV3B_HUMAN
ID KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region SIg.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC Globulin activity.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: A01892; K3HUSI.
DR HSSP: P01625; 1LVE.
DR SMR: P01620; 1-109.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 80.4%; Score 454; DB 1; Length 109;
Best Local Similarity 85.3%; Pred. No. 3.1e-39;
Matches 93; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPKGQAPRLIYDASNRATGIP 59
Db 1 EIVLTQSPGTLTLSPGERATLSCRASQSVNSFLAWYQQKPKGQAPRLIYDASNRATGIP 60

Qy 60 ARFSGSGGTFTLTISLSEPEDFAVYCCQQRNSWPPPTFGPGTKVDIK 108
Db 61 DRFSGSGGTFTLTISRLEPEDFAVYCCQYGS-SPOTFGGSKVEIK 108

RESULT 10
KV3D_HUMAN
ID KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for the
RT mechanism of antibody production.";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: A01895; K3HUTI.
DR HSSP: P01625; 1LVE.
DR SMR: P01622; 1-109.
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
DR KW Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109
FT NON_TER 109
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 80.4%; Score 454; DB 1; Length 109;
Best Local Similarity 85.3%; Pred. No. 3.1e-39;
Matches 93; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSV-SSYLAWYQQKPKGQAPRLIYDASNRATGIP 59
Db 1 EIVLTQSPGTLTLSPGERATLSCRASQSVNSFLAWYQQKPKGQAPRLIYDASNRATGIP 60

Qy 60 ARFSGSGGTFTLTISLSEPEDFAVYCCQQRNSWPPPTFGPGTKVDIK 108
Db 61 DRFSGSGGTFTLTISRLEPEDFAVYCCQYGS-SPOTFGGSKVEIK 108
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -; mRNA.
DR HSSP; P01837; IKCU.
DR SMR; Q6PJF2; 21-235.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.C1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG.C1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 80.2%; Score 453; DB 2; Length 235;
Best Local Similarity 85.3%; Pred. No. 9.8e-39;
Matches 93; Conservative 5; Mismatches 9; Indels 2; Gaps 2;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQKQKPGQAPRLIYDASNRATGIP 59
DB 21 EIVLTQSPATLSLSPGERATLSCRASQIVSSAYLAWYQKQKPGQAPRLIMFGSSSRATGIP 80

QY 60 ARFGSGSGTDTLTITISLEPEDFAVYCYQQRSNWPPFTFGPTGKVDIK 108
DB 81 DRFGSGSGTDTLTITISLEPEDFAVYCYQYGS-SQGTFGPTGKVDIK 128

RESULT 14
KV3E HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-III region WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RP PROTEIN SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group.";
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: This chain was isolated from an Igm with anti-gamma
CC globulin activity.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
DR PIR; A01896; K3HULW.
DR HSSP; P01625; ILVE.
DR SMR; P01623; 1-109.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG.V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DISULFID 23 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 79.3%; Score 448; DB 1; Length 109;
Best Local Similarity 85.3%; Pred. No. 1.3e-38;
Matches 93; Conservative 3; Mismatches 11; Indels 2; Gaps 2;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSS-YLAWYQKQKPGQAPRLIYDASNRATGIP 59
DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSGYLWYQKQKPGQAPRLIYDASNRATGIP 60

QY 60 ARFGSGSGTDTLTITISLEPEDFAVYCYQQRSNWPPFTFGPTGKVDIK 108
DB 61 DRFGSGSGTDTLTITISLEPEDFAVYCYQYGLR-TFGQGTKEIK 108

RESULT 15
Q6GMW0 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";

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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:31:09 ; Search time 70.8899 Seconds
(without alignments)
669.389 Million cell updates/sec

Title: US-10-720-323-8

Perfect score: 565

Sequence: 1 EIVLTQSPATLSLSPGERAT.....QQRNWPFFFGPTKVDIK 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	565	100.0	108	5	AAM51165 Anti-tumo
2	565	100.0	108	5	AAM51173 Human Vg/
3	565	100.0	108	5	Aau76334 Human ant
4	565	100.0	108	7	Adj73533 Erythro
5	565	100.0	108	7	Adj73534 Erythro
6	565	100.0	108	9	Adw07091 Anti-PsAa
7	565	100.0	129	5	AAM51174 Human rec
8	565	100.0	129	5	AAM51175 Human mAb
9	547	96.8	108	4	AAB72884 Human ant
10	547	96.8	108	9	AEb01062 Human IP1
11	547	96.8	109	7	Adf11411 16E1 anti
12	547	96.8	215	7	Adf11435 16E1 anti
13	546	96.6	128	8	Adm41547 Anti-inte
14	546	96.6	130	7	AdD89877 Human ant
15	546	96.6	130	8	AdS64664 Human 9E7
16	546	96.6	130	8	AdS64653 Human ant
17	546	96.6	235	8	Adm41573 Anti-inte
18	544	96.3	108	8	AdS19298 Light cha
19	542	95.9	108	8	Adw08866 IGF-IR an
20	542	95.9	109	7	Adf11395 22B3 anti
21	542	95.9	215	7	Adf11419 22B3 anti
22	541	95.8	108	8	Adi22138 Anti-plat
23	540	95.6	108	9	AEb01057 Human IP1
24	540	95.6	109	7	Adf11403 2D8 anti-

25	540	95.6	109	7	ADP11415	Adf11415 9H7 anti-
26	540	95.6	215	7	ADP11439	Adf11439 9H7 anti-
27	540	95.6	215	7	ADP11427	Adf11427 2D8 anti-
28	537.5	95.1	129	6	ABP57362	Abp57362 Anti-TRAI
29	535.5	94.8	107	6	ABR54916	ABr54916 Light cha
30	535.5	94.8	107	9	ABE19292	ABe19292 Igg kappa
31	535.5	94.8	236	9	ADZ51040	Adz51040 Amino aci
32	535	94.7	251	5	ABP45038	Abp45038 Human Bly
33	535	94.7	251	7	ADG95865	Adg95865 Single ch
34	534.5	94.6	129	7	ADJ73532	Adj73532 Erythro
35	533	94.3	128	7	ADJ73528	Adj73528 Erythro
36	531	94.0	109	4	AAAB62756	AAb62756 Human HIV
37	530.5	93.9	107	9	ADY26776	Ady26776 Anti-NGF-
38	530.5	93.9	110	9	ADX02205	Adx02205 SARS coro
39	530.5	93.9	110	9	ADX02049	Adx02049 SARS coro
40	530.5	93.9	214	8	ADH34591	Adh34591 023 light
41	530.5	93.9	251	9	ADX01956	Adx01956 SARS coro
42	530.5	93.9	252	9	ADX02034	Adx02034 SARS coro
43	530	93.8	108	9	ADM08864	Adm08864 IGF-IR an
44	530	93.8	108	9	AEb01064	AEb01064 Human IP1
45	529.5	93.7	224	4	AAAB99371	AAb99371 Human int

ALIGNMENTS

RESULT 1

AAM51165

ID AAM51165 standard; protein; 108 AA.

AC AAM51165;

DT 10-JUN-2002 (first entry)

DE Anti-tumour necrosis factor antibody light chain variable region.

XX Homo sapiens.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX  Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
PI  WPI; 2002-217194/27.
DR
XX
XX  Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT  treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT  angina pectoris, myocardial infarction, leprosy.
XX
XX  Claim 9; Page 129-130; 131pp; English.
XX
CC  The present sequence is that of the light chain variable region of an
CC  anti-tumour necrosis factor (TNF) antibody of the invention. The
CC  invention provides isolated human, primate, rodent, mammalian, chimeric,
CC  humanised and/or complementarity determining region (CDR)-grafted anti-
CC  TNF antibodies, immunoglobulins, cleavage products and other specified
CC  portions and variants, as well as anti-TNF antibody compositions,
CC  encoding or complementary nucleic acids, vectors, host cells,
CC  compositions, formulations, devices, transgenic animals, transgenic
CC  plants, and methods of making and using them. The anti-TNF antibody
CC  comprises at least a portion of an immunoglobulin molecule, especially
CC  the heavy chain and/or light chain variable regions given in AAM51164 and
CC  in the present sequence, or either all of the CDRs of the heavy chain
CC  (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
CC  63). The antibody may inhibit TNF-induced cell adhesion molecules,
CC  inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC  in a mouse model. It is useful for diagnosing or treating a TNF related
CC  condition in a cell, tissue, organ or animal (claimed) such as rheumatoid
CC  arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC  sickle cell anaemia, diabetes, a cardiovascular disease such as
CC  atherosclerosis, atherosclerosis, restenosis, angina pectoris or
CC  myocardial infarction, an infectious disease in a cell such as bacterial,
CC  viral and fungal infections, pneumonia, leprosy and malaria, a malignant
CC  disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC  lymphoma and multiple myeloma, or a neurological disease such as multiple
CC  sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC  Creutzfeldt-Jakob disease
XX
XX  Sequence 108 AA;
SQ
Query Match 100.0%; Score 565; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLTIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLTIYDASNRATGIPA 60

Qy 61 RFGSGSGTDTLTITISLPEPDFAVYVCQQRSNWPPFTFGTGKVDIK 108
Db 61 RFGSGSGTDTLTITISLPEPDFAVYVCQQRSNWPPFTFGTGKVDIK 108

RESULT 2
AAM51173
ID AAM51173 standard; protein; 108 AA.
XX
AC AAM51173;
XX
XX 10-JUN-2002 (first entry)
XX
DE Human Vg/38K-type light chain variable region.
XX
KW Tumour necrosis factor alpha; TNF; antibody; light chain; CDR;
KW complementarity determining region; antirheumatic; antiarthritic;
KW antileucic; antiaesthetic; antiallergic; antiinflammatory; antisickling;
KW antididiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW antiangiinal; cardiant; antibacterial; virucide; fungicide; antileproptic;
KW protozoacide; cyrostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy; Vg/38K.
XX
OS Homo sapiens.
XX

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PH Key Location/Qualifiers
FT Region 1..23 /label= FR1
FT Region 24..34 /label= CDR1
FT Region 35..49 /label= FR2
FT Region 50..56 /label= CDR2
FT Region 57..88 /label= FR3
FT Region 89..98 /label= CDR3
FT Region 99..108 /label= J3
XX WO200212502-A2.
XX 14-FEB-2002.
XX 07-AUG-2001; 2001WO-US024785.
XX 07-AUG-2000; 2000US-0223360P.
PR 29-SEP-2000; 2000US-0236826P.
PR 01-AUG-2000; 2001US-00920137.
XX (CENZ ) CENTOCOR INC.
XX
XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
PI WPI; 2002-217194/27.
DR N-PSDB; ABL53513.
XX
XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
PT angina pectoris, myocardial infarction, leprosy.
XX
XX Example 3; Fig 5; 131pp; English.
XX
CC The present sequence is that of a human Vg/38K-type light chain variable
CC region encoded by a human germline gene in a transgenic mouse used in
CC human monoclonal antibody (mAb) construction. A gentNV fusion was
CC performed using spleen cells from a hybrid mouse containing human
CC variable and constant region antibody transgenes that was immunised with
CC recombinant human tumour necrosis factor (TNF) alpha. Human mAbs were
CC obtained that bound immobilised human TNF alpha with apparently high
CC avidity. These mAbs had a totally human IgG1, kappa isotype. The mature
CC portion of the light chain variable region of 2 of the mAbs, TNV14 and
CC TNV15, were identical (see AAM51174) to the present sequence, while the
CC light chain variable region of 2 others, TNV14(B) and TNV196 (see
CC AAM51175), differed by a single amino acid residue. The invention
CC provides human, primate, rodent, mammalian, chimeric, humanised and/or
CC complementarity determining region (CDR)-grafted anti-TNF antibodies,
CC immunoglobulins, and cleavage products and variants, as well as anti-TNF
CC antibody compositions, encoding or complementary nucleic acids, vectors,
CC host cells, compositions, formulations, devices, transgenic animals,
CC transgenic plants, and methods of making and using them. The anti-TNF
CC antibody comprises at least a portion of an immunoglobulin molecule,
CC especially the heavy chain and/or light chain variable regions given in
CC the present sequence and in AAM51165, or either all of the CDRs of the
CC heavy chain (see AAM51158-60) or all of the CDRs of the light chain (see
CC AAM51161-63). The antibodies may inhibit TNF-induced cell adhesion
CC molecules, inhibit TNF binding to receptor, or provide Arthritic Index
CC improvement in a mouse model. They are useful for diagnosing or treating
CC a TNF related condition in a cell, tissue, organ or animal (claimed) such
CC as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis,
CC Crohn's pathology, sickle cell anaemia, diabetes, a cardiovascular
CC disease such as arteriosclerosis, atherosclerosis, restenosis, angina
CC pectoris or myocardial infarction, an infectious disease in a cell such
CC as bacterial, viral, and fungal infections, pneumonia, leprosy and
CC malaria, a malignant disease such as leukaemia, chronic myelocytic
CC leukaemia, Burkitt's lymphoma and multiple myeloma, or a neurological
CC disease such as multiple sclerosis, Parkinson's disease, spinal ataxia,

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CC Alzheimer's disease and Creutzfeldt-Jakob disease
XX Sequence 108 AA;
SQ
Query Match 100.0%; Score 565; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFSGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108
DB 61 RFSGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108
RESULT 3
AAU76334
ID AAU76334 standard; peptide; 108 AA.
XX AAU76334;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human anti-dual integrin antibody complete variable region #2.
XX
KW Human; antibody; dual integrin; HC CDR; variable region; LC CDR;
KW medical device; immune related disease; rheumatoid arthritis;
KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
KW neurological disease; multiple sclerosis; Parkinson's disease;
KW Alzheimer's disease; Creutzfeldt-Jakob disease.
XX
OS Homo sapiens.
XX
PN WO200212501-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US024784.
XX
PR 07-AUG-2000; 2000US-0223363P.
XX
PR 01-AUG-2001; 2001US-00920267.
XX
PA (CENZ ) CENTOCOR INC.
XX
PI Giles-Komar J, Heavner G, Snyder L, Trikha M;
XX
WPI; 2002-217193/27.
XX
PT Novel isolated mammalian anti-dual integrin antibody, useful for
PT diagnosing or treating dual integrin related condition such as rheumatoid
PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.
XX
PS Claim 1; Page 134; 144pp; English.
XX
CC The invention relates to an isolated mammalian anti-dual integrin
CC antibody having at least one of the human heavy chain or light chain
CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
CC included are the nucleic acids encoding the CDRs, a vector comprising the
CC nucleic acids, a host cell comprising the vector, an anti-idiotypic
CC antibody that binds to the anti-dual integrin, a medical device comprising
CC the antibody suitable for administration by parenteral, subcutaneous,
CC intramuscular, intravenous, intrarticular, intrabronchial,
CC intraabdominal, intracapsular, intracartilaginous, intracavitary,
CC intracerebellar, or other routes as given in specification. The antibody
CC is useful for diagnosing or treating a dual integrin related condition in
CC an animal for example, immune related disease such as rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC
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CC sickle cell anaemia, diabetes, cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
CC myocardial infarction, infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma, multiple myeloma; neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
CC Creutzfeldt-Jakob disease and many other diseases given in the
CC specification. The present sequence is an anti-dual integrin human
CC variable region containing at least one of the six CDRs listed above
CC (AAU76327-AAU76332)
XX
SQ Sequence 108 AA;
Query Match 100.0%; Score 565; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
DB 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIIYDASNRATGIPA 60
QY 61 RFSGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108
DB 61 RFSGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108
RESULT 4
ADJ73533
ID ADJ73533 standard; protein; 108 AA.
XX ADJ73533;
XX
DT 06-MAY-2004 (first entry)
XX
DE Erythropoietin light chain mimetibody SeqID 989.
XX
KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiac; antimicrobial; cytostatic; neuroprotective;
KW erythropoietin.
XX
OS Synthetic.
XX
PN WO2003084477-A2.
XX
PD 16-OCT-2003.
XX
PF 24-MAR-2003; 2003WO-US009139.
XX
PR 29-MAR-2002; 2002US-0368791P.
XX
PA (CENZ ) CENTOCOR INC.
XX
PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
XX
WPI; 2003-804237/75.
XX
PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.
XX
PS Example 2; SEQ ID NO 989; 97pp; English.
XX
CC This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
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CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/ or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC polypeptide sequence is an erythropoietin light chain mimetibody of the
CC invention.

XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 565; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYDASNRATGIPA 60
Qy 61 RFGSGSGTDTLTITISLEPEDFAVYQCQRSNWPPFTFGPTKVDIK 108
Db 61 RFGSGSGTDTLTITISLEPEDFAVYQCQRSNWPPFTFGPTKVDIK 108

RESULT 5

ID ADJ73534 standard; protein; 108 AA.
XX
AC ADJ73534;

DT 06-MAY-2004 (first entry)

DE Erythropoietin light chain mimetibody SeqID 990.

KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW erythropoietin.

OS Synthetic.

XX WO2003084477-A2.

XX 16-OCT-2003.

XX 24-MAR-2003; 2003WO-US009139.

XX 29-MAR-2002; 2002US-0368791P.

XX (CENZ) CENTOCOR INC.

PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;

XX WPI; 2003-804237/75.

PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.

PS Example 2; SEQ ID NO 990; 97pp; English.

XX This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products,
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms

CC of immune, cardiovascular, infectious, malignant and/ or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC polypeptide sequence is an erythropoietin light chain mimetibody of the
CC invention.

XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 565; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYDASNRATGIPA 60
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYDASNRATGIPA 60
Qy 61 RFGSGSGTDTLTITISLEPEDFAVYQCQRSNWPPFTFGPTKVDIK 108
Db 61 RFGSGSGTDTLTITISLEPEDFAVYQCQRSNWPPFTFGPTKVDIK 108

RESULT 6

ADW07091
ID ADW07091 standard; protein; 108 AA.

XX
AC ADW07091;

DT 07-APR-2005 (first entry)

DE Anti-PsAA-antibody 9A7 VK.

KW antibacterial; antiinflammatory; immunosuppressive; antibody engineering;
KW pharmaceutical; infection; pneumonia; meningitis; sepsis;
KW pneumococcal surface adhesin A; PsAA; light chain variable region.

XX Homo sapiens.

XX WO2005003174-A1.

XX 13-JAN-2005.

XX 08-JUL-2004; 2004WO-DK000492.

XX 08-JUL-2003; 2003DK-00001044.

XX 11-JUL-2003; 2003US-0486647P.

XX (GENE-) GENESTO AS.

XX Sorensen AP, Benfield TL, Lundgren JD, Kempe TD;

XX WPI; 2005-101476/11.

XX N-PSDB; ADW07090.

XX New binding member towards Streptococcus pneumoniae surface adhesin A
PT protein, useful for treating or preventing pneumonia, meningitis and/or
PT sepsis.

PS Disclosure; SEQ ID NO 40; 137pp; English.

XX The invention describes an isolated binding member comprising at least
CC one binding domain capable of specifically binding Streptococcus
CC pneumoniae surface adhesin A (PsAA) protein, the binding domain having a
CC dissociation constant Kd for PsAA which is less than 1 x10⁻⁶ M. Also
CC described are: an isolated nucleic acid molecule encoding at least a part
CC of the binding member described above; a vector comprising the nucleic
CC acid molecule of (1); a host cell comprising the nucleic acid molecule of
CC (1); a cell line engineered to express the binding member described above
CC ; detecting or diagnosing a disease or disorder associated with
CC Pneumococcus in an individual; a kit comprising at least one binding
CC member described above, the antibody being labeled; and a pharmaceutical
CC composition comprising at least one binding member described above. The
CC binding member is useful for producing a pharmaceutical composition for
CC the treatment of Pneumococcus infection. The binding member, methods and

CC composition are useful for treating or preventing an individual suffering
 CC from disorders or diseases associated with S. pneumoniae, e.g. pneumonia,
 CC meningitis and/or sepsis. This is the amino acid sequence of anti-
 CC pneumococcal surface adhesin A (PsaA)-antibody 9A7 kappa light chain
 CC variable region.
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 565; DB 9; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e-37;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108

Db 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108

RESULT 7

AAM51174

ID AAM51174 standard; protein; 129 AA.

XX AC AAM51174;

XX DT 10-JUN-2002 (first entry)

XX DE Human recombinant mAb TNV14, TNV15 light chain variable region.

XX KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
 KW complementarity determining region; antirheumatic; antiarthritic;
 KW antitumor; antidiabetic; antiallergic; antinflammatory; antitoxic;
 KW antidiabetic; antiatherosclerotic; antiatherosclerotic; vasotropic;
 KW antidiabetic; cardiac; antibacterial; virucide; fungicide; antileptotic;
 KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
 KW human; diagnosis; therapy; TNV14; TNV15; monoclonal antibody; mAb.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..20 /label= Signal_peptide

FT Protein 20..129 /label= Mature_protein

FT Region 21..43 /label= FR1

FT Region 44..54 /label= CDR1

FT Region 55..69 /label= FR2

FT Region 70..76 /label= CDR2

FT Region 77..108 /label= FR3

FT Region 109..118 /label= CDR3

FT Region 119..129 /label= J3

XX WO200212502-A2.

XX PD 14-FEB-2002.

XX PF 07-AUG-2001; 2001WO-US024785.

XX PR 07-AUG-2000; 2000US-0223360P.

XX PR 29-SEP-2000; 2000US-0236826P.

XX PR 01-AUG-2001; 2001US-0092013P.

XX PA (CENZ) CENTOCOR INC.

PI Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;
 XX WPI; 2002-217194/27.
 DR N-PSDB; ABL53514.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for
 PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,
 PT angina pectoris, myocardial infarction, leprosy.

XX Example 3; Fig 5; 131pp; English.

XX The present sequence is that of the light chain variable region of anti-
 CC tumour necrosis factor (TNF) human recombinant monoclonal antibodies
 CC (mAbs) TNV14 and TNV15. These are human mAbs produced from a GenTV
 CC fusion using spleen cells from a hybrid mouse containing human variable
 CC and constant region antibody transgenes that was immunised with human TNF
 CC alpha. The human mAbs bind immobilised human TNF alpha with high avidity
 CC and have a totally human IgG1, kappa isotype. The mature portion of the
 CC light chain variable region is identical to that of the Vg/38-type light
 CC chain germline sequence (see AAM51173). The light chain variable regions
 CC of 2 other human mAbs (see AAM51175) show a single amino acid difference.
 CC The invention provides human, primate, mammalian, rodent, chimeric,
 CC humanised and/or complementarity determining region (CDR)-grafted anti-
 CC TNF antibodies, immunoglobulins, cleavage products and other specified
 CC portions and variants, as well as anti-TNF antibody compositions,
 CC encoding or complementary nucleic acids, vectors, host cells,
 CC compositions, formulations, devices, transgenic animals, transgenic
 CC plants, and methods of making and using them. The anti-TNF antibody
 CC comprises at least a portion of an immunoglobulin molecule, especially
 CC the heavy chain and/or light chain variable regions given in the present
 CC sequence and in AAM51165, or either all of the CDRs of the heavy chain
 CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-
 CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,
 CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
 CC in a mouse model. They are useful for diagnosing or treating a TNF
 CC related condition in a cell, tissue, organ or animal (claimed) such as
 CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
 CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
 CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
 CC myocardial infarction, an infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma and multiple myeloma, or a neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
 CC Creutzfeldt-Jakob disease

XX SQ Sequence 129 AA;

Query Match 100.0%; Score 565; DB 5; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-37;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 60

Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQKPGQAPRLIIYDASNRATGIPA 80

QY 61 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 108

Db 81 RFSGSGSGTDFTLTISLSEPEDFAVYYCQQRSNWPPFTFGPKTKVDIK 128

RESULT 8

AAM51175

ID AAM51175 standard; protein; 129 AA.

XX AC AAM51175;

XX DT 10-JUN-2002 (first entry)

XX DE Human mAb TNV14(B), TNV196 light chain variable region.

XX KW Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;

XX complementarity determining region; antirheumatic; antiarthritic;

KW antiulcer; antiasthmatic; antiallergic; antiinflammatory; antisickling;
KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropic;
KW antianginal; cardiant; antibacterial; virucide; fungicide; antileprotic;
KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
KW human; diagnosis; therapy; TNV148(B); TNV196; monoclonal antibody; mAb.
XX
OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..20 /label= Signal_peptide

FT Protein 20..129 /label= Mature_protein

FT Region 21..43 /label= FR1

FT Region 44..54 /label= CDR1

FT Region 55..69 /label= FR2

FT Region 70..76 /label= CDR2

FT Region 77..108 /label= FR3

FT Region 109..118 /label= CDR3

FT Region 119..129 /label= J3

XX WO200212502-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024785.

XX 07-AUG-2000; 2000US-0223360P.

PR 29-SEP-2000; 2000US-0236826P.

PR 01-AUG-2001; 2001US-00920137.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Heavner G, Scallion B, Shealy D;

XX WPI; 2002-217194/27.

XX N-PSDB; ABL53515.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for

PT treating sickle cell anemia, diabetes, atherosclerosis, restenosis,

PT angina pectoris, myocardial infarction, leprosy.

XX Example 3; Fig 5; 131pp; English.

XX The present sequence is that of the light chain variable region of anti-

CC tumour necrosis factor (TNF) human recombinant monoclonal antibodies

CC (mAbs) TNV148(B) and TNV196. These are human mAbs produced from a GentNV

CC fusion using spleen cells from a hybrid mouse containing human variable

CC and constant region antibody transgenes that was immunised with human TNF

CC alpha. The human mAbs bind immobilised human TNF alpha with high avidity

CC and have a totally human IgG1, kappa isotype. The mature portion of the

CC light chain variable region differs from that of the Vg/38-type light

CC chain germline sequence (see AAM51173) by a single residue (Tyr-50

CC replacing Ser). The light chain variable regions of 2 other human mAbs

CC (see AAM51174) were identical to the germline sequence. The invention

CC provides isolated human, primate, rodent, mammalian, chimeric, humanised

CC and/or complementarity determining region (CDR)-grafted anti-TNF

CC antibodies, immunoglobulins, cleavage products and other specified

CC portions and variants, as well as anti-TNF antibody compositions,

CC encoding or complementary nucleic acids, vectors, host cells,

CC compositions, formulations, devices, transgenic animals, transgenic

CC plants, and methods of making and using them. The anti-TNF antibody

CC comprises at least a portion of an immunoglobulin molecule, especially

CC the heavy chain and/or light chain variable regions given in the present

CC sequence and in AAM51165, or either all of the CDRs of the heavy chain

CC (see AAM51158-60) or all of the CDRs of the light chain (see AAM51161-

CC

CC 63). The antibodies may inhibit TNF-induced cell adhesion molecules,
CC inhibit TNF binding to receptor, or provide Arthritic Index improvement
CC in a mouse model. They are useful for diagnosing or treating a TNF
CC related condition in a cell, tissue, organ or animal (claimed) such as
CC rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's
CC pathology, sickle cell anaemia, diabetes, a cardiovascular disease such
CC as arteriosclerosis, atherosclerosis, restenosis, angina pectoris or
CC myocardial infarction, an infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy and malaria, a malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma and multiple myeloma, or a neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease and
CC Creutzfeldt-Jakob disease
XX
SQ Sequence 129 AA;

Query Match 100.0%; Score 565; DB 5; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-37;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 60
Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYDASNRATGIPA 80
Qy 61 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNMPPFTFGPTKVDIK 108
Db 81 RFSGSGSGTDFTLTISISLEPEDFAVYYCQQRSNMPPFTFGPTKVDIK 128

RESULT 9
AAB72884
ID AAB72884 standard; protein; 108 AA.
XX
AC AAB72884;
XX
DT 10-MAY-2001 (first entry)
XX
DE Human anti-HER2/neu antibody 2-E8 light chain.
XX
KW Human; HER2; neu; erbB2; oncogene; cancer; antibody; immunotherapy; 3-F2;
KW 1-D2; 2-E8; growth factor receptor.
XX
OS Homo sapiens.
XX
PN WO200109187-A2.
XX
PD 08-FEB-2001.
XX
PF 25-JUL-2000; 2000WO-US020272.
XX
PR 29-JUL-1999; 99US-0146313P.
PR 10-MAR-2000; 2000US-0188539P.
XX
(MEDA-) MEDAREX INC.
XX
PI Keler T, Deo Y;
XX
XX WPI; 2001-168698/17.
DR N-PSDB; AAF5590.
XX
PT New human monoclonal antibody that specifically binds to growth factor
PT receptor HER2/neu, for treating, preventing or diagnosing diseases
PT characterized by aberrant HER2/neu expression e.g. cancers.
XX
XX Disclosure; Page 110; 113pp; English.

XX The present invention provides the protein and coding sequences for human
XX monoclonal antibodies which bind specifically to the HER2/neu growth
XX factor receptor (also known as erbB2). These are designated 3-F2, 1-D2
XX and 2-E8. They can be used in the immunotherapy-based treatment and
XX prognosis of cancers, particularly adenocarcinomas such as salivary
XX gland, stomach, kidney, mammary gland, lung and squamous cell carcinomas,
XX and ovarian cancer. The present sequence is part of an antibody of the

CC invention
XX
SQ Sequence 108 AA;

Query Match 96.8%; Score 547; DB 4; Length 108;
Best Local Similarity 96.3%; Pred. No. 3.3e-36;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYYAWYQQKPGAPRLIIYDASNRATGIPA 60
| | | | |
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYYAWYQQKPGAPRLIIYDASNRATGIPA 60
| | | | |

Qy 61 RFSGSGGTDFTLTISLSEPEFAVYQCQRNWPPTFGPGTKVDIK 108
| | | | |
Db 61 RFSGSGGTDFTLTISLSEPEFAVYQCQRNWPPTFGPGTKLEIK 108
| | | | |

RESULT 10
AEB01062
ID AEB01062 standard; protein; 108 AA.

XX AC AEB01062;
XX
DT 08-SEP-2005 (first entry)

XX Human IP10 antibody light chain variable region, SEQ ID NO 90.
DE
KW antibody; IP-10; inflammation; immune disorder; dermatological disease;
KW respiratory disease; neurological disease; degeneration; infection;
KW neuroprotective; Antiarthritis; Antirheumatic; Antiinflammatory;
KW Gastrointestinal-Gen.; Anticancer; Dermatologic; Immunosuppressive;
KW Antidiabetic; Antipsoriasis; Antithyroid; Antistomatitis;
KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
KW Antiparkinsonian; Antiangiogenic; Antiartherosclerotic; Virucide;
KW Antibacterial; light chain variable region.
XX
OS Homo sapiens.
XX
PN WO2005058815-A2.
XX
PD 30-JUN-2005.
XX
PF 10-DEC-2004; 2004WO-US041506.
XX
PR 10-DEC-2003; 2003US-0529180P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
XX
WPI: 2005-467095/47.
DR N-PSDB; AEB01088.
XX

Isolated human monoclonal antibody or an antigen-binding portion, which specifically binds to human interferon gamma inducible protein 10 (IP-10), useful for treating viral or bacterial infection, or inflammatory or autoimmune diseases.

Claim 35; SEQ ID NO 90; 179pp; English.

The invention relates to an isolated human monoclonal antibody or an antigen-binding portion, which specifically binds to human IP-10 and exhibits at least one property selected from: inhibits binding of IP-10 to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced cell migration; cross-reacts with rhesus monkey IP-10; does not cross-react with mouse IP-10; does not cross-react with human MIG; or does not cross-react with human ITAC. The isolated human monoclonal antibody is useful for treating an inflammatory or autoimmune disease including multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease), systemic lupus erythematosus, Type I diabetes, inflammatory skin disorders (e.g., psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves' disease), Hashimoto's thyroiditis), Sjogren's syndrome, pulmonary disease, inflammation (e.g., asthma, chronic obstructive pulmonary disease, pulmonary sarcoidosis, lymphocytic alveolitis), transplant rejection, spinal cord injury, brain injury (e.g., stroke), neurodegenerative diseases (e.g., Alzheimer's disease, Parkinson's disease), gingivitis, gene therapy-induced inflammation, diseases of angiogenesis, inflammatory kidney disease (e.g., IgA nephropathy, membranoproliferative glomerulonephritis, rapidly progressive glomerulonephritis), or atherosclerosis. It is also useful for treating a viral or bacterial infection involving unwanted IP-10 activity in a subject, where the viral infection is mediated by HIV, HCV, HSV-1 or SARS virus. The present sequence represents the amino acid sequence of a human IP10 monoclonal antibody light chain variable region.

Query Match 96.8%; Score 547; DB 9; Length 108;
Best Local Similarity 96.3%; Pred. No. 3.3e-36;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYYAWYQQKPGAPRLIIYDASNRATGIPA 60
| | | | |
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYYAWYQQKPGAPRLIIYDASNRATGIPA 60
| | | | |

Qy 61 RFSGSGGTDFTLTISLSEPEFAVYQCQRNWPPTFGPGTKVDIK 108
| | | | |
Db 61 RFSGSGGTDFTLTISLSEPEFAVYQCQRNWPPTFGPGTKLEIK 108
| | | | |

RESULT 11
ADF11411
ID ADF11411 standard; protein; 109 AA.

XX AC ADF11411;
XX
DT 12-FEB-2004 (first entry)

XX 16E1 anti-OPGL antibody kappa chain variable region SEQ ID NO:24.
DE
KW human; antibody; osteoprotegerin ligand; OPG; osteopenic disorder;
KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
XX
OS Homo sapiens.
XX
PN WO2003086289-A2.
XX
PD 23-OCT-2003.
XX
PF 07-APR-2003; 2003WO-US010749.
XX
PR 05-APR-2002; 2002US-0370407P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
XX
WPI: 2003-845253/78.
DR N-PSDB; ADF11410.
XX

New isolated antibody that specifically binds osteoprotegerin ligand, useful for diagnosing or treating bone disorders, such as osteoporosis, bone loss from arthritis, Paget's disease or osteopenia.

Claim 6; SEQ ID NO 24; 156pp; English.

The present invention describes an isolated human antibody (I) that specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of (I); (2) methods of treating an osteopenic disorder in a patient, comprising administering to a patient the pharmaceutical composition of (1) or a pharmaceutical amount of (I); and (3) a method for detecting OPGL in a biological sample, comprising contacting the

CC invention
XX
SQ Sequence 108 AA;

Query Match 96.8%; Score 547; DB 4; Length 108;
Best Local Similarity 96.3%; Pred. No. 3.3e-36;
Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYYAWYQQKPGAPRLIIYDASNRATGIPA 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYYAWYQQKPGAPRLIIYDASNRATGIPA 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRNWPPTFGPGTKVDIK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 RFSGSGGTDFLTITISLSEDPFAVYQCQRNWPPTFGPGTKLEIK 108
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
AEB01062
ID AEB01062 standard; protein; 108 AA.

XX AC AEB01062;
XX
DT 08-SEP-2005 (first entry)
XX
DE Human IP10 antibody light chain variable region, SEQ ID NO 90.
XX
KW antibody; IP-10; inflammation; immune disorder; dermatological disease;
KW respiratory disease; neurological disease; degeneration; infection;
KW neuroprotective; Antiarthritis; Antirheumatic; Antiinflammatory;
KW Gastrointestinal-Gen.; Anticancer; Dermatologic; Immunosuppressive;
KW Antidiabetic; Antipsoriasis; Antithyroid; Antiasthmatic;
KW Respiratory-Gen.; Cerebroprotective; Vasotropic; Nootropic;
KW Antiparkinsonian; Antiangiogenic; Antiartherosclerotic; Virucide;
KW Antibacterial; light chain variable region.
XX
OS Homo sapiens.
XX
PN WO2005058815-A2.
XX
PD 30-JUN-2005.
XX
PF 10-DEC-2004; 2004WO-US041506.
XX
PR 10-DEC-2003; 2003US-0529180P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Deshpande S, Huang H, Srinivasan M, Cardarelli JM, Wang C;
PI Passmore D, Rangan VS, Lane TE, Keirstead HS, Liu MT;
XX
WPI: 2005-467095/47.
DR N-PSDB; AEB01088.
XX

Isolated human monoclonal antibody or an antigen-binding portion, which specifically binds to human interferon gamma inducible protein 10 (IP-10), useful for treating viral or bacterial infection, or inflammatory or autoimmune diseases.

Claim 35; SEQ ID NO 90; 179pp; English.

The invention relates to an isolated human monoclonal antibody or an antigen-binding portion, which specifically binds to human IP-10 and exhibits at least one property selected from: inhibits binding of IP-10 to CXCR3; inhibits IP-10 induced calcium flux; inhibits IP-10 induced cell migration; cross-reacts with rhesus monkey IP-10; does not cross-react with mouse IP-10; does not cross-react with human MIG; or does not cross-react with human ITAC. The isolated human monoclonal antibody is useful for treating an inflammatory or autoimmune disease including multiple sclerosis, rheumatoid arthritis, inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease), systemic lupus erythematosus, Type I diabetes, inflammatory skin disorders (e.g., psoriasis, lichen planus), autoimmune thyroid disease (e.g., Graves' disease).

CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 109 AA;

Query Match 96.8%; Score 547; DB 7; Length 109;
 Best Local Similarity 96.3%; Pred. No. 3.4e-36;
 Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGAPRLLIYDASNRATGIPA 60
 |||||
 Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGAPRLLIYDASNRATGIPA 60
 |||||
 QY 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRSNWPPYTFGGTKVDIK 108
 |||||
 Db 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRSNWPPYTFGGTKLEIK 108
 |||||

RESULT 12
 ADF11435
 ID ADF11435 standard; protein; 215 AA.
 AC ADF11435;
 XX
 DT 12-FEB-2004 (first entry)
 XX

DE 1651 anti-OPGL antibody light chain SEQ ID NO:48.

XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
 XX
 OS Homo sapiens.

XX WO2003086289-A2.
 XX
 XX 23-OCT-2003.
 XX
 PF 07-APR-2003; 2003WO-US010749.
 XX
 XX 05-APR-2002; 2002US-0370407P.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
 XX

XX WPI; 2003-845253/78.
 DR N-PSDB; ADF11434.
 XX
 XX New isolated antibody that specifically binds osteoprotegerin ligand,
 PT useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.

XX
 PS Claim 16; SEQ ID NO 48; 156pp; English.

XX The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or

CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 215 AA;

Query Match 96.8%; Score 547; DB 7; Length 215;
 Best Local Similarity 96.3%; Pred. No. 6.4e-36;
 Matches 104; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGAPRLLIYDASNRATGIPA 60
 |||||
 Db 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQQKPGAPRLLIYDASNRATGIPA 60
 |||||
 QY 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRSNWPPYTFGGTKVDIK 108
 |||||
 Db 61 RFGSGSGTDFTLTISLSEPEDFAVYCCQQRSNWPPYTFGGTKLEIK 108
 |||||

RESULT 13
 ADM41547
 ID ADM41547 standard; protein; 128 AA.
 XX ADM41547;
 AC ADM41547;
 XX

DT 03-JUN-2004 (first entry)

DE Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.

XX Human; monoclonal antibody; antibody; interleukin-1; receptor;
 KW antiasthmatic; antiinflammatory; dermatological; antiallergic;
 KW prozoscicide; antirheumatic; antiarthritic; osteopathic; vasotropic;
 KW analgesic; antidiabetic; nephrotropic; antinaemic; neutropic;
 KW anticonvulsant; dermatological; antitumor; antiparkinsonian; antidiabetic;
 KW cytostatic.
 XX
 OS Homo sapiens.

XX WO2004022718-A2.

XX 18-MAR-2004.

XX 05-SEP-2003; 2003WO-US027978.

XX 06-SEP-2002; 2002US-0408719P.

XX (AMGE-) AMGEN INC.

XX Varnum B, Vezina C, Witte A, Qian X, Martin F, Huang H;
 PI Elliott G;
 XX

XX WPI; 2004-248462/23.
 DR N-PSDB; ADM41546.

XX Isolated human antibody that specifically binds interleukin-1 receptor
 PT type 1 (IL-1R1) useful for treating IL-1 mediated diseases such as
 PT rheumatoid arthritis, osteoarthritis and inflammatory conditions.

XX
 PS Claim 2; SEQ ID NO 12; 179pp; English.

XX The present sequence is that of human anti-interleukin-1 receptor type 1
 CC (IL-1R1) monoclonal antibody (Mab) 26f5 kappa chain variable region.
 CC Human MAb5 to IL-1R1 were prepared using the HCO7 strain of transgenic
 CC mice, which expresses human antibody genes. These mice were immunised
 CC with purified recombinant IL-1R1, and splenocytes from immunised mice
 CC were fused to a mouse myeloma cell line to generate hybridomas.
 CC Hybridomas which secreted a Mab that bound with high avidity to IL-1R1
 CC were selected. The MAb5 inhibit IL-1 signalling by competing with IL-
 CC beta and IL-1alpha binding to IL-1R. These MAb5, as well as single chain
 CC antibodies single chain Fv antibodies, Fab antibodies, Fab' antibodies
 CC and (Fab')2 antibodies derived from them, are used in methods of treating

CC IL-1 mediated diseases or for detecting the amount of IL-1R1 in a sample.
 CC IL-1 mediated diseases include acute pancreatitis, amyotrophic lateral
 CC sclerosis, Alzheimer's disease, cachexia, anorexia, asthma,
 CC atherosclerosis, autoimmune vasculitis, chronic fatigue syndrome,
 CC Clostridium associated illnesses, coronary conditions, cancer including
 CC leukaemia and tumour metastasis, diabetes, endometriosis, fever,
 CC fibromyalgia, glomerulonephritis, graft versus host disease,
 CC osteoarthritis, rheumatoid arthritis, inflammatory eye disease,
 CC ischaemia, Kawasaki's disease, learning impairment, lung diseases,
 CC multiple sclerosis, myopathy, osteoporosis, pain, Parkinson's disease,
 CC periodontal disease, pre-term labour, psoriasis, reperfusion injury,
 CC septic shock, side effects of radiation therapy, temporal mandibular
 CC joint disease, sleep disturbance, uveitis, or an inflammatory condition
 CC resulting from strain, sprain, cartilage damage, trauma, orthopaedic
 CC surgery, infection or other disease processes.
 XX
 SQ Sequence 128 AA;

Query Match 96.6%; Score 546; DB 8; Length 128;
 Best Local Similarity 97.2%; Pred. No. 4.7e-36;
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
 Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 80
 Qy 61 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGGPKVDIK 108
 Db 81 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGGPKVVEIK 128

RESULT 14

ADD89877
 ID ADD89877 standard; protein; 130 AA.

XX AC ADD89877;
 XX 29-JAN-2004 (first entry)
 XX Human anti-TNF antibody 9E7 light chain variable region.
 DE Human anti-TNF antibody 9E7 light chain variable region.
 XX Human; Tumour necrosis factor; TNF; antibody; cytostatic; anabolic;
 KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;
 KW neuroprotective.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Region 44..54
 FT /note= "CDR1"
 FT Region 65..71
 FT /note= "CDR2"
 FT Region 109..118
 FT /note= "CDR3"
 XX WO2003083061-A2.
 XX 09-OCT-2003.
 XX 24-MAR-2003; 2003WO-US009072.
 XX 26-MAR-2002; 2002US-0367903P.
 XX (CENZ) CENTOCOR INC.
 XX Giles-Komar J, Scallion BJ, Carton JM;
 XX WPI; 2003-804040/75.
 XX N-PSDB; ADD89883.
 XX New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful
 PT for diagnosing or treating an anti-TNF related condition, e.g. cancer,
 PT anorexia, cachexia, or bacterial infection.

XX Claim 1; Fig 3B; 87pp; English.
 XX

CC The present sequence is that of the light chain variable region of human
 CC anti-tumour necrosis factor (TNF) monoclonal antibody 9E7. This human TNF
 CC reactive IgG monoclonal antibody was generated by cloning variable and
 CC constant region DNA in vector pC4 and expression in CHO cells. The
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,
 CC humanized and/or CDK-grafted anti-TNF antibodies, immunoglobulins, their
 CC cleavage products, other specified portions and variants, as well as anti-
 CC -TNF antibody compositions, nucleic acids encoding these, vectors, host
 CC cells, methods for producing the antibodies using a host cell, transgenic
 CC animal or transgenic plant or plant cell, and therapeutic compositions,
 CC methods and devices. The antibody, nucleic acid, protein, composition and
 CC methods are useful for diagnosing or treating an anti-TNF related
 CC condition, e.g. cancer, anorexia, cachexia, or an immune, cardiovascular,
 CC infectious, and/or neurological disease.
 XX

SQ Sequence 130 AA;

Query Match 96.6%; Score 546; DB 7; Length 130;
 Best Local Similarity 97.2%; Pred. No. 4.8e-36;
 Matches 105; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 60
 Db 21 EIVLTQSPATLSLSPGERATLSCRASQSVSYLAWYQOKPGQAPRLLIYDASNRATGIPA 80
 Qy 61 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGGPKVDIK 108
 Db 81 RFSGSGGTDFTLTISSLEPEDFAVYQCQRSNWPPFTFGGPKVVEIK 128

RESULT 15

ADS64664
 ID ADS64664 standard; protein; 130 AA.

XX AC ADS64664;
 XX 16-DEC-2004 (first entry)
 XX Human 9E7LC light chain protein.
 DE Human 9E7LC light chain protein.
 XX Tumour necrosis factor; TNF; immunotherapy; TNF related diseases;
 KW obesity; immune related disease; rheumatoid arthritis;
 KW cardiovascular disease; stroke; malignant disease; leukaemia;
 KW neurological disease; multiple sclerosis; infection; hepatitis;
 KW anorectic; antiarthritic; cerebroprotective; vasotrophic; cytostatic;
 KW neuroprotective; antibacterial; antiinflammatory; hepatotropic; virucide;
 KW human; 9E7LC; light chain.
 XX Homo sapiens.
 XX US2004185047-A1.
 XX 23-SEP-2004.
 XX 21-MAR-2003; 2003US-00394471.
 XX 21-MAR-2003; 2003US-00394471.
 XX (GILE/) GILES-KOMAR J.
 XX (SCAL/) SCALLON B J.
 XX (CART/) CARTON J M.
 XX Giles-Komar J, Scallion BJ, Carton JM;
 XX WPI; 2004-676151/66.
 XX N-PSDB; ADS64661.
 XX Novel isolated mammalian anti-tumor necrosis factor (TNF) alpha antibody
 PT capable of inhibiting binding of TNF alpha to TNF receptor, useful for
 PT treating TNF-related diseases such as obesity or rheumatoid arthritis.

Hadad, M.
10/720323
Seq IDs 1-8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:11:28 ; Search time 28.4483 Seconds
(without alignments)
77.224 Million cell updates/sec

Title: US-10-720-323-1

Perfect score: 30

Sequence: 1 RYTMH 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	5	AAW51158	Aam51158 Anti-tumo
2	30	100.0	5	AAU76327	Aau76327 Human ant
3	30	100.0	10	ADV66152	Adv66152 Mutant CD
4	30	100.0	10	ADV14578	Adv14578 CDR1 pept
5	30	100.0	10	ADZ83466	Adz83466 Anti-CD3
6	30	100.0	10	ADZ83462	Adz83462 Anti-CD3
7	30	100.0	10	ADZ83464	Adz83464 Anti-CD3
8	30	100.0	114	AAAR21273	Aar21273 Murine VH
9	30	100.0	119	AAAR13097	Aar13097 Grafted h
10	30	100.0	119	AAAR13092	Aar13092 Grafted h
11	30	100.0	119	AAAR13100	Aar13100 Grafted h
12	30	100.0	119	AAAR13096	Aar13096 Grafted h
13	30	100.0	119	AAAR13095	Aar13095 Grafted h
14	30	100.0	119	AAAR13098	Aar13098 Grafted h
15	30	100.0	119	AAAR13105	Aar13105 Grafted h
16	30	100.0	119	AAAR13104	Aar13104 Grafted h
17	30	100.0	119	AAAR13094	Aar13094 Grafted h
18	30	100.0	119	AAAR13102	Aar13102 Grafted h
19	30	100.0	119	AAAR13101	Aar13101 Grafted h
20	30	100.0	119	AAAR13103	Aar13103 Grafted h
21	30	100.0	119	AAAR13093	Aar13093 Grafted h
22	30	100.0	119	AAAR13099	Aar13099 Grafted h
23	30	100.0	119	AAAR67449	Aar67449 OKT3 huma
24	30	100.0	119	AAAR75224	Aar75224 OKT3 huma

25	30	100.0	119	2	AAW67447	Aar67447 OKT3 huma
26	30	100.0	119	2	AAW73531	Aaw73531 Humanised
27	30	100.0	119	2	AAW73529	Aaw73529 Humanised
28	30	100.0	119	4	ADW80851	Adw80851 Anti-CD3
29	30	100.0	119	5	AAU76333	Aau76333 Human ant
30	30	100.0	119	6	AAO16693	Aao16693 Anti-ovar
31	30	100.0	119	8	ADQ91061	Adq91061 Murine OK
32	30	100.0	119	8	ADR48645	Adr48645 Novel bis
33	30	100.0	119	8	ADR42625	Adr42625 Mouse ant
34	30	100.0	119	9	ADV66154	Adv66154 CD3-speci
35	30	100.0	119	9	ADV66149	Adv66149 CD3-speci
36	30	100.0	119	9	ADV26037	Adv26037 Mouse OKT
37	30	100.0	119	9	ADV26043	Adv26043 Mouse OKT
38	30	100.0	119	9	ADV26040	Adv26040 Mouse OKT
39	30	100.0	119	9	ADV26044	Adv26044 Mouse OKT
40	30	100.0	119	9	ADV26039	Adv26039 Mouse OKT
41	30	100.0	119	9	ADV26038	Adv26038 Mouse OKT
42	30	100.0	119	9	ADV26041	Adv26041 Mouse OKT
43	30	100.0	119	9	ADV26042	Adv26042 Mouse OKT
44	30	100.0	119	9	ADZ64964	Adz64964 Deimmuniz
45	30	100.0	119	9	ADZ64960	Adz64960 Deimmuniz
46	30	100.0	119	9	ADZ64962	Adz64962 Deimmuniz
47	30	100.0	119	9	ADZ64970	Adz64970 Deimmuniz
48	30	100.0	119	9	ADZ64968	Adz64968 Deimmuniz
49	30	100.0	119	9	ADZ64966	Adz64966 Deimmuniz
50	30	100.0	119	9	ADZ64980	Adz64980 Non-deimm
51	30	100.0	119	9	ADZ64972	Adz64972 Deimmuniz
52	30	100.0	119	9	ADZ83448	Adz83448 Deimmuniz
53	30	100.0	119	9	ADZ83450	Adz83450 Deimmuniz
54	30	100.0	119	9	ADZ83454	Adz83454 Deimmuniz
55	30	100.0	119	9	ADZ83452	Adz83452 Deimmuniz
56	30	100.0	119	9	ADZ83488	Adz83488 Non-deimm
57	30	100.0	119	9	ADZ83484	Adz83484 Non-deimm
58	30	100.0	121	5	AAE22195	Aae22195 CD3-speci
59	30	100.0	121	8	ADQ91076	Adq91076 Modified
60	30	100.0	123	9	ADV26052	Adv26052 Mouse OKT
61	30	100.0	123	9	ADW18339	Adw18339 Murine OK
62	30	100.0	125	7	ADMF60842	Admf60842 Mouse hor
63	30	100.0	125	8	ADM80371	Adm80371 Murine ho
64	30	100.0	138	8	ADQ91059	Adq91059 Murine OK
65	30	100.0	138	9	ADW1844	Adw1844 Human OKT
66	30	100.0	138	9	ADW1854	Adw1854 APEX-3Pmo
67	30	100.0	142	3	AAV43871	Aav43871 Heavy cha
68	30	100.0	186	7	ADC31702	Adc31702 Human nov
69	30	100.0	219	9	ADZ00217	Adz00217 Mouse OKT
70	30	100.0	236	2	AAAR67436	Aar67436 OKT3 mono
71	30	100.0	240	9	ADV14577	Adv14577 VL(CD3)-V
72	30	100.0	243	8	ADZ43341	Adz43341 SCFV anti
73	30	100.0	243	9	ADV14573	Adv14573 VH(CD3)-V
74	30	100.0	243	9	ADZ64929	Adz64929 Anti-CD3
75	30	100.0	243	9	ADZ64943	Adz64943 Anti-CD3
76	30	100.0	243	9	ADZ64955	Adz64955 Anti-CD3
77	30	100.0	243	9	ADZ64919	Adz64919 Anti-CD3
78	30	100.0	243	9	ADZ64927	Adz64927 Anti-CD3
79	30	100.0	243	9	ADZ64951	Adz64951 Anti-CD3
80	30	100.0	243	9	ADZ64931	Adz64931 Anti-CD3
81	30	100.0	243	9	ADZ64912	Adz64912 Anti-CD3
82	30	100.0	243	9	ADZ64925	Adz64925 Anti-CD3
83	30	100.0	243	9	ADZ64937	Adz64937 Anti-CD3
84	30	100.0	243	9	ADZ64941	Adz64941 Anti-CD3
85	30	100.0	243	9	ADZ64933	Adz64933 Anti-CD3
86	30	100.0	243	9	ADZ64939	Adz64939 Anti-CD3
87	30	100.0	243	9	ADZ64945	Adz64945 Anti-CD3
88	30	100.0	243	9	ADZ64921	Adz64921 Anti-CD3
89	30	100.0	243	9	ADZ64953	Adz64953 Anti-CD3
90	30	100.0	243	9	ADZ64947	Adz64947 Anti-CD3
91	30	100.0	243	9	ADZ64949	Adz64949 Anti-CD3
92	30	100.0	243	9	ADZ64935	Adz64935 Anti-CD3
93	30	100.0	243	9	ADZ64917	Adz64917 Anti-CD3
94	30	100.0	243	9	ADZ64915	Adz64915 Anti-CD3
95	30	100.0	243	9	ADZ64923	Adz64923 Anti-CD3
96	30	100.0	243	9	ADZ83383	Adz83383 Anti-CD3
97	30	100.0	243	9	ADZ83389	Adz83389 Anti-CD3

98 30 100.0 243 9 ADZ83397 Adz83397 Anti-CD3
 99 30 100.0 243 9 ADZ83405 Adz83405 Anti-CD3
 100 30 100.0 243 9 ADZ83380 Adz83380 Non-deimm

ALIGNMENTS

RESULT 1
 AAM51158
 ID AAM51158 standard; peptide; 5 AA.

AC AAM51158;
 DT 10-JUN-2002 (first entry)
 XX
 DE Anti-tumour necrosis factor antibody heavy chain CDR1.

XX Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;
 KW complementarity determining region; antirheumatic; antiarthritic;
 KW antidiabetic; antiasthmatic; antiallergic; antiinflammatory; antisickling;
 KW antidiabetic; antiarteriosclerotic; antiatherosclerotic; vasotropism;
 KW antidiabetic; antidiabetic; antidiabetic; virucide; fungicide; antileptotic;
 KW protozoacide; cytostatic; neuroprotective; antiparkinsonian; nootropic;
 KW human; diagnosis; therapy.

XX Homo sapiens.

OS WO200212502-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024785.

XX 07-AUG-2000; 2000US-0223360P.

XX 29-SEP-2000; 2000US-0236826P.

XX 01-AUG-2001; 2001US-00920137.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Heavner G, Scallan B, Shealy D;

XX WPI; 2002-217194/27.

XX N-PSDB; ABL53501.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for

XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,

XX angina pectoris, myocardial infarction, leprosy.

XX Claim 21; Page 128; 131pp; English.

XX This sequence is that of complementarity determining region 1 (CDR1) of
 CC the heavy chain of an anti-tumour necrosis factor (TNF) antibody. The
 CC invention provides isolated human, primate, rodent, mammalian, chimeric,
 CC humanised and/or CDR-grafted anti-TNF antibodies, immunoglobulins,
 CC cleavage products and other specified portions and variants, as well as
 CC anti-TNF antibody compositions, encoding or complementary nucleic acids,
 CC vectors, host cells, compositions, formulations, devices, transgenic
 CC animals, transgenic plants, and methods of making and using them. The
 CC anti-TNF antibody comprises at least a portion of an immunoglobulin
 CC molecule, especially the heavy chain and/or light chain variable regions
 CC given in AAM51165-66, or either all of the CDRs of the heavy chain (see
 CC AAM51158-60) or all of the CDRs of the light chain (see AAM51161-63). The
 CC antibody may inhibit TNF-induced cell adhesion molecules, inhibit TNF
 CC binding to receptor, or provide Arthritic index improvement in a mouse
 CC model. It is useful for diagnosing or treating a TNF related condition in
 CC a cell, tissue, organ or animal (Claimed) such as rheumatoid arthritis,
 CC gastric ulcer, asthma, allergic rhinitis, Crohn's pathology, sickle cell
 CC anaemia, diabetes, a cardiovascular disease such as arteriosclerosis,
 CC atherosclerosis, restenosis, angina pectoris or myocardial infarction, an
 CC infectious disease in a cell such as bacterial, viral, and fungal
 CC infections, pneumonia, leprosy and malaria, a malignant disease such as
 CC leukaemia, chronic myelocytic leukaemia, Burkitt's lymphoma and multiple

CC myeloma, or a neurological disease such as multiple sclerosis,
 CC Parkinson's disease, spinal ataxia, Alzheimer's disease and Creutzfeldt-
 CC Jakob disease
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
 DB 1 RYTMH 5

RESULT 2

AAU76327
 ID AAU76327 standard; peptide; 5 AA.

XX AAU76327;

XX 21-MAY-2002 (first entry)

XX Human anti-dual integrin antibody heavy chain variable region CDR1.

XX Human; antibody; dual integrin; CDR; heavy chain variable region; HC CDR;
 KW medical device; immune related disease; rheumatoid arthritis;
 KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
 KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
 KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
 KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
 KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
 KW neurological disease; multiple sclerosis; Parkinson's disease;
 KW Alzheimer's disease; Creutzfeldt-Jakob disease.

XX Homo sapiens.

XX WO200212501-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024784.

XX 07-AUG-2000; 2000US-0223363P.

XX 01-AUG-2001; 2001US-00920267.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Heavner G, Snyder L, Trikha M;

XX WPI; 2002-217193/27.

XX N-PSDB; ABK10114.

XX Novel isolated mammalian anti-dual integrin antibody, useful for

XX diagnosing or treating dual integrin related condition such as rheumatoid

XX arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

XX Claim 29; Page 133; 144pp; English.

XX The invention relates to an isolated mammalian anti-dual integrin
 CC antibody having at least one of the human heavy chain or light chain
 CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
 CC included are the nucleic acids encoding the CDRs, a vector comprising the
 CC nucleic acids, a host cell comprising the vector, an anti-idiotypic
 CC antibody that binds to the anti-dual integrin, a medical device comprising
 CC the antibody suitable for administration by parenteral, subcutaneous,
 CC intramuscular, intravenous, intracapsular, intracartilaginous, intracavitary,
 CC intracerebellar, or other routes as given in specification. The antibody
 CC is useful for diagnosing or treating a dual integrin related condition in
 CC an animal for example, immune related disease such as rheumatoid
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
 CC sickle cell anaemia, diabetes, cardiovascular disease such as

CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
 CC myocardial infarction, infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma, multiple myeloma; neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
 CC Creutzfeldt-Jakob disease and many other diseases given in the
 CC specification. The present sequence is an anti-dual integrin human heavy
 CC chain CDR

XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 30; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
 DB 1 RYTMH 5
 |||||

RESULT 3
 ID ADV66152 standard; peptide; 10 AA.
 XX
 AC ADV66152;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE Mutant CDRH3 peptide - SEQ ID 75.
 XX
 KW bispecific single chain antibody; CDRH3; tumor; cancer; cytostatic;
 KW mutin.
 XX
 OS Synthetic.
 GS Unidentified.
 OS
 XX WO2004106383-A1.
 XX
 *PD 09-DEC-2004.
 XX
 PF 26-MAY-2004; 2004WO-EP005687.
 XX
 PR 31-MAY-2003; 2003EP-00012133.
 PR
 PR 31-MAY-2003; 2003EP-00012134.
 XX
 XX (MICR-) MICROMET AG.
 XX
 XX Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
 PI Kohleisen B, Lenkkeri-Schuetz U, Baeuerle P;
 XX
 DR WPI; 2005-021271/02.
 XX
 PT New pharmaceutical composition having a bispecific single chain antibody
 PT construct, useful for preventing, treating or ameliorating a tumorous
 PT disease, such as an epithelial or minimal residual cancer.
 XX
 PS Example 1; SEQ ID NO 75; 227pp; English.
 XX
 CC The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents a mutant
 CC CDRH3 peptide that was used in an example of the invention.

XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
 DB 6 RYTMH 10
 |||||

RESULT 4
 ID ADV14578 standard; peptide; 10 AA.
 XX
 AC ADV14578;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE CDR1 peptide of the VH(CD3) antibody fragment Seq 52.
 XX
 KW antibody; antibody engineering; antibody therapy; CD3; tumor;
 KW B-cell leukemia; inflammation; immune disorder; autoimmune disease;
 KW rheumatoid arthritis; viral infection; allergy; parasitic infection;
 KW graft-versus-host disease; cytostatic; antiinflammatory;
 KW immunosuppressive; antimicrobial-gen.; antirheumatic; antiarthritic;
 KW virucide; antiparasitic; antiallergic; proliferative disorders; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2004106381-A1.
 XX
 PD 09-DEC-2004.
 XX
 PF 26-MAY-2004; 2004WO-EP005685.
 XX
 PR 31-MAY-2003; 2003EP-00012136.
 XX
 XX (MICR-) MICROMET AG.
 XX
 XX Kufer P, Lutterbuese R, Kohleisen B, Zeman S, Baeuerle P;
 DR WPI; 2005-021270/02.
 XX
 PT Use of bispecific single chain antibody construct, nucleic acid sequence
 PT encoding the antibody construct, vector containing the nucleic acid or
 PT host transformed with the vector for the treatment of e.g. proliferative
 PT and autoimmune disease.

XX
 PS Claim 5; SEQ ID NO 52; 115pp; English.
 XX
 CC This invention relates to novel pharmaceutical compositions that comprise
 CC a bispecific single chain antibody construct, a nucleic acid sequence
 CC encoding the antibody construct and a vector that contains the nucleic
 CC acid sequence. Specifically, it refers to an antibody construct that
 CC contains binding domains specific for the human T cell differentiation
 CC antigens CD3 and CD19, with specific variable heavy and light chain
 CC regions. In particular such constructs include, from the N- to C-termini,
 CC in the order, VH(CD19)-VL(CD19)-VH(CD3)-VL(CD3), VH(CD3)-VL(CD3)-VH(CD19)
 CC -VL(CD19), or VH(CD3)-VL(CD3)-VL(CD19)-VH(CD19). The present invention
 CC describes a method of culturing the host transformed with this vector in
 CC order to recover expressed bispecific single chain antibodies from the
 CC culture solution. Note that the pharmaceutical composition additionally
 CC comprises a proteinaceous compound that provides an activation signal for
 CC immune effector cells. Furthermore, this invention provides compositions
 CC that can be used for the treatment, prevention or amelioration of
 CC proliferative disease, minimal residual cancer, tumorous disease (e.g. B-
 CC cell leukemia), inflammatory disease, immunological disorder, autoimmune
 CC disease (e.g. rheumatoid arthritis), infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, host
 CC -versus-graft diseases and B-cell malignancies. As such, these
 CC compositions exhibit cytostatic, antiinflammatory, immunosuppressive,
 CC antimicrobial, antirheumatic, antiarthritic, virucide, antiparasitic and
 CC antiallergic activities. In addition, these compositions provide well-
 CC tolerated and convenient medicaments that are highly active and potent at
 CC low concentrations and as such avoid adverse side effects including
 CC hypersensitivity and inflammatory events caused by excessive protein
 CC concentrations. This peptide sequence is a complementarity determining

CC region (CDR) peptide of a variable heavy chain antibody protein molecule
 CC that targets human CD3 antigens, as given in an exemplification of the
 CC invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 9; Length 10;
 - Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
 |||||
 Db 6 RYTMH 10

RESULT 5
 ADZ83466
 ID ADZ83466 standard; protein; 10 AA.

XX AC ADZ83466;

XX 14-JUL-2005 (first entry)

XX Anti-CD3 cassette heavy chain variable region CDR1 #3.

XX neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
 KW CD3; heavy chain variable region.

XX Synthetic.

XX WO2005040220-A1.

XX 06-MAY-2005.

XX 15-OCT-2004; 2004WO-EP011646.

XX 16-OCT-2003; 2003EP-00023581.

XX (MICR-) MICROMET AG.

XX Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
 PI Carr FJ, Hamilton AA, Williams S;

XX WPI; 2005-333494/34.

DR N-PSDB; ADZ83702.

XX New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.

XX Claim 8; SEQ ID NO 88; 639pp; English.

XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral diseases,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral diseases,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a non-deimmunized anti-CD3 cassette heavy chain variable
 CC region CDR.

SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
 |||||
 Db 6 RYTMH 10

RESULT 6
 ADZ83462
 ID ADZ83462 standard; protein; 10 AA.

XX AC ADZ83462;

XX 14-JUL-2005 (first entry)

XX Anti-CD3 cassette heavy chain variable region CDR1 #1.

XX neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
 KW CD3; heavy chain variable region.

XX Synthetic.

XX WO2005040220-A1.

XX 06-MAY-2005.

XX 15-OCT-2004; 2004WO-EP011646.

XX 16-OCT-2003; 2003EP-00023581.

XX (MICR-) MICROMET AG.

XX Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
 PI Carr FJ, Hamilton AA, Williams S;

XX WPI; 2005-333494/34.

DR N-PSDB; ADZ83461.

XX New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.

XX Example 1; SEQ ID NO 84; 639pp; English.

XX The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral diseases,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral diseases,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a non-deimmunized anti-CD3 cassette heavy chain variable
 CC region CDR.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 30; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 |||||
 Db 6 RYTMH 10

RESULT 7
 ADZ83464
 ID ADZ83464 standard; protein; 10 AA.
 XX AC ADZ83464;
 XX 14-JUL-2005 (first entry)
 DT Anti-CD3 cassette heavy chain variable region CDR1 #2.
 DE neoplasm; inflammation; immune disorder; infection; allergy;
 KW graft versus host disease; Cytostatic; Antiinflammatory;
 KW Immunosuppressive; Virucide; Antibacterial; Antiallergic; Antiparasitic;
 KW CD3; heavy chain variable region.
 XX OS Synthetic.
 XX WO2005040220-A1.
 FN 06-MAY-2005.
 PD 15-OCT-2004; 2004WO-EP011646.
 PF 16-OCT-2003; 2003EP-00023581.
 PR (MICR-) MICROMET AG.
 XX PA
 XX Hofmeister R, Kohleisen B, Lenkkeri-Schuetz U, Itin C, Baeuerle P;
 PI Carr FJ, Hamilton AA, Williams S;
 XX WPI; 2005-333494/34.
 DR N-PSDB; ADZ83463.

2XX New cytotoxically active CD3 specific binding construct comprises a first
 PT domain specifically binding to human CD3 and an Ig-derived second binding
 PT domain, useful for treating, preventing, or ameliorating, e.g.
 PT proliferative disease.
 XX Example 1; SEQ ID NO 86; 639pp; English.

CC The invention relates to a cytotoxically active CD3 specific binding
 CC construct comprising a first domain specifically binding to human CD3 and
 CC an Ig-derived second binding domain. The CD3 specific binding construct
 CC above or the construct produced by the process, nucleic acid molecule,
 CC vector, or host is useful for the preparation of a pharmaceutical
 CC composition for the prevention, treatment, or amelioration of a
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The cytotoxically active CD3 specific binding
 CC construct is useful for treating, preventing, or ameliorating
 CC proliferative disease, a tumor, an inflammatory disease, an immunological
 CC disorder, an autoimmune disease, an infectious disease, viral disease,
 CC allergic reactions, parasitic reactions, graft-versus-host diseases, or
 CC host-versus-graft diseases. The present sequence represents the amino
 CC acid sequence of a non-deimmunized anti-CD3 cassette heavy chain variable
 CC region CDR.

XX Sequence 10 AA;
 SQ

Query Match 100.0%; Score 30; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 |||||

Db 6 RYTMH 10

RESULT 8
 AAR21273
 ID AAR21273 standard; protein; 114 AA.
 XX AC AAR21273;
 XX 21-MAY-1992 (first entry)
 DT Murine VH group 1 chain J specific for pHOX.
 DE Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
 KW gp; binding; adsorption; gene VIII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package.
 XX OS Synthetic.
 XX Key Location/Qualifiers
 FH Binding-site 31..35
 FT /label= CDR1
 FT Binding-site 50..66
 FT /label= CDR2
 FT Binding-site 99..103
 FT /label= CDR3
 FT /note= " D/N-X-G-X-X motif "
 XX WO9201047-A.
 PN 23-JAN-1992.
 PD 10-JUL-1990; 90GB-00015198.
 XX 10-JUL-1990; 90GB-00015198.
 PR 19-OCT-1990; 90GB-00022845.
 PR 12-NOV-1990; 90GB-00024503.
 PR 06-MAR-1991; 91GB-00004744.
 PR 15-MAY-1991; 91GB-00010549.
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA (MEDI-) MED RES COUNCIL.
 PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD;
 XX WPI; 1992-056862/07.

XX Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic display
 PT package.
 XX Example 22; Fig 24; 209pp; English.

XX The VH sequence is one of 22 (AAR21264-85) expressed from a single chain
 CC Fv library. The library produces a diverse repertoire of antibody
 CC fragments specific for 2-phenyl-5-oxazolone (pHOX). It was prep. using
 CC cDNA generated from mRNA from mice immunised with pHOX coupled to chicked
 CC serum albumin. The VH and VL kappa sequences were separately amplified by
 CC PCR (AAQ23474-84) and ligated into fdCAT2 (AAQ23463) for expression on
 CC the phage surface as fusions with gene III. The resulting library of
 CC clones was diverse; 23 hapten binding clones were sequenced revealing 8
 CC VH genes (A-H; AAR21264-71) in a variety of pairings with 7 V_k genes (a-g
 CC ; AAR21286-92). Most clones were V_k-d combinations so a further
 CC hierarchical library was prep. by "crossing" V_k-d with the VH
 CC repertoire. The resulting library was screened for hapten binding and 24
 CC clones sequenced. 13 new partners (AAR21272-85) for V_k-d were identified.
 CC Nearly all the VH genes belonged to gp 1, with only one, "E", being of gp
 CC 2 (VHOx1). Of the 24 hierarchical clones, only one was of type "J". The
 CC Kd of VH-B/V_k-d for pHOX-CABA was 10 nM, one of the highest values found.
 CC This suggests that phage bearing scFv fragments having weak affinities
 CC can be selected with antigen, probably due to the avidity of the multiple
 CC antibody heads on the phage. The different combinations could also be

CC isolated on a basis of antigen affinity. See also AAR21260-307, 309-311;
CC AAR22450, 565-581
XX
SQ Sequence 114 AA;
Query Match 100.0%; Score 30; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db ||||| 31 RYTMH 35
RESULT 9
AAR13097
ID AAR13097 standard; protein; 119 AA.
XX
AC AAR13097;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341D/JA197.
XX
XX humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 6 /label= OKT 3 heavy chain residue
FT Region 23..34
FT /label= from OKT 3 heavy chain
FT Region 48..66
FT /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Misc-difference 72 /label= OKT 3 heavy chain residue
FT Misc-difference 74
FT /label= OKT 3 heavy chain residue
FT Region 99..106
FT /label= from OKT 3 heavy chain
XX
PN WO9109967-A.
XX
XX 11-JUL-1991.
XX
XX 21-DEC-1989; 89GB-00028874.
XX
XX 21-DEC-1989; 89GB-00028874.
XX 21-DEC-1990; 90WO-GB002017.
XX (CLLT) CELLTech LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX WPI; 1991-222915/30.
XX
XX New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in vivo therapy and diagnosis.
XX Example 15; Fig 5; 91pp; English.
XX
XX This is an example of a CDR-grafted heavy chain region of the invention. It comprises the human KOL heavy chain sequence except where certain regions have been replaced by corresponding regions from the murine OKT3 antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109. NOTE: Data found in patent WO9109968 has been used to index this entry. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003

CC to correct PA field.)
XX
SQ Sequence 119 AA;
Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db ||||| 31 RYTMH 35
RESULT 10
AAR13092
ID AAR13092 standard; protein; 119 AA.
XX
AC AAR13092;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341/JA178.
XX
XX humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Region 25..35
FT /label= from murine OKT 3 heavy chain
FT Region 50..66
FT /label= from murine OKT 3 heavy chain
FT Region 99..106
FT /label= from murine OKT 3 heavy chain
XX
PN WO9109967-A.
XX
XX 11-JUL-1991.
XX
XX 21-DEC-1989; 89GB-00028874.
XX 21-DEC-1989; 89GB-00028874.
XX 21-DEC-1990; 90WO-GB002017.
XX (CLLT) CELLTech LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX WPI; 1991-222915/30.
XX
XX New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in vivo therapy and diagnosis.
XX Example 15; Fig 5; 91pp; English.
XX
XX This is an example of a CDR-grafted heavy chain region of the invention. It comprises the human KOL heavy chain sequence except where certain regions have been replaced by corresponding regions from the murine OKT3 antibody heavy chain (see features). See also AAQ12636-7 and AAR13093-R13109. NOTE: Data found in patent WO9109968 has been used to index this entry. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 119 AA;
Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RYTMH 5
Db      31 RYTMH 35

RESULT 11
AAR13100
ID  AAR13100 standard; protein; 119 AA.
XX
AC  AAR13100;
XX
XX  25-MAR-2003 (revised)
DT  09-JAN-2003 (revised)
DT  04-OCT-1991 (first entry)
XX
XX  Grafted heavy chain variable region GH341*/JA203.
XX
XX  humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS  Homo sapiens.
OS  Mus sp.
OS  Synthetic.
XX
XX  Key
FH  Location/Qualifiers
FT  Misc-difference 6
FT  /label= OKT 3 heavy chain residue
FT  Region
FT  24..34
FT  /label= from OKT 3 heavy chain
FT  Region
FT  48..66
FT  /label= from OKT3 heavy chain
FT  /note= "Val(64) is from KOL sequence"
FT  Misc-difference 72
FT  /label= OKT 3 heavy chain residue
FT  Misc-difference 74
FT  /label= OKT 3 heavy chain residue
FT  Misc-difference 77
FT  /label= OKT 3 heavy chain residue
FT  Misc-difference 79
FT  /label= OKT 3 heavy chain residue
FT  Misc-difference 92
FT  /label= OKT 3 heavy chain residue
FT  Misc-difference 95
FT  /label= OKT 3 heavy chain residue
FT  Region
FT  99..106
FT  /label= from OKT 3 heavy chain
FT  /label= from OKT 3 heavy chain
XX
XX  WO9109967-A.
XX
XX  11-JUL-1991.
XX
XX  21-DEC-1989; 89GB-00028874.
XX
XX  21-DEC-1989; 89GB-00028874.
XX  21-DEC-1990; 90WO-GB002017.
XX
XX  (CLLT ) CELLTech LTD.
XX
XX  Adair JR, Achwal DS, Emtage JS;
XX  WPI; 1991-222915/30.
XX
XX  New humanised antibodies comprising CDR grafted antibody - with heavy and
XX  light chains, for use in vivo therapy and diagnosis.
XX
XX  Example 15; Fig 5; 91pp; English.
XX
XX  This is an example of a CDR-grafted heavy chain region of the invention.
XX  It comprises the human KOL heavy chain sequence except where certain
XX  regions have been replaced by corresponding regions from the murine OKT3
XX  antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109.
XX  NOTE: Data found in patent WO9109968 has been used to index this entry.
XX  (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
XX  to correct PA field.)

Qy      1 RYTMH 5
Db      31 RYTMH 35

Query Match      100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
Db      31 RYTMH 35

RESULT 12
AAR13096
ID  AAR13096 standard; protein; 119 AA.
XX
AC  AAR13096;
XX
XX  25-MAR-2003 (revised)
DT  09-JAN-2003 (revised)
DT  04-OCT-1991 (first entry)
XX
XX  Grafted heavy chain variable region GH341*/JA209.
XX
XX  humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS  Homo sapiens.
OS  Mus sp.
OS  Synthetic.
XX
XX  Key
FH  Location/Qualifiers
FT  Misc-difference 6
FT  /label= OKT 3 heavy chain residue
FT  Region
FT  23..34
FT  /label= from OKT 3 heavy chain
FT  Region
FT  48..66
FT  /label= from OKT3 heavy chain
FT  /note= "Val(64) is from KOL sequence"
FT  Misc-difference 79
FT  /label= OKT 3 heavy chain residue
FT  Region
FT  99..106
FT  /label= from OKT 3 heavy chain
XX
XX  WO9109967-A.
XX
XX  11-JUL-1991.
XX
XX  21-DEC-1989; 89GB-00028874.
XX
XX  21-DEC-1989; 89GB-00028874.
XX  21-DEC-1990; 90WO-GB002017.
XX
XX  (CLLT ) CELLTech LTD.
XX
XX  Adair JR, Achwal DS, Emtage JS;
XX  WPI; 1991-222915/30.
XX
XX  New humanised antibodies comprising CDR grafted antibody - with heavy and
XX  light chains, for use in vivo therapy and diagnosis.
XX
XX  Example 15; Fig 5; 91pp; English.
XX
XX  This is an example of a CDR-grafted heavy chain region of the invention.
XX  It comprises the human KOL heavy chain sequence except where certain
XX  regions have been replaced by corresponding regions from the murine OKT3
XX  antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109.
XX  NOTE: Data found in patent WO9109968 has been used to index this entry.
XX  (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
XX  to correct PA field.)

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Query Match      100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 RYTMH 35

RESULT 13
AAR13095
ID AAR13095 standard; protein; 119 AA.
XX
AC AAR13095;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341*/JA207.
XX
KW humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Misc-difference 6 /label= OKT 3 heavy chain residue
FT Region 23..34 /label= from OKT 3 heavy chain
FT Region 48..66 /label= from OKT3 heavy chain
FT /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Misc-difference 72 /label= OKT 3 heavy chain residue
FT Misc-difference 74 /label= OKT 3 heavy chain residue
FT Misc-difference 79 /label= OKT 3 heavy chain residue
FT Region 99..106 /label= from OKT 3 heavy chain
FT
FT WO9109967-A.
XX
XX 11-JUL-1991.
XX
XX 21-DEC-1989; 89GB-00028874.
XX
XX 21-DEC-1989; 89GB-00028874.
XX 21-DEC-1990; 90WO-GB002017.
XX
XX (CLLT ) CELLTECH LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX WPI; 1991-222915/30.
XX
XX New humanised antibodies comprising CDR grafted antibody - with heavy and
XX light chains, for use in vivo therapy and diagnosis.
XX
XX Example 15; Fig 5; 91pp; English.
XX
XX This is an example of a CDR-grafted heavy chain region of the invention.
XX It comprises the human KOL heavy chain sequence except where certain
XX regions have been replaced by corresponding regions from the murine OKT3
XX antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109.
XX NOTE: Data found in patent WO9109968 has been used to index this entry.
XX (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
XX to correct PA field.)
XX
XX Sequence 119 AA;

Query Match      100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 RYTMH 35

RESULT 14
AAR13098
ID AAR13098 standard; protein; 119 AA.
XX
AC AAR13098;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341*/JA199.
XX
KW humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Misc-difference 6 /label= OKT 3 heavy chain residue
FT Region 23..34 /label= from OKT 3 heavy chain
FT Region 48..66 /label= from OKT3 heavy chain
FT /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Region 99..106 /label= from OKT 3 heavy chain
FT
FT WO9109967-A.
XX
XX 11-JUL-1991.
XX
XX 21-DEC-1989; 89GB-00028874.
XX
XX 21-DEC-1989; 89GB-00028874.
XX 21-DEC-1990; 90WO-GB002017.
XX
XX (CLLT ) CELLTECH LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX WPI; 1991-222915/30.
XX
XX New humanised antibodies comprising CDR grafted antibody - with heavy and
XX light chains, for use in vivo therapy and diagnosis.
XX
XX Example 15; Fig 5; 91pp; English.
XX
XX This is an example of a CDR-grafted heavy chain region of the invention.
XX It comprises the human KOL heavy chain sequence except where certain
XX regions have been replaced by corresponding regions from the murine OKT3
XX antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109.
XX NOTE: Data found in patent WO9109968 has been used to index this entry.
XX (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
XX to correct PA field.)
XX
XX Sequence 119 AA;

Query Match      100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RYTMH 5
Db      31 RYTMH 35

RESULT 15
AAR13105
ID AAR13105 standard; protein; 119 AA.
XX
AC AAR13105;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341*/JA208.
XX
KW humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= OKT 3 heavy chain residue
FT Region 24..34 /label= from OKT 3 heavy chain
FT Region 48..66 /label= from OKT 3 heavy chain
FT /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Misc-difference 72 /label= OKT 3 heavy chain residue
FT Misc-difference 74 /label= OKT 3 heavy chain residue
FT Misc-difference 79 /label= OKT 3 heavy chain residue
FT Region 99..106 /label= OKT 3 heavy chain residue
FT /label= from OKT 3 heavy chain
XX
PN WO9109967-A.
XX
PD 11-JUL-1991.
XX
PF 21-DEC-1989; 89GB-00028874.
XX
PR 21-DEC-1989; 89GB-00028874.
PR 21-DEC-1990; 90WO-GB002017.
XX
PA (CLLT ) CELLTECH LTD.
XX
PI Adair JR, Athwal DS, Emtage JS;
XX
DR WPI; 1991-222915/30.
XX
PT New humanised antibodies comprising CDR grafted antibody - with heavy and
PT light chains, for use in vivo therapy and diagnosis.
XX
PS Example 15; Fig 5; 91pp; English.
XX
CC This is an example of a CDR-grafted heavy chain region of the invention.
CC It comprises the human KOL heavy chain sequence except where certain
CC regions have been replaced by corresponding regions from the murine OKT3
CC antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109.
CC NOTE: Data found in patent WO9109968 has been used to index this entry.
CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
AAR13104
ID AAR13104 standard; protein; 119 AA.
XX
AC AAR13104;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341*/JA206.
XX
KW humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 24..34 /label= from OKT 3 heavy chain
FT Region 48..66 /label= from OKT3 heavy chain
FT /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Misc-difference 72 /label= OKT 3 heavy chain residue
FT Misc-difference 74 /label= OKT 3 heavy chain residue
FT Misc-difference 77 /label= OKT 3 heavy chain residue
FT Misc-difference 79 /label= OKT 3 heavy chain residue
FT Misc-difference 92 /label= OKT 3 heavy chain residue
FT Region 99..106 /label= from OKT 3 heavy chain
XX
PN WO9109967-A.
XX
PD 11-JUL-1991.
XX
PF 21-DEC-1989; 89GB-00028874.
XX
PR 21-DEC-1989; 89GB-00028874.
PR 21-DEC-1990; 90WO-GB002017.
XX
PA (CLLT ) CELLTECH LTD.
XX
PI Adair JR, Athwal DS, Emtage JS;
XX
DR WPI; 1991-222915/30.
XX
PT New humanised antibodies comprising CDR grafted antibody - with heavy and
PT light chains, for use in vivo therapy and diagnosis.
XX
PS Example 15; Fig 5; 91pp; English.
XX
CC This is an example of a CDR-grafted heavy chain region of the invention.
CC It comprises the human KOL heavy chain sequence except where certain
CC regions have been replaced by corresponding regions from the murine OKT3
CC antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109.
CC NOTE: Data found in patent WO9109968 has been used to index this entry.
CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
SQ Sequence 119 AA;

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Query Match      100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 RYTMH 35

RESULT 17
ID AAR13094 standard; protein; 119 AA.
XX
AC AAR13094;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341B/JA198.
XX
KW humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= OKT 3 heavy chain residue
FT Region 23..34 /label= from OKT 3 heavy chain
FT Region 48..56 /label= from OKT3 heavy chain
FT /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Misc-difference 72 /label= OKT 3 heavy chain residue
FT Misc-difference 74 /label= OKT 3 heavy chain residue
FT Misc-difference 77 /label= OKT 3 heavy chain residue
FT Misc-difference 79 /label= OKT 3 heavy chain residue
FT Region 99..106 /label= from OKT 3 heavy chain
FT
XX WO9109967-A.
XX
XX 11-JUL-1991.
XX
XX 21-DEC-1989; 89GB-00028874.
XX
XX 21-DEC-1989; 89GB-00028874.
XX 21-DEC-1990; 90WO-GH002017.
XX (CLLT ) CELLTECH LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX WPI; 1991-222915/30.
XX
XX New humanised antibodies comprising CDR grafted antibody - with heavy and
XX light chains, for use in vivo therapy and diagnosis.
XX
XX Example 15; Fig 5; 91pp; English.
XX
XX This is an example of a CDR-grafted heavy chain region of the invention.
XX It comprises the human KOL heavy chain sequence except where certain
XX regions have been replaced by corresponding regions from the murine OKT3
XX antibody heavy chain (see features). See AAQ2636-7 and AAR13092-R1109.
XX NOTE: Data found in patent WO9109968 has been used to index this entry.
XX (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
XX to correct PA field.)

XX
SQ      Sequence 119 AA;
Query Match      100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 RYTMH 35

RESULT 18
AAR13102
ID AAR13102 standard; protein; 119 AA.
XX
AC AAR13102;
XX
DT 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
DE Grafted heavy chain variable region GH341B/JA183.
XX
KW humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 25..34 /label= from OKT 3 heavy chain
FT Region 48..66 /label= from OKT3 heavy chain
FT /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Misc-difference 72 /label= OKT 3 heavy chain residue
FT Misc-difference 74 /label= OKT 3 heavy chain residue
FT Misc-difference 77 /label= OKT 3 heavy chain residue
FT Misc-difference 79 /label= OKT 3 heavy chain residue
FT Misc-difference 92 /label= OKT 3 heavy chain residue
FT Misc-difference 95 /label= OKT 3 heavy chain residue
FT Region 99..106 /label= from OKT 3 heavy chain
FT
XX WO9109967-A.
XX
XX 11-JUL-1991.
XX
XX 21-DEC-1989; 89GB-00028874.
XX
XX 21-DEC-1989; 89GB-00028874.
XX 21-DEC-1990; 90WO-GH002017.
XX (CLLT ) CELLTECH LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX WPI; 1991-222915/30.
XX
XX New humanised antibodies comprising CDR grafted antibody - with heavy and
XX light chains, for use in vivo therapy and diagnosis.
XX
XX Example 15; Fig 5; 91pp; English.
XX
XX This is an example of a CDR-grafted heavy chain region of the invention.
XX It comprises the human KOL heavy chain sequence except where certain
XX regions have been replaced by corresponding regions from the murine OKT3
XX antibody heavy chain (see features). See AAQ2636-7 and AAR13092-R1109.
XX NOTE: Data found in patent WO9109968 has been used to index this entry.
XX (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
XX to correct PA field.)
```


CC regions have been replaced by corresponding regions from the murine OKT3
 CC antibody heavy chain (see features). See AAQ12636-7 and AAR13092-RI3109.
 CC NOTE: Data found in patent WO9109968 has been used to index this entry.
 CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
 CC to correct PA field.)

XX Sequence 119 AA;

Query Match 100.0%; Score 30; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 |||||
 Db 31 RYTMH 35

RESULT 19

AAR13101
 ID AAR13101 standard; protein; 119 AA.

XX AAR13101;

XX 25-MAR-2003 (revised)
 DT 09-JAN-2003 (revised)
 DT 04-OCT-1991 (first entry)

XX Grafted heavy chain variable region GH341*/JA205.

XX humanised antibody; CDR graft; heavy chain variable region; mouse.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Region 24..34 /label= from OKT 3 heavy chain
 FT Region 48..66 /label= from OKT3 heavy chain
 FT /note= "Val(64) is from KOL sequence"
 FT Misc-difference 72 /label= OKT 3 heavy chain residue
 FT Misc-difference 74 /label= OKT 3 heavy chain residue
 FT Misc-difference 77 /label= OKT 3 heavy chain residue
 FT Misc-difference 79 /label= OKT 3 heavy chain residue
 FT Misc-difference 92 /label= OKT 3 heavy chain residue
 FT Misc-difference 95 /label= OKT 3 heavy chain residue
 FT Region 99..106 /label= from OKT 3 heavy chain

XX WO9109967-A.

FN 11-JUL-1991.

XX 21-DEC-1989; 89GB-00028874.

XX 21-DEC-1989; 89GB-00028874.

XX 21-DEC-1990; 90WO-GB002017.

XX (CLLT) CELLTech LTD.

XX Adair JR, Athwal DS, Emtage JS;

XX WPI; 1991-222915/30.

XX New humanised antibodies comprising CDR grafted antibody - with heavy and
 PT light chains, for use in vivo therapy and diagnosis.

XX Example 15; Fig 5; 91pp; English.

XX This is an example of a CDR-grafted heavy chain region of the invention.
 CC It comprises the human KOL heavy chain sequence except where certain
 CC regions have been replaced by corresponding regions from the murine OKT3
 CC antibody heavy chain (see features). See AAQ12636-7 and AAR13092-RI3109.
 CC NOTE: Data found in patent WO9109968 has been used to index this entry.
 CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
 CC to correct PA field.)

XX Sequence 119 AA;

Query Match 100.0%; Score 30; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 |||||
 Db 31 RYTMH 35

RESULT 20

AAR13103
 ID AAR13103 standard; protein; 119 AA.

XX AAR13103;

XX 25-MAR-2003 (revised)

DT 09-JAN-2003 (revised)

DT 04-OCT-1991 (first entry)

XX Grafted heavy chain variable region GH341*/JA204.

XX humanised antibody; CDR graft; heavy chain variable region; mouse.

XX Homo sapiens.

OS Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 6 /label= OKT 3 heavy chain residue
 FT Region 24..34 /label= from OKT 3 heavy chain
 FT Region 48..66 /label= from OKT3 heavy chain
 FT /note= "Val(64) is from KOL sequence"
 FT Misc-difference 72 /label= OKT 3 heavy chain residue
 FT Misc-difference 74 /label= OKT 3 heavy chain residue
 FT Misc-difference 77 /label= OKT 3 heavy chain residue
 FT Misc-difference 79 /label= OKT 3 heavy chain residue
 FT Region 99..106 /label= from OKT 3 heavy chain

XX WO9109967-A.

XX 11-JUL-1991.

XX 21-DEC-1989; 89GB-00028874.

XX 21-DEC-1989; 89GB-00028874.

XX 21-DEC-1990; 90WO-GB002017.

XX (CLLT) CELLTech LTD.

XX Adair JR, Athwal DS, Emtage JS;

XX WPI; 1991-222915/30.

XX New humanised antibodies comprising CDR grafted antibody - with heavy and
PT light chains, for use in vivo therapy and diagnosis.
XX
XX Example 15; Fig 5; 91pp; English.
XX
XX This is an example of a CDR-grafted heavy chain region of the invention.
CC It comprises the human KOL heavy chain sequence except where certain
CC regions have been replaced by corresponding regions from the murine OKT3
CC antibody heavy chain (see features). See AAK12636-7 and AAR13092-R13109.
CC NOTE: Data found in patent WO9109968 has been used to index this entry.
CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
DB 31 RYTMH 35
RESULT 21
AAR13093
ID AAR13093 standard; protein; 119 AA.
XX
XX AAR13093;
XX
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
XX Grafted heavy chain variable region GH341A/JA175.
DE
XX humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 6 /label= OKT 3 heavy chain residue
FT Region 23..34 /label= from OKT 3 heavy chain
FT Region 48..66 /label= from OKT3 heavy chain
FT /note= "Val(64) is from KOL sequence"
FT Misc-difference 72
FT Misc-difference 74 /label= OKT 3 heavy chain residue
FT Misc-difference 74 /label= OKT 3 heavy chain residue
FT Misc-difference 77 /label= OKT 3 heavy chain residue
FT Misc-difference 79 /label= OKT 3 heavy chain residue
FT Misc-difference 79 /label= OKT 3 heavy chain residue
FT Misc-difference 92 /label= OKT 3 heavy chain residue
FT Misc-difference 95 /label= OKT 3 heavy chain residue
FT Region 100..106 /label= from OKT 3 heavy chain
FT
XX
XX WO9109967-A.
PN
XX
XX 11-JUL-1991.
PD
XX
XX 21-DEC-1989; 89GB-00028874.
PF
XX
XX 21-DEC-1989; 89GB-00028874.
PR

PR 21-DEC-1990; 90WO-GB002017.
XX
XX (CLLT) CELLTECH LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX
XX WPI; 1991-222915/30.
DR
XX New humanised antibodies comprising CDR grafted antibody - with heavy and
PT light chains, for use in vivo therapy and diagnosis.
XX
XX Example 15; Fig 5; 91pp; English.
PS
XX This is an example of a CDR-grafted heavy chain region of the invention.
CC It comprises the human KOL heavy chain sequence except where certain
CC regions have been replaced by corresponding regions from the murine OKT3
CC antibody heavy chain (see features). See AAK12636-7 and AAR13092-R13109.
CC NOTE: Data found in patent WO9109968 has been used to index this entry.
CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
CC to correct PA field.)
XX
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
DB 31 RYTMH 35
RESULT 22
AAR13099
ID AAR13099 standard; protein; 119 AA.
XX
XX AAR13099;
XX
XX 25-MAR-2003 (revised)
DT 09-JAN-2003 (revised)
DT 04-OCT-1991 (first entry)
XX
XX Grafted heavy chain variable region GH341C/JA184.
DE
XX humanised antibody; CDR graft; heavy chain variable region; mouse.
XX
XX Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 6 /label= OKT 3 heavy chain residue
FT Region 23..34 /label= from OKT 3 heavy chain
FT Region 50..66 /label= from OKT3 heavy chain
FT Region 99..106 /label= from OKT 3 heavy chain
FT
XX
XX WO9109967-A.
PN
XX
XX 11-JUL-1991.
PD
XX
XX 21-DEC-1989; 89GB-00028874.
PF
XX
XX 21-DEC-1989; 89GB-00028874.
PR
XX
XX 21-DEC-1990; 90WO-GB002017.
XX
XX (CLLT) CELLTECH LTD.
XX
XX Adair JR, Athwal DS, Emtage JS;
XX

DR WPI; 1991-222915/30.
 XX New humanised antibodies comprising CDR grafted antibody - with heavy and
 PT light chains, for use in vivo therapy and diagnosis.
 XX
 XX
 PS Example 15; Fig 5; 91pp; English.
 XX
 CC This is an example of a CDR-grafted heavy chain region of the invention.
 CC It comprises the human KOL heavy chain sequence except where certain
 CC regions have been replaced by corresponding regions from the murine OKT3
 CC antibody heavy chain (see features). See AAQ12636-7 and AAR13092-R13109.
 CC NOTE: Data found in patent WO9109968 has been used to index this entry.
 CC (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003
 CC to correct PA field.)
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 30; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 Db 31 RYTMH 35
 RESULT 23
 AAR67449
 ID AAR67449 standard; protein; 119 AA.
 XX
 AC AAR67449;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 08-JUL-1995 (first entry)
 XX
 DE OKT3 humanized antibody heavy chain variable region (gHA).
 XX
 KW OKT3; humanized antibody; 3C10; antibody engineering; immunosuppressive;
 *XX monoclonal antibody.
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Region 6
 FT /note= "mouse residue"
 FT Region 23..24
 FT /note= "mouse residues"
 FT Region 27..28
 FT /note= "mouse residues"
 FT Region 29..35
 FT /note= "CDR region of 3C10 heavy chain"
 FT Region 30
 FT /note= "mouse residue"
 FT Region 47..48
 FT /note= "mouse residues"
 FT Region 50..66
 FT /note= "CDR region of 3C10 heavy chain"
 FT Region 72
 FT /note= "mouse residue"
 FT Region 74
 FT /note= "mouse residue"
 FT Region 77
 FT /note= "mouse residue"
 FT Region 79
 FT /note= "mouse residue"
 FT Region 92
 FT /note= "mouse residue"
 FT Region 95
 FT /note= "mouse residue"
 FT Region 99..108

FT /note= "CDR region of 3C10 heavy chain"
 XX
 PN WO9428027-A1.
 XX
 PD 08-DEC-1994.
 XX
 PF 01-JUN-1994; 94WO-US0006198.
 XX
 PR 01-JUN-1993; 93US-00070116.
 XX
 PA (ARCH-) ARCH DEV CORP.
 XX
 PI Bluestone JA, Zivin RA, Jolliffe L;
 XX WPI; 1995-022721/03.
 XX
 DT New humanised OKT3 antibody with mutated Fc receptor binding region -
 PT useful as immunosuppressant to reduce transplant rejection, lacks the T-
 PT cell activating side effects of wild type antibody.
 XX
 PS Disclosure; Page 98-99; 135pp; English.
 XX
 CC The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) can be
 CC engineered to contain a human Fc region. By transferring the binding
 CC specificity into a human framework, the immunogenicity is reduced without
 CC affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to
 CC correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 30; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 Db 31 RYTMH 35
 RESULT 24
 AAR75224
 ID AAR75224 standard; protein; 119 AA.
 XX
 AC AAR75224;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 08-JUL-1995 (first entry)
 XX
 DE OKT3 humanized antibody heavy chain variable region (gHG).
 XX
 KW OKT3; humanized antibody; 3C10; antibody engineering; immunosuppressive;
 XX monoclonal antibody.
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Region 6
 FT /note= "mouse residue"
 FT Region 23..24
 FT /note= "mouse residues"
 FT Region 27..28
 FT /note= "mouse residues"
 FT Region 29..35
 FT /note= "CDR region of 3C10 heavy chain"
 FT Region 30
 FT /note= "mouse residue"
 FT Region 47..48
 FT /note= "mouse residues"
 FT Region 50..66
 FT /note= "CDR region of 3C10 heavy chain"

```

FT Region 79
FT /note= "mouse residue"
FT Region 99..108
FT /note= "CDR region of 3C10 heavy chain"
XX
PN WO9428027-A1.
XX
PD 08-DEC-1994.
XX
XX 01-JUN-1994; 94WO-US006198.
XX
XX 01-JUN-1993; 93US-00070116.
XX
XX (ARCH-) ARCH DEV CORP.
XX
PI Bluestone JA, Zivin RA, Jolliffe L;
XX
XX WPI; 1995-022721/03.
XX
XX New humanised OKT3 antibody with mutated Fc receptor binding region -
PT useful as immunosuppressant to reduce transplant rejection, lacks the T-
PT cell activating side effects of wild type antibody.
XX
XX Disclosure; Page 98-99; 135pp; English.
XX
XX The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) can be
CC engineered to contain a human Fc region. By transferring the binding
CC specificity into a human framework, the immunogenicity is reduced without
CC affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 119 AA;
XX
XX Query Match 100.0%; Score 30; DB 2; Length 119;
XX Best Local Similarity 100.0%; Pred. No. 71;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
DB 31 RYTMH 35
XX
XX RESULT 26
XX AAW73531
XX ID AAW73531 standard; protein; 119 AA.
XX
XX AC AAW73531;
XX
XX DT 03-MAR-1999 (first entry)
XX
XX DE Humanised OKT3 variable region.
XX
XX OKT3; variable region; immune system modulator; theta chain; infection;
KW T-cell receptor; TCR complex; ZAP-70; tyrosine kinase; human; cancer;
KW haematopoietic tissue transplant; autoimmune disease; therapy.
XX
XX OS Synthetic.
XX
XX PN WO9847531-A2.
XX
XX PD 29-OCT-1998.
XX
XX PF 21-APR-1998; 98WO-US008029.
XX
XX PR 21-APR-1997; 97US-0044084P.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX PI Smith JA, Tso J, Yunciark MR, Cole M, Sbluestone JA;
XX
XX WPI; 1998-609934/51.
XX
XX Modulating mammalian immune system e.g. in tissue transplants - using Fc
PT receptor non-binding anti-CD3 antibodies that inactivate Th1 and promote
PT Th2 type T cells.
XX
XX Example 2; Fig 1b; 120pp; English.
XX
XX This sequence represents a humanised variable region of OKT3. The OKT3
CC sequence can be used in the method of the invention. The method is for
CC modulating the immune system of a mammal, and comprises obtaining an
CC immunomodulatory compound that selectively induces theta chain tyrosine

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FT Region 79
FT /note= "mouse residue"
FT Region 99..108
FT /note= "CDR region of 3C10 heavy chain"
XX
PN WO9428027-A1.
XX
PD 08-DEC-1994.
XX
XX 01-JUN-1994; 94WO-US006198.
XX
XX 01-JUN-1993; 93US-00070116.
XX
XX (ARCH-) ARCH DEV CORP.
XX
PI Bluestone JA, Zivin RA, Jolliffe L;
XX
XX WPI; 1995-022721/03.
XX
XX New humanised OKT3 antibody with mutated Fc receptor binding region -
PT useful as immunosuppressant to reduce transplant rejection, lacks the T-
PT cell activating side effects of wild type antibody.
XX
XX Disclosure; Page 98-99; 135pp; English.
XX
XX The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) can be
CC engineered to contain a human Fc region. By transferring the binding
CC specificity into a human framework, the immunogenicity is reduced without
CC affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to
CC correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
XX Sequence 119 AA;
XX
XX Query Match 100.0%; Score 30; DB 2; Length 119;
XX Best Local Similarity 100.0%; Pred. No. 71;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
DB 31 RYTMH 35
XX
XX RESULT 25
XX AAR67447
XX ID AAR67447 standard; protein; 119 AA.
XX
XX AC AAR67447;
XX
XX DT 16-OCT-2003 (revised)
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 08-JUL-1995 (first entry)
XX
XX DE OKT3 humanized antibody heavy chain variable region (GH).
XX
XX OKT3; humanized antibody; 3C10; antibody engineering; immunosuppressive;
KW monoclonal antibody.
XX
XX OS Mus musculus.
XX
XX OS Homo sapiens.
XX
XX OS Chimeric.
XX
XX Key Location/Qualifiers
XX Region 29..35
XX /note= "CDR region of 3C10 heavy chain"
XX Region 50..56
XX /note= "CDR region of 3C10 heavy chain"
XX Region 99..108
XX /note= "CDR region of 3C10 heavy chain"
XX
XX WO9428027-A1.
XX
XX 08-DEC-1994.
XX

```

CC phosphorylation of a p21 form of theta of the T-cell receptor (TCR)
 CC complex without induction of the highly phosphorylated form of theta and
 CC triggers ZAP-70 association, but does not induce tyrosine phosphorylation
 CC of associated ZAP-70 tyrosine kinase. The immunomodulatory compound is
 CC then combined in a pharmaceutically acceptable vehicle and administered
 CC to the mammal. The method is used to modulate the immune system in a
 CC human receiving haematopoietic tissue transplant. It can also be used in
 CC the treatment of diseases such as an autoimmune disease, an infection
 CC cancer, or other malignancy or immunodeficiency
 XX
 SQ Sequence 119 AA;

Query Match 100.0%; Score 30; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 |||||
 Db 31 RYTMH 35

RESULT 27
 AAW73529
 ID AAW73529 standard; protein; 119 AA.

XX AC AAW73529;

XX DT 03-MAR-1999 (first entry)

XX DE Humanised OKT3 variable region.

XX KW OKT3; variable region; immune system modulator; theta chain; infection;
 KW T-cell receptor; TCR complex; ZAP-70; tyrosine kinase; human; cancer;
 KW haematopoietic tissue transplant; autoimmune disease; therapy.

XX OS Synthetic.

XX PN W09847531-A2.

XX PD 29-OCT-1998.

XX PF 21-APR-1998; 98WO-US008029.

XX PR 21-APR-1997; 97US-0044084P.

XX PA (ARCH-) ARCH DEV CORP.

XX PI Smith JA, Tso J, Yuncclark MR, Cole M, Sbluestone JA;

XX DR WPI; 1998-609934/51.

XX PT Modulating mammalian immune system e.g. in tissue transplants - using Fc
 PT receptor non-binding anti-CD3 antibodies that inactivate Th1 and promote
 PT Th2 type T cells.

XX PS Example 2; Fig 1b; 120pp; English.

XX This sequence represents a humanised variable region of OKT3. The OKT3
 CC sequence can be used in the method of the invention. The method is for
 CC modulating the immune system of a mammal, and comprises obtaining an
 CC immunomodulatory compound that selectively induces theta chain tyrosine
 CC phosphorylation of a p21 form of theta of the T-cell receptor (TCR)
 CC complex without induction of the highly phosphorylated form of theta and
 CC triggers ZAP-70 association, but does not induce tyrosine phosphorylation
 CC of associated ZAP-70 tyrosine kinase. The immunomodulatory compound is
 CC then combined in a pharmaceutically acceptable vehicle and administered
 CC to the mammal. The method is used to modulate the immune system in a
 CC human receiving haematopoietic tissue transplant. It can also be used in
 CC the treatment of diseases such as an autoimmune disease, an infection
 CC cancer, or other malignancy or immunodeficiency

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 30; DB 2; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 |||||
 Db 31 RYTMH 35

RESULT 28

ADW80851
 ID ADW80851 standard; protein; 119 AA.

XX AC ADW80851;

XX DT 07-APR-2005 (first entry)

XX DE Anti-CD3 monoclonal antibody heavy chain protein Seq 3.

XX KW CD3; tumor suppressor; organ transplant rejections; immunosuppressive;
 KW cytostatic; antibody.

XX OS Unidentified.

XX PN CN1298020-A.

XX PD 06-JUN-2001.

XX PF 30-NOV-1999; 99CN-00125250.

XX PR 30-NOV-1999; 99CN-00125250.

XX PA (NOSO-) NOSOHEMIA HOSPITAL INST HEMATOLOGY.

XX PI Yang C, Zhu Z, Xiong D;

XX DR WPI; 2001-489689/54.

XX DR N-PSDB; ADW80849.

XX PT CD3-resisting single clone antibody heavy-chain and light-chain variable-
 PT area gene, useful for treating tumors.

XX PS Claim 2; SEQ ID NO 3; 15pp; Chinese.

XX This invention relates to the novel anti-CD3 monoclonal antibody heavy
 CC chain and light chain variable-area and the encoded proteins thereof.
 CC Specifically, it refers to using these genes and polypeptides for the
 CC preparation of medicines for the diagnosis and treatment of tumor growth.
 CC The present invention further describes the development of composition
 CC that can be used to inhibit immunological rejection during organ
 CC transplantation i.e. graft versus host disease. Accordingly, these
 CC compositions exhibit immunosuppressive and cytostatic activities. This
 CC polypeptide sequence is the anti-CD3 monoclonal antibody heavy chain
 CC protein of the invention.

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 30; DB 4; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 |||||
 Db 31 RYTMH 35

RESULT 29

AAU76333

ID AAU76333 standard; peptide; 119 AA.

XX AC AAU76333;

XX DT 21-MAY-2002 (first entry)

XX Human anti-dual integrin antibody complete variable region #1.
 DE
 XX Human; antibody; dual integrin; HC CDR; variable region; LC CDR;
 KW medical device; immune related disease; rheumatoid arthritis;
 KW gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
 KW sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
 KW atherosclerosis; restenosis; angina pectoris; myocardial infarction;
 KW infectious disease; pneumonia; leprosy; malaria; malignant disease;
 KW leukaemia; chronic myelocytic leukaemia; multiple myeloma;
 KW neurological disease; multiple sclerosis; Parkinson's disease;
 KW Alzheimer's disease; Creutzfeldt-Jakob disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200212501-A2.
 PN
 XX 14-FEB-2002.
 PD
 XX 07-AUG-2001; 2001WO-US024784.
 PF
 XX 07-AUG-2000; 2000US-0223363P.
 PR
 PR 01-AUG-2001; 2001US-00920267.
 XX
 XX (CENZ) CENTOCOR INC.
 PA
 XX Giles-Komar J, Heavner G, Snyder L, Trikha M;
 PI
 XX WPI; 2002-217193/27.
 DR
 XX Novel isolated mammalian anti-dual integrin antibody, useful for
 PT diagnosing or treating dual integrin related condition such as rheumatoid
 PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.
 PT
 XX Claim 1; Page 134; 144pp; English.
 PS
 XX The invention relates to an isolated mammalian anti-dual integrin
 CC antibody having at least one of the human heavy chain or light chain
 CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
 CC included are the nucleic acids encoding the CDRs, a vector comprising the
 CC nucleic acids, a host cell comprising the vector, an anti-idiotype
 CC antibody that binds to the anti-dual integrin, a medical device comprising
 CC the antibody suitable for administration by parenteral, subcutaneous,
 CC intramuscular, intravenous, intrarticular, intrabronchial,
 CC intrabdominal, intracapsular, intracartilaginous, intracavitary,
 CC intracerebellar, or other routes as given in specification. The antibody
 CC is useful for diagnosing or treating a dual integrin related condition in
 CC an animal for example, immune related disease such as rheumatoid
 CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
 CC sickle cell anaemia, diabetes, cardiovascular disease such as
 CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
 CC myocardial infarction, infectious disease in a cell such as bacterial,
 CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
 CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
 CC lymphoma, multiple myeloma; neurological disease such as multiple
 CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
 CC Creutzfeldt-Jakob disease and many other diseases given in the
 CC specification. The present sequence is an anti-dual integrin human
 CC variable region containing at least one of the six CDRs listed above
 CC (AAU76327-AAU76332)
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 30; DB 5; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 DB |||||
 31 RYTMH 35
 RESULT 30
 ADQ91061
 ID ADQ91061 standard; peptide; 119 AA.
 XX
 AC ADQ91061;
 XX
 XX 23-SEP-2004 (first entry)
 DT
 XX Murine OKT3 VH region without signal peptide SEQ ID NO:42.
 DE
 XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
 KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
 KW immunological disorder; autoimmune disease; infectious disease; OKT3;
 KW heavy chain variable region; antibody.
 XX
 OS Mus sp.
 XX
 XX CA2403313-A1.
 PN
 XX 11-APR-2004.
 PD

AAO16693
 ID AAO16693 standard; protein; 119 AA.
 XX
 AC AAO16693;
 XX
 DT 15-MAY-2003 (first entry)
 XX
 DE Anti-ovarian cancer bispecific antibody-related protein #3.
 XX
 KW Anti-ovarian cancer bispecific antibody; anti-ovarian cancer antibody;
 KW anti-CD3 antibody; tumour; ovarian cancer.
 XX
 OS Unidentified.
 XX
 PN WO2003004648-A1.
 XX
 PD 16-JAN-2003.
 XX
 PF 23-MAY-2002; 2002WO-CN000347.
 XX
 PR 24-MAY-2001; 2001CN-00118247.
 XX
 XX (GENE-) INST GENETICS & DEV BIOL CAS.
 PA (BEIJ-) BEIJING ABT GENETIC ENG TECHNOLOGY CO LT.
 XX
 XX Huang H, Jiang X, Fang M, Feng J, Zhou P, Yu X, Lin Q;
 PI
 XX WPI; 2003-210366/20.
 DR N-PSDB; AAL52078.
 XX
 XX Anti human ovarian cancer-anti CD3 bispecific antibody, applicable in
 PT drug compositions for preventing or treating tumor e.g. ovarian cancer.
 PT
 XX Claim 5; Fig 5; 51pp; Chinese.
 PS
 XX The invention comprises an anti-ovarian cancer bispecific antibody. The
 CC bispecific antibody of the invention contains an anti-ovarian cancer
 CC antibody region and an anti-CD3 antibody region. The antibody of the
 CC invention is useful for treating tumours, particularly ovarian cancer.
 CC The present amino acid sequence is used in the exemplification of the
 CC invention
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 30; DB 6; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 DB |||||
 31 RYTMH 35
 RESULT 31
 ADQ91061
 ID ADQ91061 standard; peptide; 119 AA.
 XX
 AC ADQ91061;
 XX
 XX 23-SEP-2004 (first entry)
 DT
 XX Murine OKT3 VH region without signal peptide SEQ ID NO:42.
 DE
 XX CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
 KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
 KW immunological disorder; autoimmune disease; infectious disease; OKT3;
 KW heavy chain variable region; antibody.
 XX
 OS Mus sp.
 XX
 XX CA2403313-A1.
 PN
 XX 11-APR-2004.
 PD

XX 11-OCT-2002; 2002CA-02403313.
 XX
 PR 11-OCT-2002; 2002CA-02403313.
 XX
 XX (MICR-) MICROMET AG.
 XX
 PA Lanzavecchia A;
 XX
 PI
 XX WPI; 2004-390792/37.
 DR
 DR N-PSDB; ADQ91062.
 XX
 XX Antibody construct, useful in treating, e.g., cancer and inflammatory
 PT diseases comprises at least one mutated CDR3 region.
 XX
 PS Claim 8; SEQ ID NO 42; 80pp; English.
 XX
 XX The invention relates to a novel polypeptide construct comprising at
 CC least one CDR3 region comprising at least one mutation in a fully defined
 CC sequence of 6 amino acids. A construct of the invention has
 CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
 CC immunosuppressive activity. The polypeptide construct, polynucleotide,
 CC vector or composition are useful for the prevention, treatment or
 CC amelioration of a proliferative disease, a tumorous disease, an
 CC inflammatory disease, an immunological disorder, an autoimmune disease or
 CC an infectious disease in a human subject. The present sequence represents
 CC the OKT3 antibody heavy chain variable region without the signal peptide.
 XX
 XX Sequence 119 AA;
 SQ

Query Match 100.0%; Score 30; DB 8; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
 Db 31 RYTMH 35
 |||||

RESULT 32
 ADR48645
 ID ADR48645 standard; protein; 119 AA.
 XX
 AC ADR48645;
 XX
 XX 18-NOV-2004 (first entry)
 DT
 DE Novel bispecific antibody-related OKT3 antibody VH partial protein.
 XX
 XX diabody; bispecific antibody;
 KW human epithelial cell growth factor receptor; HER; phagocytosis;
 KW cell damage; cytostatic; cancer immunotherapy; anti-tumour agent;
 KW increased cytokine production; phagocytic; cell-damage; tumour cell;
 KW OKT3; VH; humanised.
 XX
 OS Unidentified.
 OS Chimeric.
 XX
 XX JP2004242638-A.
 PN
 XX 02-SEP-2004.
 PD
 XX 17-FEB-2003; 2003JP-00038643.
 PF
 XX 17-FEB-2003; 2003JP-00038643.
 PR
 XX (TOHO-) TOHOKU TECHNOARCH KK.
 PA
 XX WPI; 2004-629611/61.
 DR
 DR N-PSDB; ADR48639.
 XX
 XX Novel diabody-type bispecific antibody having first specificity to human
 PT epithelial cell growth factor receptor and second specificity to surface

PT antigen expressed in cell having phagocytosis activity, useful in cancer
 FT immunotherapy.
 XX
 PS Example 12; Fig 21; 49pp; Japanese.
 XX
 XX This invention relates to a novel diabody type bispecific antibody having
 CC a first specificity with respect to a human epithelial cell growth factor
 CC receptor (HER) and a second specificity with respect to the surface
 CC antigen expressed in a cell having phagocytosis or cell damage activity.
 CC The invention may be useful for the production of compounds with a
 CC cytostatic activity. Hence it is useful in cancer immunotherapy as an
 CC anti-tumour agent. The antibody increases cytokine production in a cell
 CC having phagocytic or cell-damage activity. The invention may be useful in
 CC preparing pharmaceutical composition for excluding, for killing or
 CC harming, for traumatizing and/or decreasing tumour cells. The antibody
 CC exhibits an excellent in vivo cell damage activity and has the advantage
 CC that it maintains its activity and exhibits outstanding stability even
 CC when preserved for several months. The present sequence is that of the
 CC humanised OKT3 antibody VH chain and which was used in the
 CC exemplification of the invention.
 XX
 XX Sequence 119 AA;
 SQ

Query Match 100.0%; Score 30; DB 8; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
 Db 31 RYTMH 35
 |||||

RESULT 33
 ADR42625
 ID ADR42625 standard; protein; 119 AA.
 XX
 AC ADR42625;
 XX
 XX 18-NOV-2004 (first entry)
 DT
 DE Mouse anti-human PD-1 bispecific antibody.
 XX
 XX antiallergic; antiinflammatory; vasotropic; dermatological; nootropic;
 KW antiarthritic; antidiabetic; nephrotropic; immunosuppressive;
 KW thymimetic; anticonvulsant; hepatotropic; muscular; antiparkinsonian;
 KW antianaemic; ophthalmological; neuropathic; gastrointestinal;
 KW antirheumatic; antiulcer; antithyroid; immune therapy; human; PD-1;
 KW bispecific antibody; senile dementia; Alzheimer's disease;
 KW Down's syndrome; Parkinson's disease; Creutzfeldt-Jacob disease;
 KW amyotrophic lateral sclerosis; diabetic neuropathy; Huntington's disease;
 KW Machado-Joseph disease; autoimmune disease; glomerulonephritis;
 KW arthritis; extended myocardiosis disease; ulcerative colitis;
 KW Sjogren's syndrome; Crohn's disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; dry bright;
 KW allergic contact dermatitis; multiple myelitis; scleroderma;
 KW polyarteritis nodosa; rheumatic fever; vitiligo vulgaris;
 KW insulin-dependent diabetes mellitus; Hashimoto's disease; Bechet disease;
 KW Addison's disease; sterility; dermatomyositis; myasthenia gravis;
 KW Reiter's syndrome; Graves' disease; pernicious anaemia;
 KW Goodpasture's syndrome; chronic active liver disease; pemphigus;
 KW autoimmune thrombocytopenic purpura; autoimmune haemolytic anaemia;
 KW angitis.
 XX
 OS Mus sp.
 XX
 XX WO2004072286-A1.
 PN
 XX 26-AUG-2004.
 PD
 XX 22-JAN-2004; 2004WO-JP000549.
 PF
 XX 23-JAN-2003; 2003JP-00014793.
 PR
 XX

PA (ONOEY) ONO PHARM CO LTD.
PA (HONGI/) HONJO T.
XX Honjo T, Shibayama S, Takeda K, Matsuo M, Yoshida T, Miyamoto M;
PI WPI; 2004-625878/60.
XX N-PSDB; ADR42624.
DR Substances specific to human PD-1, comprises region recognizing human PD-1, region recognizing membrane protein existing in cytoplasmic membrane expressing human PD-1, and linker.
XX Disclosure; SEQ ID NO 6; 70pp; Japanese.
XX The invention relates to a substance (I) specific to human PD-1, comprising a region recognizing human PD-1, a region recognizing a membrane protein existing in cytoplasmic membrane in which human PD-1 is expressed, and a linker. Also disclosed are: (a) a bispecific antibody (II) comprising an antibody with respect to human PD-1 or its partial fragment, an antibody with respect to B-cell receptor composite or its partial fragment, and a linker; (b) a polypeptide (III) comprising the antibody with respect to human PD-1, and comprising a sequence in which 10 amino acids are deleted, substituted and/or added; (c) a polynucleotide (IV) encoding (III); (d) an expression vector (V) consisting of (IV); and (e) a host cell (VI) transformed by (V). (I) is useful as a pharmaceutical composition for preventing or treating a disease concerned in human PD-1, such as neurodegenerative disease chosen from senile dementia, Alzheimer's disease, Down's syndrome, Parkinson's disease, Creutzfeldt-Jacob disease, amyotrophic lateral sclerosis, diabetic neuropathy, Parkinson's, Huntington's disease, Machado-Joseph disease, autoimmune diseases chosen from glomerulonephritis, arthritis, extended myocardiosis disease, ulcerative colitis, Sjogren's syndrome, Crohn's disease, systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, dry bright, allergic contact dermatitis, vitiligo myositis, scleroderma, polyarteritis nodosa, rheumatic fever, vitiligo vulgaris, insulin-dependent diabetes mellitus, Hashimoto's disease, Bechet disease, Addison's disease, sterility, dermatomyositis, myasthenia gravis, Reiter's syndrome, Graves' disease, pernicious anaemia, Goodpasture's syndrome, chronic active liver disease, pemphigus, autoimmune thrombocytopenic purpura, autoimmune haemolytic anaemia, and angitis. This sequence corresponds to a bispecific antibody targeted to the human PD-1.
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 30; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db |||||
31 RYTMH 35
RESULT 34
ADV66154
ID ADV66154 standard; protein; 119 AA.
XX AC ADV66154;
XX DT 24-FEB-2005 (first entry)
XX DE CD3-specific antibody heavy chain variable domain - SEQ ID 77.
XX KW bispecific single chain antibody; CD3; tumor; cancer; cytostatic;
XX KM heavy chain variable region.
XX OS Unidentified.
XX PN WO2004106383-A1.
XX PD 09-DEC-2004.
XX PF 26-MAY-2004; 2004WO-EP005687.
XX PR 31-MAY-2003; 2003EP-00012133.
XX PR 31-MAY-2003; 2003EP-00012134.
XX PA (MICR-) MICROMET AG.
XX PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
XX PI Kohleisen B, Lenkner-Schuetz U, Baeuerle P;
XX WPI; 2005-021271/02.
XX N-PSDB; ADV66148.
XX New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous disease, such as an epithelial or minimal residual cancer.
XX Disclosure; SEQ ID NO 77; 227pp; English.
XX The invention comprises a composition that contains a bispecific single chain antibody consisting of at least two domains, where one of domains binds to human epithelial cell adhesion molecule (EpCAM) antigen, and the second domain binds to human CD3 antigen. The bispecific antibody construct of the invention is useful for the prevention, treatment or amelioration of a tumorous disease, such as an epithelial or minimal residual cancer. The present amino acid sequence represents an antibody heavy chain variable domain that is specific for the CD3 antigen.
XX Sequence 119 AA;
SQ
Query Match 100.0%; Score 30; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db |||||
31 RYTMH 35
RESULT 35
ADV66149
ID ADV66149 standard; protein; 119 AA.
XX AC ADV66149;
XX DT 24-FEB-2005 (first entry)
XX DE CD3-specific antibody heavy chain variable domain - SEQ ID 72.
XX KW bispecific single chain antibody; CD3; tumor; cancer; cytostatic;
XX KM heavy chain variable region.
XX OS Unidentified.
XX PN WO2004106383-A1.
XX PD 09-DEC-2004.
XX PF 26-MAY-2004; 2004WO-EP005687.
XX PR 31-MAY-2003; 2003EP-00012133.
XX PR 31-MAY-2003; 2003EP-00012134.
XX PA (MICR-) MICROMET AG.
XX PI Kufer P, Berry M, Offner S, Brischwein K, Wolf A, Raum T;
XX PI Kohleisen B, Lenkner-Schuetz U, Baeuerle P;
XX WPI; 2005-021271/02.
XX N-PSDB; ADV66148.
XX New pharmaceutical composition having a bispecific single chain antibody construct, useful for preventing, treating or ameliorating a tumorous

PT disease, such as an epithelial or minimal residual cancer.
 XX Disclosure; SEQ ID NO 72; 227pp; English.
 XX
 CC The invention comprises a composition that contains a bispecific single
 CC chain antibody consisting of at least two domains, where one of domains
 CC binds to human epithelial cell adhesion molecule (EPCAM) antigen, and the
 CC second domain binds to human CD3 antigen. The bispecific antibody
 CC construct of the invention is useful for the prevention, treatment or
 CC amelioration of a tumorous disease, such as an epithelial or minimal
 CC residual cancer. The present amino acid sequence represents an antibody
 CC heavy chain variable domain that is specific for the CD3 antigen.
 XX
 XX Sequence 119 AA;
 SQ
 Query Match 100.0%; Score 30; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYTMH 5
 Db 31 RYTMH 35
 |||||
 31 RYTMH 35
 RESULT 36
 ADV26037
 ID ADV26037 standard; protein; 119 AA.
 XX
 AC ADV26037;
 DT 10-MAR-2005 (first entry)
 XX
 DE Mouse OKT3 VH protein.
 XX
 DE immunostimulant; immunogenicity; antibody.
 XX
 OS Mus sp.
 XX
 PN WO2004108158-A1.
 XX
 PD 16-DEC-2004.
 XX
 PF 28-MAY-2004; 2004WO-US017219.
 XX
 PR 02-JUN-2003; 2003US-0475155P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Rother RP, Faas-Knight S, Wu D, Carr FJ, Hamilton A;
 XX
 DR WPI; 2005-031597/03.
 XX
 PT New de-immunized anti-CD3 antibody, useful for stimulating an immune
 PT response against infections and for treating infections.
 XX
 PS Claim 2; SEQ ID NO 16; 75pp; English.
 CC
 CC The invention relates to a de-immunized anti-CD3 antibody. The antibody,
 CC composition and methods are useful for stimulating an immune response
 CC against infections and for treating infections. The present sequence
 CC represents the amino acid sequence of a mouse OKT3 deimmunized VH
 CC protein.
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 30; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYTMH 5
 Db 31 RYTMH 35
 |||||
 31 RYTMH 35
 RESULT 37
 ADV26043
 ID ADV26043 standard; protein; 119 AA.
 XX
 AC ADV26043;
 DT 10-MAR-2005 (first entry)
 XX
 DE Mouse OKT3 deimmunized VH protein v6.
 XX
 DE immunostimulant; immunogenicity; antibody.
 XX
 OS Mus sp.
 XX
 PN WO2004108158-A1.
 XX
 PD 16-DEC-2004.
 XX
 PF 28-MAY-2004; 2004WO-US017219.
 XX
 PR 02-JUN-2003; 2003US-0475155P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Rother RP, Faas-Knight S, Wu D, Carr FJ, Hamilton A;
 XX
 DR WPI; 2005-031597/03.
 XX
 PT New de-immunized anti-CD3 antibody, useful for stimulating an immune
 PT response against infections and for treating infections.
 XX
 PS Claim 2; SEQ ID NO 16; 75pp; English.
 CC
 CC The invention relates to a de-immunized anti-CD3 antibody. The antibody,
 CC composition and methods are useful for stimulating an immune response
 CC against infections and for treating infections. The present sequence
 CC represents the amino acid sequence of a mouse OKT3 deimmunized VH
 CC protein.
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 30; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYTMH 5
 Db 31 RYTMH 35
 |||||
 31 RYTMH 35
 RESULT 38
 ADV26040
 ID ADV26040 standard; protein; 119 AA.
 XX
 AC ADV26040;
 DT 10-MAR-2005 (first entry)
 XX
 DE Mouse OKT3 deimmunized VH protein v3.
 XX
 DE immunostimulant; immunogenicity; antibody.
 XX
 OS Mus sp.
 XX
 PN WO2004108158-A1.
 XX
 PD 16-DEC-2004.
 XX
 PF 28-MAY-2004; 2004WO-US017219.
 XX
 PR 02-JUN-2003; 2003US-0475155P.
 XX
 PA (ALEX-) ALEXION PHARM INC.

```
XX Rother RP, Faas-Knight S, Wu D, Carr FJ, Hamilton A;
PI WPI; 2005-031597/03.
XX
XX New de-immunized anti-CD3 antibody, useful for stimulating an immune
PT response against infections and for treating infections.
XX
PS Claim 2; SEQ ID NO 13; 75pp; English.
XX
CC The invention relates to a de-immunized anti-CD3 antibody. The antibody,
CC composition and methods are useful for stimulating an immune response
CC against infections and for treating infections. The present sequence
CC represents the amino acid sequence of a mouse OKT3 deimmunized VH
CC protein.
XX
SQ Sequence 119 AA;
Query Match 100.0%; Score 30; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
DB 31 RYTMH 35
|||||
RESULT 39
ADV26044
.ID ADV26044 standard; protein; 119 AA.
XX
AC ADV26044;
XX
DT 10-MAR-2005 (first entry)
XX
DE Mouse OKT3 deimmunized VH protein v7.
XX
DE Mouse OKT3 deimmunized VH protein v7.
XX immunostimulant; immunogenicity; antibody.
XX
OS Mus sp.
XX
PN WO2004108158-A1.
XX
PD 16-DEC-2004.
XX
PF 28-MAY-2004; 2004WO-US017219.
XX
PR 02-JUN-2003; 2003US-0475155P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Rother RP, Faas-Knight S, Wu D, Carr FJ, Hamilton A;
XX
XX WPI; 2005-031597/03.
XX
PS Claim 2; SEQ ID NO 17; 75pp; English.
XX
CC The invention relates to a de-immunized anti-CD3 antibody. The antibody,
CC composition and methods are useful for stimulating an immune response
CC against infections and for treating infections. The present sequence
CC represents the amino acid sequence of a mouse OKT3 deimmunized VH
CC protein.
XX
SQ Sequence 119 AA;
Query Match 100.0%; Score 30; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
DB 31 RYTMH 35
|||||
RESULT 40
ADV26039
.ID ADV26039 standard; protein; 119 AA.
XX
AC ADV26039;
XX
DT 10-MAR-2005 (first entry)
XX
DE Mouse OKT3 deimmunized VH protein v2.
XX
KW immunostimulant; immunogenicity; antibody.
XX
OS Mus sp.
XX
PN WO2004108158-A1.
XX
PD 16-DEC-2004.
XX
PF 28-MAY-2004; 2004WO-US017219.
XX
PR 02-JUN-2003; 2003US-0475155P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Rother RP, Faas-Knight S, Wu D, Carr FJ, Hamilton A;
XX
XX WPI; 2005-031597/03.
XX
PS New de-immunized anti-CD3 antibody, useful for stimulating an immune
PT response against infections and for treating infections.
XX
PS Claim 2; SEQ ID NO 12; 75pp; English.
XX
CC The invention relates to a de-immunized anti-CD3 antibody. The antibody,
CC composition and methods are useful for stimulating an immune response
CC against infections and for treating infections. The present sequence
CC represents the amino acid sequence of a mouse OKT3 deimmunized VH
CC protein.
XX
SQ Sequence 119 AA;
Query Match 100.0%; Score 30; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
DB 31 RYTMH 35
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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	100.0	114	2	US-09-196-522-223
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4	30	100.0	118	2	US-09-348-224-10
5	30	100.0	119	1	US-08-303-569B-11
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67	30	100.0	119	2	US-09-348-224-22
68	30	100.0	119	2	US-09-348-224-23
69	30	100.0	119	2	US-09-348-224-24
70	30	100.0	119	2	US-09-348-224-25
71	30	100.0	121	2	US-09-948-004-26
72	30	100.0	142	2	US-09-069-628-27
73	30	100.0	236	1	US-08-070-116A-2
74	30	100.0	236	2	US-08-557-050-2
75	30	100.0	468	1	US-08-303-569B-7
76	30	100.0	468	1	US-08-116-247-7
77	30	100.0	468	2	US-09-795-515-7
78	30	100.0	468	2	US-09-348-224-7
79	30	100.0	495	2	US-09-948-004-18
80	27	90.0	115	2	US-09-640-211A-660
81	27	90.0	115	2	US-09-640-211A-2127
82	27	90.0	203	2	US-09-552-991A-17282
83	27	90.0	216	2	US-09-489-039A-11117
84	27	90.0	371	2	US-09-302-540-13676
85	27	90.0	676	2	US-09-061-768A-2
86	27	90.0	676	2	US-09-764-246-2
87	27	90.0	676	2	US-09-949-016-6027
88	27	90.0	677	2	US-09-061-768A-4
89	27	90.0	677	2	US-09-764-246-4
90	27	90.0	679	2	US-09-949-016-8912
91	27	90.0	704	2	US-09-949-002-407
92	27	90.0	705	2	US-09-949-016-11418
93	27	90.0	705	2	US-09-949-002-557
94	27	90.0	826	2	US-09-489-039A-10341
95	27	90.0	915	2	US-09-489-039A-8249
96	27	90.0	1297	2	US-09-540-245A-17
97	27	90.0	1297	2	US-10-289-776-17
98	26	86.7	86	1	US-08-933-750C-40
99	26	86.7	86	2	US-09-234-613-40
100	26	86.7	159	2	US-09-270-767-31841

Sequence 16, Appl
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Sequence 660, App
Sequence 2127, Ap
Sequence 17282, A
Sequence 11117, A
Sequence 13676, A
Sequence 2, Appl
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Sequence 6277, Ap
Sequence 4, Appl
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Sequence 8912, Ap
Sequence 407, App
Sequence 11419, A
Sequence 557, App
Sequence 10341, A
Sequence 8249, Ap
Sequence 17, Appl
Sequence 17, Appl
Sequence 40, Appl
Sequence 31841, A

ALIGNMENTS

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RESULT 1
US-09-726-219A-223
; Sequence 223, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-726-219A-223

Query Match      100.0%; Score 30; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
DB      31 RYTMH 35

RESULT 2
US-09-196-522-223
; Sequence 223, Application US/09196522
; Patent No. 6916605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
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; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00004
; CURRENT APPLICATION NUMBER: US/09/196,522
; CURRENT FILING DATE: 1998-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-09-196-522-223

Query Match      100.0%; Score 30; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
DB      31 RYTMH 35

RESULT 3
US-08-116-247-10
; Sequence 10, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Achwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 118 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-116-247-10

Query Match 100.0%; Score 30; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 4
US-09-348-224-10
; Sequence 10, Application US/09348224
; Patent No. 6750325
; GENERAL INFORMATION:
; APPLICANT: Jollieffe, Linda Kay
; APPLICANT: Zivin, Robert Allan
; APPLICANT: Adair, John Robert
; APPLICANT: Athwal, Diljeet Singh
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; FILE REFERENCE: CARP0066
; CURRENT APPLICATION NUMBER: US/09/348,224
; CURRENT FILING DATE: 1993-07-06
; EARLIER APPLICATION NUMBER: 08/116,247
; EARLIER FILING DATE: 1993-09-03
; EARLIER APPLICATION NUMBER: 07/743,377
; EARLIER FILING DATE: 1991-10-04
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Mouse
; US-09-348-224-10

Query Match 100.0%; Score 30; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 5
US-08-303-569B-11
; Sequence 11, Application US/08303569B
; Patent No. 5859205

; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-303-569B-11

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 6
US-08-303-569B-12
; Sequence 12, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-303-569B-12

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 7
US-08-303-569B-13
; Sequence 13, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-303-569B-13

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 8
US-08-303-569B-14
; Sequence 14, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-303-569B-14

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 9
US-08-303-569B-15
; Sequence 15, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-303-569B-15

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 10

; US-08-303-569B-16;
; Sequence 16, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-303-569B-16

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

Db 31 RYTMH 35

RESULT 11

; US-08-303-569B-17
; Sequence 17, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-303-569B-17

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 12

; US-08-303-569B-18
; Sequence 18, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/303,569B
/ FILING DATE: 07-SEP-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trujillo, Doreen Yanko
/ REGISTRATION NUMBER: 35,719
/ REFERENCE/DOCKET NUMBER: CARP-0032
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-303-569B-18
Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 13
US-08-303-569B-19
; Sequence 19, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-303-569B-19
Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 14
US-08-303-569B-20
; Sequence 20, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-303-569B-20
Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 15
US-08-303-569B-21
; Sequence 21, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
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US-08-303-569B-22
Query Match          100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 RYTMH 35

RESULT 17
US-08-303-569B-23
; Sequence 23, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-303-569B-23

Query Match          100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 RYTMH 35

RESULT 18
US-08-303-569B-24
; Sequence 24, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris

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/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/303,569B
/ FILING DATE: 07-SEP-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trujillo, Doreen Yanko
/ REGISTRATION NUMBER: 35,719
/ REFERENCE/DOCKET NUMBER: CARP-0032
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-303-569B-24

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 19
US-08-303-569B-30
/ Sequence 30, Application US/08303569B
/ Patent No. 5859205
/ GENERAL INFORMATION:
/ APPLICANT: Agair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ APPLICANT: Emage, John S.
/ TITLE OF INVENTION: Humanised Antibodies
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/303,569B
/ FILING DATE: 07-SEP-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trujillo, Doreen Yanko
/ REGISTRATION NUMBER: 35,719
/ REFERENCE/DOCKET NUMBER: CARP-0032
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-303-569B-30

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 20
US-08-070-116A-10
/ Sequence 10, Application US/08070116A
/ Patent No. 5885573
/ GENERAL INFORMATION:
/ APPLICANT: Zivin, Robert A.
/ APPLICANT: Jolliffe, Linda K.
/ APPLICANT: Bluestone, Jeffrey A.
/ TITLE OF INVENTION: Methods and Materials For Modulation
/ TITLE OF INVENTION: of the Immuno-suppressive Activity and
/ TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: United States of America
/ ZIP: 77210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/070,116A
/ FILING DATE: 01-JUN-1993
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wilson, Mark B.
/ REGISTRATION NUMBER: 37,259
/ REFERENCE/DOCKET NUMBER: ARCD:082
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-070-116A-10

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 21
US-08-070-116A-12
/ Sequence 12, Application US/08070116A
/ Patent No. 5885573
/ GENERAL INFORMATION:
```

;; APPLICANT: Zivin, Robert A.
;; APPLICANT: Jolliffe, Linda K.
;; APPLICANT: Bluestone, Jeffrey A.
;; TITLE OF INVENTION: Methods and Materials For Modulation
;; TITLE OF INVENTION: of the Immuno-suppressive Activity and
;; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
;; NUMBER OF SEQUENCES: 18
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: United States of America
;; ZIP: 77210
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Wordperfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/070,116A
;; FILING DATE: 01-JUN-1993
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: ARCD:082
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-070-116A-12

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 22
US-08-070-116A-13
; Sequence 13, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/070,116A
;; FILING DATE: 01-JUN-1993
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wilson, Mark B.
;; REGISTRATION NUMBER: 37,259
;; REFERENCE/DOCKET NUMBER: ARCD:082
;; TELEPHONE: (512) 418-3000
;; TELEFAX: (512) 474-7577
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-070-116A-13

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 23
US-08-070-116A-14
; Sequence 14, Application US/08070116A
; Patent No. 5885573
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Bluestone, Jeffrey A.
; TITLE OF INVENTION: Methods and Materials For Modulation
; TITLE OF INVENTION: of the Immuno-suppressive Activity and
; TITLE OF INVENTION: Toxicity of Monoclonal Antibodies
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/070,116A
; FILING DATE: 01-JUN-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:082
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-070-116A-14

Query Match 100.0%; Score 30; DB 1; Length 119;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

*RESULT 24

US-08-116-247-12
; Sequence 12, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-247-12

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 25

US-08-116-247-13
; Sequence 13, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-247-13

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 26

US-08-116-247-14
; Sequence 14, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991

REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-704-352-22

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 39
US-10-704-352-23
Sequence 23, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-704-352-23

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 40
US-10-704-352-24
Sequence 24, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-704-352-24

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

Search completed: December 14, 2005, 07:37:50
Job time : 23.931 secs

ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-14

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 27

US-08-116-247-15
Sequence 15, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,247
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-15

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 28

US-08-116-247-16
Sequence 16, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,247
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-16

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 29

US-08-116-247-17
Sequence 17, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor

City: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/116,247
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-17

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 30
US-08-116-247-18
Sequence 18, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,247
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-19

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 30
US-08-116-247-18
Sequence 18, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,247
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-19

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-18

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 31
US-08-116-247-19
Sequence 19, Application US/08116247
Patent No. 5929212
GENERAL INFORMATION:
APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,247
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Paintin, Francis A.
REGISTRATION NUMBER: 19,386
REFERENCE/DOCKET NUMBER: CARP-0011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-247-19

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 32
US-08-116-247-20
; Sequence 20, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-247-20
Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYTMH 5
Db 31 RYTMH 35
RESULT 33
US-08-116-247-21
; Sequence 21, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-247-20
Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYTMH 5
Db 31 RYTMH 35
RESULT 34
US-08-116-247-22
; Sequence 22, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100

ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-116-247-21
Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYTMH 5
Db 31 RYTMH 35
RESULT 34
US-08-116-247-22
; Sequence 22, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100

/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-116-247-22

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 35
US-08-116-247-23
/ Sequence 23, Application US/08116247
/ Patent No. 5929212
/ GENERAL INFORMATION:
/ APPLICANT: Jolliffe, Linda K.
/ APPLICANT: Zivin, Robert A.
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ TITLE OF INVENTION: CD3 Specific Recombinant Antibody
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/116,247
/ FILING DATE:
/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/743,377
/ FILING DATE: 10-OCT-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paintin, Francis A.
/ REGISTRATION NUMBER: 19,386
/ REFERENCE/DOCKET NUMBER: CARP-0011
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-116-247-23

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

, RESULT 36

US-08-116-247-24
/ Sequence 24, Application US/08116247
/ Patent No. 5929212
/ GENERAL INFORMATION:
/ APPLICANT: Jolliffe, Linda K.
/ APPLICANT: Zivin, Robert A.
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ TITLE OF INVENTION: CD3 Specific Recombinant Antibody
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/116,247
/ FILING DATE:
/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/743,377
/ FILING DATE: 10-OCT-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paintin, Francis A.
/ REGISTRATION NUMBER: 19,386
/ REFERENCE/DOCKET NUMBER: CARP-0011
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-116-247-24

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 37
US-08-116-247-25
/ Sequence 25, Application US/08116247
/ Patent No. 5929212
/ GENERAL INFORMATION:
/ APPLICANT: Jolliffe, Linda K.
/ APPLICANT: Zivin, Robert A.
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ TITLE OF INVENTION: CD3 Specific Recombinant Antibody
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-116-247-25

Query Match 100.0%; Score 30; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 38
US-08-557-050-10
; Sequence 10, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION NUMBER: US 08/070,116
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 474-7577
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-557-050-12

Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5

; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-557-050-10

Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 39
US-08-557-050-12
; Sequence 12, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION NUMBER: US 08/070,116
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-557-050-12

Query Match 100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5

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Db          31 RYTMH 35
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RESULT 40
US-08-557-050-13
; Sequence 13, Application US/08557050
; Patent No. 6491916
; GENERAL INFORMATION:
; APPLICANT: Bluestone, Jeffrey A.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF
; TITLE OF INVENTION: THE IMMUNO-SUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,050
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06198
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/070,116
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:208
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-557-050-13

Query Match          100.0%; Score 30; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. NO. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 RYTMH 5
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Db          31 RYTMH 35

Search completed: December 14, 2005, 07:33:18
Job time : 7.32759 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:19:54 ; Search time 22.931 Seconds
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91.106 Million cell updates/sec

File: US-10-720-323-1
Effect score: 30
Sequence: 1 RYTMH 5

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per of hits satisfying chosen parameters: 1867569

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Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.Main.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30	100.0	5	4	US-10-720-323-1
3	30	100.0	5	5	US-10-954-300A-1
4	30	100.0	71	4	US-10-424-599-246908
5	30	100.0	114	4	US-10-803-622-223
6	30	100.0	114	4	US-10-803-653-223
7	30	100.0	119	3	US-09-795-515-11
8	30	100.0	119	3	US-09-795-515-12
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ALIGNMENTS

RESULT 1
US-09-920-267C-1
; Sequence 1, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc. Jill
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-1

Query Match 100.0%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 1 RYTMH 5

RESULT 2
US-10-720-323-1
; Sequence 1, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-1

Query Match 100.0%; Score 30; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 1 RYTMH 5

RESULT 3
US-10-954-900A-1

; Sequence 1, Application US/10954900A
; Publication No. US20050123541A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallon
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-1

Query Match 100.0%; Score 30; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 1 RYTMH 5

RESULT 4
US-10-424-599-246908
; Sequence 246908, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246908
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64989C.1.pgp
US-10-424-599-246908

Query Match 100.0%; Score 30; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 63 RYTMH 67

RESULT 5
US-10-803-622-223
; Sequence 223, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology

APPLICANT: Cambridge Antibody Technology Limited
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803.622
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 223
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-622-223

Query Match 100.0%; Score 30; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 6
US-10-803-653-223
Sequence 223, Application US/10803653
Publication No. US20040157215A1
GENERAL INFORMATION:
APPLICANT: Cambridge Antibody Technology
APPLICANT: Medical Research Council
APPLICANT: McCafferty, John
APPLICANT: Pope, Anthony
APPLICANT: Johnson, Kevin
APPLICANT: Hoogenboom, Hendricus
APPLICANT: Griffiths, Andrew
APPLICANT: Jackson, Ronald
APPLICANT: Holliger, Kasper
APPLICANT: Marks, James
APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David

APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 13839-00013
CURRENT APPLICATION NUMBER: US/10/803.653
CURRENT FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
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PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 223
LENGTH: 114
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VH of scFv from mouse immunized with 2-phenyl-5-oxazolone
US-10-803-653-223

Query Match 100.0%; Score 30; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 7
US-09-795-515-11
Sequence 11, Application US/09795515
Publication No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/795,515
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:

```
/ NAME: Trujillo, Doreen Yatko
/ REGISTRATION NUMBER: 35,719
/ REFERENCE/DOCKET NUMBER: CARP-0057
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-795-515-11

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 8
US-09-795-515-12
/ Sequence 12, Application US/09795515
/ Publication No. US20030039645A1
/ GENERAL INFORMATION:
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ APPLICANT: Emage, John S.
/ TITLE OF INVENTION: Humanised Antibodies
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/795,515
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/846,658
/ FILING DATE: 01-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trujillo, Doreen Yatko
/ REGISTRATION NUMBER: 35,719
/ REFERENCE/DOCKET NUMBER: CARP-0057
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-795-515-13

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 9
US-09-795-515-13
/ Sequence 13, Application US/09795515
/ Publication No. US20030039645A1
/ GENERAL INFORMATION:
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ APPLICANT: Emage, John S.
/ TITLE OF INVENTION: Humanised Antibodies
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/795,515
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/846,658
/ FILING DATE: 01-MAY-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Trujillo, Doreen Yatko
/ REGISTRATION NUMBER: 35,719
/ REFERENCE/DOCKET NUMBER: CARP-0057
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 119 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-09-795-515-13

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 10
US-09-795-515-14
/ Sequence 14, Application US/09795515
/ Publication No. US20030039645A1
/ GENERAL INFORMATION:
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ APPLICANT: Emage, John S.
/ TITLE OF INVENTION: Humanised Antibodies
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 11
US-09-795-515-15
/ Sequence 15, Application US/09795515
/ Publication No. US20030039645A1
/ GENERAL INFORMATION:
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ APPLICANT: Emage, John S.
/ TITLE OF INVENTION: Humanised Antibodies
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19103

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35
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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatkco
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-795-515-14

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 11
US-09-795-515-15
; Sequence 15, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtege, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatkco
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-795-515-15

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 12
US-09-795-515-16
; Sequence 16, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtege, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatkco
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-795-515-16

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 13
US-09-795-515-17
; Sequence 17, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
```

APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1r1s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-795-515-17

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 14
US-09-795-515-18
Sequence 18, Application US/09795515
Publication No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1r1s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-795-515-18

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 15
US-09-795-515-19
Sequence 19, Application US/09795515
Publication No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1r1s
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-795-515-19

Query Match 100.0%; Score 30; DB 3; Length 119;

```
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 16
US-09-795-515-20
; Sequence 20, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-795-515-21

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 17
US-09-795-515-20
; Sequence 21, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-795-515-20

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35

RESULT 18
US-09-795-515-22
; Sequence 22, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-795-515-21

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTMH 35
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; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-795-515-22

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 19
US-09-795-515-23
; Sequence 23, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-795-515-24

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 21
US-09-795-515-30
; Sequence 30, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-795-515-30

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 22

US-09-920-267C-7
; Sequence 7, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-7

Query Match 100.0%; Score 30; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 23

US-10-267-286A-10
; Sequence 10, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.

; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; APPLICATION NUMBER: US/10-267-286A
; FILING DATE: 2003-01-28
; CURRENT APPLICATION NUMBER: US/10/267,286A
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-10

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 24

US-10-267-286A-12
; Sequence 12, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; APPLICATION NUMBER: US/10-267-286A
; FILING DATE: 2003-01-28
; CURRENT APPLICATION NUMBER: US/10/267,286A
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-12

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 25
US-10-267-286A-13
; Sequence 13, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/10/267,286A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-13
Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db 31 RYTMH 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-14
Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db 31 RYTMH 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-267-286A-14

Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db 31 RYTMH 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-704-352-11
; Sequence 11, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,858
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-704-352-11
Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
Db 31 RYTMH 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-704-352-12
; Sequence 12, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies

;;
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/704,352
;; FILING DATE: 07-Nov-2003
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/795,515
;; FILING DATE: 28-FEB-2001
;; APPLICATION NUMBER: 08/846,658
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Trujillo, Doreen Yatkoo
;; REGISTRATION NUMBER: 35,719
;; REFERENCE/DOCKET NUMBER: CARP-0057
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;;
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-704-352-12
;
Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 RYTMH 5
Db 31 RYTMH 35
;
RESULT 29
US-10-704-352-13
; Sequence 13, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>

;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/795,515
;; FILING DATE: 28-FEB-2001
;; APPLICATION NUMBER: 08/846,658
;; FILING DATE: 01-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Trujillo, Doreen Yatkoo
;; REGISTRATION NUMBER: 35,719
;; REFERENCE/DOCKET NUMBER: CARP-0057
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;;
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 119 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-704-352-13
;
Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 1 RYTMH 5
Db 31 RYTMH 35
;
RESULT 30
US-10-704-352-14
; Sequence 14, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatkoo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-704-352-17

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 34
US-10-704-352-18
Sequence 18, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-704-352-18

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 35
US-10-704-352-19
Sequence 19, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-704-352-19

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-704-352-18

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

RESULT 35
US-10-704-352-19
Sequence 19, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-704-352-19

Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 31 RYTMH 35

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RESULT 36
US-10-704-352-20
; Sequence 20, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-704-352-20
Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 37
US-10-704-352-21
; Sequence 21, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-704-352-21
Query Match 100.0%; Score 30; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 31 RYTMH 35

RESULT 38
US-10-704-352-22
; Sequence 22, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:25:44 ; Search time 1.55172 Seconds
(without alignments)
21.698 Million cell updates/sec

Title: US-10-720-323-1
Perfect score: 30
Sequence: 1 RYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51441 seqs, 6734002 residues

Total number of hits satisfying chosen parameters: 51441

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	90.0	247	US-11-054-515-1307	Sequence 1307, Ap
2	27	90.0	248	US-11-054-515-877	Sequence 877, App
3	27	90.0	248	US-11-054-515-953	Sequence 953, App
4	27	90.0	248	US-11-054-515-965	Sequence 965, App
5	27	90.0	248	US-11-054-515-980	Sequence 980, App
6	27	90.0	248	US-11-054-515-984	Sequence 984, App
7	27	90.0	248	US-11-054-515-987	Sequence 987, App
8	27	90.0	248	US-11-054-515-1181	Sequence 1181, App
9	27	90.0	248	US-11-054-515-1182	Sequence 1182, App
10	27	90.0	248	US-11-054-515-1293	Sequence 1293, App
11	27	90.0	248	US-11-054-515-1306	Sequence 1306, App
12	27	90.0	248	US-11-054-515-1417	Sequence 1417, App
13	27	90.0	248	US-11-054-515-1588	Sequence 1588, App
14	27	90.0	248	US-11-054-515-1609	Sequence 1609, App
15	27	90.0	248	US-11-054-515-1622	Sequence 1622, App
16	27	90.0	248	US-11-054-515-1623	Sequence 1623, App
17	27	90.0	248	US-11-054-515-1624	Sequence 1624, App
18	27	90.0	248	US-11-054-515-1643	Sequence 1643, App
19	27	90.0	248	US-11-054-515-1657	Sequence 1657, App
20	27	90.0	248	US-11-054-515-1660	Sequence 1660, App
21	27	90.0	248	US-11-054-515-1667	Sequence 1667, App
22	27	90.0	248	US-11-054-515-1668	Sequence 1668, App
23	27	90.0	248	US-11-054-515-1670	Sequence 1670, App
24	27	90.0	248	US-11-054-515-1679	Sequence 1679, App
25	27	90.0	248	US-11-054-515-1681	Sequence 1681, App

26	27	90.0	248	US-11-054-515-1755	Sequence 1755, Ap
27	27	90.0	248	US-11-054-515-1765	Sequence 1765, Ap
28	27	90.0	248	US-11-054-515-1823	Sequence 1823, Ap
29	27	90.0	250	US-11-054-515-859	Sequence 859, App
30	27	90.0	250	US-11-054-515-3247	Sequence 3247, App
31	27	90.0	251	US-11-054-515-845	Sequence 845, App
32	27	90.0	251	US-11-054-515-852	Sequence 852, App
33	27	90.0	251	US-11-054-515-853	Sequence 853, App
34	27	90.0	251	US-11-054-515-875	Sequence 875, App
35	27	90.0	251	US-11-054-515-879	Sequence 879, App
36	27	90.0	251	US-11-054-515-884	Sequence 884, App
37	27	90.0	251	US-11-054-515-886	Sequence 886, App
38	27	90.0	251	US-11-054-515-887	Sequence 887, App
39	27	90.0	251	US-11-054-515-940	Sequence 940, App
40	27	90.0	251	US-11-054-515-944	Sequence 944, App
41	27	90.0	251	US-11-054-515-961	Sequence 961, App
42	27	90.0	251	US-11-054-515-962	Sequence 962, App
43	27	90.0	251	US-11-054-515-968	Sequence 968, App
44	27	90.0	251	US-11-054-515-975	Sequence 975, App
45	27	90.0	251	US-11-054-515-978	Sequence 978, App
46	27	90.0	251	US-11-054-515-986	Sequence 986, App
47	27	90.0	251	US-11-054-515-1051	Sequence 1051, App
48	27	90.0	251	US-11-054-515-1052	Sequence 1052, App
49	27	90.0	251	US-11-054-515-1055	Sequence 1055, App
50	27	90.0	251	US-11-054-515-1057	Sequence 1057, App
51	27	90.0	251	US-11-054-515-1059	Sequence 1059, App
52	27	90.0	251	US-11-054-515-1062	Sequence 1062, App
53	27	90.0	251	US-11-054-515-1064	Sequence 1064, App
54	27	90.0	251	US-11-054-515-1072	Sequence 1072, App
55	27	90.0	251	US-11-054-515-1073	Sequence 1073, App
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57	27	90.0	251	US-11-054-515-1076	Sequence 1076, App
58	27	90.0	251	US-11-054-515-1078	Sequence 1078, App
59	27	90.0	251	US-11-054-515-1082	Sequence 1082, App
60	27	90.0	251	US-11-054-515-1085	Sequence 1085, App
61	27	90.0	251	US-11-054-515-1086	Sequence 1086, App
62	27	90.0	251	US-11-054-515-1103	Sequence 1103, App
63	27	90.0	251	US-11-054-515-1106	Sequence 1106, App
64	27	90.0	251	US-11-054-515-1107	Sequence 1107, App
65	27	90.0	251	US-11-054-515-1132	Sequence 1132, App
66	27	90.0	251	US-11-054-515-1172	Sequence 1172, App
67	27	90.0	251	US-11-054-515-1176	Sequence 1176, App
68	27	90.0	251	US-11-054-515-1187	Sequence 1187, App
69	27	90.0	251	US-11-054-515-1292	Sequence 1292, App
70	27	90.0	251	US-11-054-515-1297	Sequence 1297, App
71	27	90.0	251	US-11-054-515-1338	Sequence 1338, App
72	27	90.0	251	US-11-054-515-1343	Sequence 1343, App
73	27	90.0	251	US-11-054-515-1408	Sequence 1408, App
74	27	90.0	251	US-11-054-515-1437	Sequence 1437, App
75	27	90.0	251	US-11-054-515-1473	Sequence 1473, App
76	27	90.0	251	US-11-054-515-1478	Sequence 1478, App
77	27	90.0	251	US-11-054-515-1479	Sequence 1479, App
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81	27	90.0	251	US-11-054-515-1749	Sequence 1749, App
82	27	90.0	251	US-11-054-515-1752	Sequence 1752, App
83	27	90.0	251	US-11-054-515-1758	Sequence 1758, App
84	27	90.0	251	US-11-054-515-1763	Sequence 1763, App
85	27	90.0	251	US-11-054-515-1769	Sequence 1769, App
86	27	90.0	251	US-11-054-515-1774	Sequence 1774, App
87	27	90.0	251	US-11-054-515-1775	Sequence 1775, App
88	27	90.0	251	US-11-054-515-1783	Sequence 1783, App
89	27	90.0	251	US-11-054-515-1792	Sequence 1792, App
90	27	90.0	251	US-11-054-515-1793	Sequence 1793, App
91	27	90.0	251	US-11-054-515-1795	Sequence 1795, App
92	27	90.0	251	US-11-054-515-1798	Sequence 1798, App
93	27	90.0	251	US-11-054-515-1800	Sequence 1800, App
94	27	90.0	251	US-11-054-515-1801	Sequence 1801, App
95	27	90.0	251	US-11-054-515-1803	Sequence 1803, App
96	27	90.0	251	US-11-054-515-1805	Sequence 1805, App
97	27	90.0	251	US-11-054-515-1808	Sequence 1808, App
98	27	90.0	251	US-11-054-515-1811	Sequence 1811, App

99 27 90.0 251 7 US-11-054-515-1822
100 27 90.0 251 7 US-11-054-515-1824

ALIGNMENTS

RESULT 1

US-11-054-515-1307
; Sequence 1307, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1307
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1307

Query Match Best Local Similarity 90.0%; Score 27; DB 7; Length 247;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
:||||
Db 30 KYTMH 34

RESULT 2

US-11-054-515-877
; Sequence 877, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817

Sequence 1822, Ap
Sequence 1824, Ap

; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 877
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-877

Query Match Best Local Similarity 90.0%; Score 27; DB 7; Length 248;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
:||||
Db 31 KYTMH 35

RESULT 3

US-11-054-515-953
; Sequence 953, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 953
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-953

Query Match Best Local Similarity 90.0%; Score 27; DB 7; Length 248;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
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Db 31 KYTMH 35

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RESULT 4
US-11-054-515-965
; Sequence 965, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 965
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-965

Query Match      90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 KYTMH 35

RESULT 5
US-11-054-515-980
; Sequence 980, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 984
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-984
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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 980
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-980

Query Match      90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 KYTMH 35

RESULT 6
US-11-054-515-984
; Sequence 984, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 984
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-984

Query Match      90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
Db      31 KYTMH 35

RESULT 7
US-11-054-515-987
; Sequence 987, Application US/11054515
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; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1293
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1293
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Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 RYTMH 5
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Db      31 KYTMH 35
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RESULT 11
US-11-054-515-1306
; Sequence 1306, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1306
; LENGTH: 248
```

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1306
```

```

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 RYTMH 5
       :||||
Db      31 KYTMH 35
```

```

RESULT 12
US-11-054-515-1417
; Sequence 1417, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1417
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1417

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 RYTMH 5
       :||||
Db      31 KYTMH 35
```

```

RESULT 13
US-11-054-515-1588
; Sequence 1588, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
```

```
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1588
/ TYPE: PRT
/ LENGTH: 248
/ ORGANISM: Homo sapiens
US-11-054-515-1588

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
       :||||
Db      31 KYTMH 35

RESULT 14
US-11-054-515-1609
/ Sequence 1609, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1609
/ TYPE: PRT
/ LENGTH: 248
/ ORGANISM: Homo sapiens
US-11-054-515-1609

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
       :||||
Db      31 KYTMH 35

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
       :||||
Db      31 KYTMH 35

RESULT 15
US-11-054-515-1622
/ Sequence 1622, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1622
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1622

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RYTMH 5
       :||||
Db      31 KYTMH 35

RESULT 16
US-11-054-515-1623
/ Sequence 1623, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
```


;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1623
;; LENGTH: 248
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1623

Query Match 90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
:||||
Db 31 KYTMH 35

RESULT 17
US-11-054-515-1624
;; Sequence 1624, Application US/11054515
;; Publication No. US2005025532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1624
;; LENGTH: 248
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1624

Query Match 90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 RYTMH 5
:||||

Db 31 KYTMH 35

RESULT 18
US-11-054-515-1643
;; Sequence 1643, Application US/11054515
;; Publication No. US2005025532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1643
;; LENGTH: 248
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1643

Query Match 90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
:||||
Db 31 KYTMH 35

RESULT 19
US-11-054-515-1657
;; Sequence 1657, Application US/11054515
;; Publication No. US2005025532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499

;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1657
;; LENGTH: 248
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1657

Query Match 90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 :||||
Db 31 KYTMH 35

RESULT 20
US-11-054-515-1660
; Sequence 1660, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1660
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1660

Query Match 90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 :||||
Db 31 KYTMH 35

RESULT 21
US-11-054-515-1667

;; Sequence 1667, Application US/11054515
;; Publication No. US20050255532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1667
;; LENGTH: 248
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1667

Query Match 90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 :||||
Db 31 KYTMH 35

RESULT 22
US-11-054-515-1668
; Sequence 1668, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1668
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1668

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       :||||
Db      31 KYTMH 35

RESULT 23
US-11-054-515-1670
; Sequence 1670, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1670
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1670

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       :||||
Db      31 KYTMH 35

RESULT 24
US-11-054-515-1679
; Sequence 1679, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

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; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1681

Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       :||||
Db      31 KYTMH 35

RESULT 25
US-11-054-515-1681
; Sequence 1681, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1681
```

LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1681

Query Match
Best Local Similarity 90.0%; Score 27; DB 7; Length 248;
Best Local 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
: ||||
Db 31 KYTMH 35

RESULT 26
US-11-054-515-1755
Sequence 1755, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1755
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1755

Query Match
Best Local Similarity 90.0%; Score 27; DB 7; Length 248;
Best Local 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
: ||||
Db 31 KYTMH 35

RESULT 27
US-11-054-515-1765
Sequence 1765, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1765
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1765

Query Match
Best Local Similarity 90.0%; Score 27; DB 7; Length 248;
Best Local 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
: ||||
Db 31 KYTMH 35

RESULT 28
US-11-054-515-1823
Sequence 1823, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE REFERENCE: PF523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1823
LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1823

```
Query Match          90.0%; Score 27; DB 7; Length 248;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       : |||
Db      31 KYTMH 35

RESULT 29
US-11-054-515-859
; Sequence 859, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 859
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-859

Query Match          90.0%; Score 27; DB 7; Length 250;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       : |||
Db      31 KYTMH 35

RESULT 30
US-11-054-515-3247
; Sequence 3247, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR APPLICATION NUMBER: 60/331,469
```

```
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3247
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3247

Query Match          90.0%; Score 27; DB 7; Length 250;
Best Local Similarity 80.0%; Pred. No. 10;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       : |||
Db      31 KYTMH 35

RESULT 31
US-11-054-515-845
; Sequence 845, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 845
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-845

Query Match          90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
```

Db 31 KYTMH 35

RESULT 32

US-11-054-515-852
; Sequence 852, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT FILING DATE: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 852
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-852

Query Match 90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
:||||
Db 31 KYTMH 35

RESULT 33

US-11-054-515-853
; Sequence 853, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT FILING DATE: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 853
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-853

Query Match 90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
:||||
Db 31 KYTMH 35

RESULT 34

US-11-054-515-875
; Sequence 875, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT FILING DATE: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 875
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-875

Query Match 90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
:||||
Db 31 KYTMH 35

RESULT 35

```
US-11-054-515-879
; Sequence 879, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 879
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-879

Query Match          90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       : ||||
Db      31 KYTMH 35

RESULT 36
US-11-054-515-884
; Sequence 884, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 886
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-886
```

```
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 884
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-884

Query Match          90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       : ||||
Db      31 KYTMH 35

RESULT 37
US-11-054-515-886
; Sequence 886, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 886
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-886

Query Match          90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
       : ||||
Db      31 KYTMH 35

RESULT 38
US-11-054-515-887
; Sequence 887, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 887
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-887

Query Match      90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RYTMH 5
       :||||
Db       31 KYTMH 35
```

```
RESULT 39
US-11-054-515-940
; Sequence 940, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
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; SEQ ID NO 940
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-940
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Query Match      90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RYTMH 5
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Db       31 KYTMH 35
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RESULT 40
US-11-054-515-944
; Sequence 944, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 944
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-944
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Query Match      90.0%; Score 27; DB 7; Length 251;
Best Local Similarity 80.0%; Pred. No. 11;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RYTMH 5
       :||||
Db       31 KYTMH 35
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Search completed: December 14, 2005, 07:38:14
Job time : 1.55172 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 14, 2005, 07:17:38 ; Search time 5.43103 Seconds
(without alignments)
88.581 Million cell updates/sec

Title: US-10-720-323-1

Perfect score: 30
Sequence: 1 RYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	96	2	SI1610
2	27	90.0	61	2	C81896
3	27	90.0	195	2	G83629
4	27	90.0	205	2	A82789
5	27	90.0	275	2	C69808
6	27	90.0	292	2	H89921
7	27	90.0	393	2	B71857
8	27	90.0	398	2	C71857
9	27	90.0	423	2	T29549
10	27	90.0	431	2	A64658
11	27	90.0	541	2	S46794
12	27	90.0	613	2	T52465
13	27	90.0	661	2	A55877
14	27	90.0	792	2	AB0704
15	27	90.0	792	2	B85778
16	27	90.0	792	2	A90930
17	27	90.0	792	2	S20554
18	27	90.0	889	2	JC6015
19	27	90.0	907	2	F96617
20	27	90.0	1002	2	T09438
21	27	90.0	1013	2	B82276
22	27	90.0	1044	2	B72338
23	27	90.0	1273	2	T42405
24	27	90.0	1568	2	T41013
25	27	90.0	1273	2	T17428
26	27	86.7	94	2	B82847
27	26	86.7	119	1	GHUN1
28	26	86.7	139	1	RKML5
29	26	86.7	204	2	T51012

30	26	86.7	243	2	A63251
31	26	86.7	281	2	C72712
32	26	86.7	304	2	F72378
33	26	86.7	316	2	S35516
34	26	86.7	319	2	S44235
35	26	86.7	320	2	E71696
36	26	86.7	321	2	G98288
37	26	86.7	326	2	AC2995
38	26	86.7	337	2	D87354
39	26	86.7	403	2	H98327
40	26	86.7	453	2	AE2955
41	26	86.7	467	2	B82567
42	26	86.7	484	2	SE0050
43	26	86.7	536	2	C96652
44	26	86.7	564	2	T18776
45	26	86.7	567	2	S43415
46	26	86.7	657	2	A46128
47	26	86.7	657	2	A36087
48	26	86.7	816	2	T21713
49	26	86.7	889	2	A44154
50	26	86.7	889	2	AB0790
51	26	86.7	898	2	B84471
52	26	86.7	907	2	T04820
53	26	86.7	956	2	A89153
54	26	86.7	1200	2	T43148
55	25	83.3	95	2	G90774
56	25	83.3	96	2	S17621
57	25	83.3	96	2	S17230
58	25	83.3	96	2	S17620
59	25	83.3	98	2	S26929
60	25	83.3	102	2	S26471
61	25	83.3	102	2	S53076
62	25	83.3	111	2	PH0990
63	25	83.3	113	2	E33936
64	25	83.3	114	2	S20707
65	25	83.3	120	2	S44111
66	25	83.3	128	2	C37267
67	25	83.3	128	2	A37267
68	25	83.3	128	2	I37267
69	25	83.3	136	2	D64764
70	25	83.3	138	2	TT0011
71	25	83.3	151	2	PL0011
72	25	83.3	162	2	T49484
73	25	83.3	178	2	C75059
74	25	83.3	178	2	G02272
75	25	83.3	193	2	T50693
76	25	83.3	217	2	T33890
77	25	83.3	240	2	JB0011
78	25	83.3	277	2	S71222
79	25	83.3	296	1	S55795
80	25	83.3	297	2	F4206
81	25	83.3	299	1	S68863
82	25	83.3	301	2	D84143
83	25	83.3	315	2	T32059
84	25	83.3	318	2	G70131
85	25	83.3	321	2	T52537
86	25	83.3	323	1	S45455
87	25	83.3	323	2	T38739
88	25	83.3	324	2	F75208
89	25	83.3	324	2	F71243
90	25	83.3	328	1	E54392
91	25	83.3	332	2	JC1239
92	25	83.3	347	2	T37995
93	25	83.3	348	2	T66447
94	25	83.3	356	2	T19792
95	25	83.3	361	2	S74789
96	25	83.3	389	2	T04390
97	25	83.3	391	2	A42973
98	25	83.3	429	2	D64414
99	25	83.3	441	1	QRHUT1
100	25	83.3	453	2	A95212

conserved hypotnet
probable methionin
conserved hypotnet
type II site-speci
amidinotransferase
rare lipoprotein A
hypothetical prote
conserved hypotnet
conserved hypotnet
enantiomer-selecti
glutamyl-rRNA amid
Gunc protein XF236
vacuolar processin
protein F23N19.7 l
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hypothetical prote
probable two-compo
cytoplasmic aconit
aconitate hydratase
protein C24B5.3 (l
probable protein-t
hypothetical prote
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Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V-D
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
hypothetical prote
thyrotropin beta c
Ig heavy chain pre
hypothetical prote
hypothetical prote
heat shock protein
interferon - chick
hypothetical prote
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xyloglucan endo-1,
arginase (EC 3.5.3
lipopolysaccharide
arginase (EC 3.5.3
arginase BH3948 (l
hypothetical prote
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arginase (EC 3.5.3
arginase (EC 3.5.3
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translational initia
probable translati
nup protein - Ent
adenosine receptor
probable fatty aci
hypothetical prote
hypothetical prote
NBS-LRR type resis
serum protein MSB5
ribonuclease II fa
microtubule-associ
anthranilate synth

ALIGNMENTS

RESULT 1

S17610

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997

C/Accession: S17610

R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.

Nature 352, 624-628, 1991

A>Title: Making antibody fragments using phage display libraries.

A/Reference number: S17230; MUID:91326098; PMID:1907718

A/Accession: S17610

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-96 <CLAs>

A/Cross-references: UNIPARC:UPI0000176E7D

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/8-91/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 30; DB 2; Length 96;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 24 RYTMH 28

RESULT 2

C81896

hypothetical protein NMA1281 [imported] - Neisseria meningitidis (strain Z2491 serogroup C/Species: Neisseria meningitidis

C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: C81896

R:Parikh, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Church, C.; Klee, S.R.; Morel

Nature 404, 502-506, 2000

A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: C81896

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-61 <PAR>

A/Cross-references: UNIPROT:Q9JUH8; UNIPARC:UPI00000C4B6B; GB:AL162755; GB:AL157959; NID

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: NMA1280; NMA1281

Query Match

Best Local Similarity 90.0%; Score 27; DB 2; Length 61;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 44 RYTMH 48

RESULT 3

G83629

hypothetical protein PA0118 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: G83629

R:Stover, C.K.; Plam, X.Q.; Ewain, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: G83629

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-195 <STO>

A/Cross-references: UNIPROT:Q9J714; UNIPARC:UPI0000C4F47; GB:AE004450; GB:AE004091; NID:

A/Experimental source: strain PA01

C/Genetics:

A/Accession: PA0118

C/Superfamily: HCCA isomerase/mitochondrial glutathione S-transferase

Query Match

Best Local Similarity 90.0%; Score 27; DB 2; Length 195;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 61 RYTMH 65

RESULT 4

A82789

hypothetical protein XF0583 [imported] - Xylella fastidiosa (strain 9a5c)

C/Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C/Accession: A82789

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A/Reference number: A82515; MUID:20365717; PMID:10910347

A/Note: for a complete list of authors see reference number A59328 below

A/Accession: A82789

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-205 <SIM>

A/Cross-references: UNIPROT:Q9PFS4; UNIPARC:UPI0000C246D; GB:AE003904; GB:AE003849; NID:

A/Experimental source: strain 9a5c

R:Simpon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Brienes, M.R.S.; Bueno, W.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carier, H

as-Velho, E.; Docena, C.; El-Doroty, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramé, E.E.; Laigre

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A/Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J.; de M., de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak

A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvair

M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zé

A/Reference number: A59328

A/Contents: annotation

C/Genetics:

A/Gene: XF0583

Query Match

Best Local Similarity 90.0%; Score 27; DB 2; Length 205;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 34 RYTMH 38

RESULT 5

C69808

transporter homolog yfkh - Bacillus subtilis

C/Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: C69808

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertier

C.; Bron, S.; Brouillet, S.; Brunsch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi

A.; Ehrlich, S.D.; Emerson, P.T.; Eutian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizi, A.; Gallier

tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, V.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Serot, Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tempstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K. A.; Authors: Yoshikawa, H.F.; Zumbstein, H.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A6580; MUID:98044033; PMID:9384377
A:Accession: C69808
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KUN>
A:Cross-references: UNIPROT:Q34437; UNIPARC:UP100000600AE; GB:Z99108; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: yfkH

Query Match
Best Local Similarity 90.0%; Score 27; DB 2; Length 275;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYTMH 5
|||:
Db 10 RYTLH 14

RESULT 6
H8921
hypothetical protein SA1273 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89921
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, ma, A.; Mizutani-Ut, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hirataesu, K.
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89756; MUID:21311952; PMID:11418146
A:Accession: H89921
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292 <KUN>
A:Cross-references: UNIPROT:Q99U48; UNIPARC:UP100000CACOA; GB:BA000018; PID:g13701238; F
C:Genetics:
A:Experimental source: strain N315
A:Gene: SA1273

Query Match
Best Local Similarity 90.0%; Score 27; DB 2; Length 292;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYTMH 5
|||:
Db 162 RYTLH 166

RESULT 7
B71857
probable lipopolysaccharide biosynthesis protein - *Helicobacter pylori* (strain J99)
C:Species: *Helicobacter pylori*
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: B71857
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: B71857
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-393 <ARN>
A:Cross-references: UNIPROT:Q9ZKA8; UNIPARC:UP10000047C3D; GB:AE001531; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1031

Query Match
Best Local Similarity 90.0%; Score 27; DB 2; Length 393;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYTMH 5
|||:
Db 49 RYTLH 53

RESULT 8
C71857
probable lipopolysaccharide biosynthesis protein - *Helicobacter pylori* (strain J99)
C:Species: *Helicobacter pylori*
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: C71857
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: C71857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-398 <ARN>
A:Cross-references: UNIPROT:Q9ZKA7; UNIPARC:UP100000D36DE; GB:AE001531; GB:AE001439; NID
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1032

Query Match
Best Local Similarity 90.0%; Score 27; DB 2; Length 398;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYTMH 5
|||:
Db 49 RYTLH 53

RESULT 9
T29549
hypothetical protein ZK377.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T29549
R:Nhan, M.; Hawkins, J.
A:Submitted to the EMBL Data Library, February 1997
A:Description: The sequence of *C. elegans* cosmid ZK377.
A:Reference number: Z20639
A:Accession: T29549
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-423 <NHA>
A:Cross-references: UNIPARC:UP1000017BD05; EMBL:U88183; PIDN:AA852658.1; GSPDB:GN00028;
A:Experimental source: strain Bristol N2; clone ZK377
C:Genetics:
A:Gene: CESP:ZK377.3
A:Map position: X
A:Introns: 24/1; 142/3; 229/3; 284/2; 408/3

Query Match
Best Local Similarity 90.0%; Score 27; DB 2; Length 423;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RYTMH 5
|||:
Db 180 RYTLH 184

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RESULT 10
A64658
LPS biosynthesis protein - Helicobacter pylori (strain 26695)
C/Species: Helicobacter pylori
C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C/Accession: A64658
R/Tomb, J.F.; White, O.; Kierlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, R.; Dodson, R.; Khalaf, H.G.; Giodok, A.; McKen-
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.
Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A/Reference number: A64520; PMID:97394467; PMID:9252185
A/Accession: A64658
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-431 <TOM>
A/Cross-references: UNIPROT:O25733; UNIPARC:UPI0000047C3E; GB:A5000617; GB:A5000511; NID:

Query Match          90.0%; Score 27; DB 2; Length 431;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 49 RYTLH 53

RESULT 11
S46794
Hypothetical protein YHR006w - Yeast (Saccharomyces cerevisiae)
C/Species: Saccharomyces cerevisiae
C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Oct-2004
C/Accession: S46794
R/Favell, T.
Submitted to the EMBL Data Library, June 1994
A/Description: The sequence of S. cerevisiae cosmid 9780.
A/Reference number: S46797
A/Accession: S46794
A/Molecule type: DNA
A/Residues: 1-541 <FAV>
A/Cross-references: UNIPROT:P36704; UNIPARC:UPI000013B236; EMBL:U10555; NID:G500813; PII:
C/Genetics:
A/Gene: SGD:SRP2
A/Cross-references: SGD:S0001048; MIPS:YHR006w
A/Map position: 8R
C/Superfamily: zinc finger protein
C/Keywords: nucleus

Query Match          90.0%; Score 27; DB 2; Length 541;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 441 RYTLH 445

RESULT 12
T52465
Hypothetical protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Aug-2001
C/Accession: T52465
R/Kato, A.; Suzuki, M.; Kuwahara, A.; Ooe, H.; Higano-Inaba, K.; Komeda, Y.
Gene 239, 309-316, 1999
A/Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic reg
A/Reference number: Z25171
A/Accession: T52465
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
```

```
A/Residues: 1-613 <KAT>
A/Cross-references: UNIPARC:UPI00000A700A; EMBL:AB008016; PIDN:BA08265.1
A/Experimental source: cultivar Columbia
C/Genetics:
A/Map position: 1
C/Superfamily: disease resistance protein RPS2; leucine-rich alpha-2-glycoprotein repeat

Query Match          90.0%; Score 27; DB 2; Length 613;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 377 RYTLH 381

RESULT 13
A55877
Tumor necrosis factor type 1 receptor associated protein TRAP-1 - human
C/Species: Homo sapiens (man)
C/Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 05-Nov-1999
C/Accession: A55877
R/Song, H.Y.; Dunbar, J.D.; Zhang, Y.X.; Guo, D.; Donner, D.B.
J. Biol. Chem. 270, 3574-3581, 1995
A/Title: Identification of a protein with homology to hsp90 that binds the type 1 tumor r
A/Reference number: A55877; PMID:95181307; PMID:7876093
A/Accession: A55877
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-661 <SON>
A/Cross-references: UNIPARC:UPI000016A0FC; GB:U12595; NID:9687236; PIDN:AA087704.1; PID:
C/Superfamily: heat shock protein 90

Query Match          90.0%; Score 27; DB 2; Length 661;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 311 RYTLH 315

RESULT 14
AB0704
pyruvate, water dikinase (EC 2.7.9.2) - Salmonella enterica subsp. enterica serovar Typh
C/Species: Salmonella enterica subsp. enterica serovar Typh
A/Note: this species has also been called Salmonella typh
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Nov-2002
C/Accession: AB0704
R/ParKhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 648-652, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmoneilla enterica serov
A/Reference number: AB0502; PMID:21534947; PMID:11677608
A/Accession: AB0704
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-792 <PAR>
A/Cross-references: UNIPARC:UPI0000059DD6; GB:AL513382; PIDN:CAD02003.1; PID:G16502841; C
C/Genetics:
A/Gene: ppsA
C/Superfamily: Baccherichia coli pyruvate, water dikinase; phosphotransferase system enzyme
C/Keywords: transferase

Query Match          90.0%; Score 27; DB 2; Length 792;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 349 RYTLH 353
```

RESULT 15
E85778
phosphoenolpyruvate synthase [imported] - Escherichia coli (strain O157:H7, substrain ED
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: E85778
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Llm, A.; Dimalanta, E.; Potlamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A65480; MUID:21074935; PMID:11206551
A:Accession: E85778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-792 <STO>
A:Cross-references: UNIPROT:O8XEC4, UNIPARC:UPI00000D0268, GB:AE005174, NID:g12515710, F
A:Experimental source: strain O157:H7, substrain ED933
C:Genetics:
A:Gene: ppsa
C:Superfamily: Escherichia coli pyruvate,water dikinase; phosphotransferase system enzym
Query Match 90.0%; Score 27; DB 2; Length 792;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RYTMH 5
Db 349 RYTLH 353

RESULT 16
A90930
phosphoenolpyruvate synthase [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A90930
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A:Reference number: A96629; MUID:21156231; PMID:11258796
A:Accession: A90930
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-792 <HAV>
A:Cross-references: UNIPROT:Q8XEC4, UNIPARC:UPI0000165476, GB:BA000007, PIDN:BA035832.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC62409
C:Superfamily: Escherichia coli pyruvate,water dikinase; phosphotransferase system enzym
Query Match 90.0%; Score 27; DB 2; Length 792;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RYTMH 5
Db 349 RYTLH 353

RESULT 17
S20554
pyruvate, water dikinase (EC 2.7.9.2) ppsa [validated] - Escherichia coli (strain K-12)
N:Alternate names: phosphoenolpyruvate synthase
C:Species: Escherichia coli
A:Variety: strain K12
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: S20554; F64928; S14818
R:Nierbach, M.; Kreuzaler, F.; Geerse, R.H.; Postma, P.W.; Hirsch, H.J.
Mol. Gen. Genet. 231, 332-336, 1992
A:Title: Cloning and nucleotide sequence of the Escherichia coli K-12 ppsa gene, encodin

A:Reference number: S20554; MUID:92140374; PMID:1310524
A:Accession: S20554
A:Molecule type: DNA
A:Residues: 1-792 <NIR>
A:Cross-references: UNIPROT:P23338, UNIPARC:UPI00001680C9, EMBL:X59381, NID:g42480; PIDN
A:Experimental source: strain K-12, substrain DH1
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64928
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-792 <BLAT>
A:Cross-references: UNIPARC:UPI00001680C9; GB:AE00265; GB:U00096; NID:g2367122; PIDN:AA
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ppsa
C:Function:
A:Description: EC 2.7.9.2 [validated, MUID:66071519]; catalyzes the ATP-dependent conver
A:Pathway: gluconeogenesis
C:Superfamily: Escherichia coli pyruvate,water dikinase; phosphotransferase system enzym
C:Keywords: phosphoprotein, transferase
Query Match 90.0%; Score 27; DB 2; Length 792;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RYTMH 5
Db 349 RYTLH 353

RESULT 18
JC6015
chitin synthase (EC 2.4.1.16) C - Aspergillus fumigatus
N:Alternate names: chitin-UDP N-acetylglucosaminyltransferase C; ChSC protein
C:Species: Aspergillus fumigatus
C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC6015
R:Medlao, E.; Aufauvre-Brown, A.; Gow, N.A.R.; Holden, D.W.
Mol. Microbiol. 20, 667-679, 1996
A:Title: The Aspergillus fumigatus chsc and chsg genes encode class III chitin synthases
A:Reference number: JC6015; MUID:96347138; PMID:8736545
A:Accession: JC6015
A:Molecule type: mRNA
A:Residues: 1-889 <MBL>
A:Cross-references: UNIPROT:Q92197, UNIPARC:UPI000012794E, EMBL:X94245; NID:g1197185; PI
A:Experimental source: strain 237
C:Comment: This enzyme belongs to class III zymogen-type enzymes, it is a target for ant
C:Genetics:
A:Gene: chsc
A:Introns: 28/3; 169/2; 289/3; 633/2; 844/3
C:Function:
A:Description: catalyzes the alpha-1,4-glycosylation of chitin by UDP-N-acetyl-D-glucosa
C:Superfamily: chitin synthase chsa
C:Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; zymogen
F1524,845/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 90.0%; Score 27; DB 2; Length 889;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 RYTMH 5
Db 69 RYTLH 73

RESULT 19
F96617
probable disease resistance protein P9K23.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C/Accession: F96617
R/Theologias, A.; Ecker, J.R.; Palm, C.J.; Federici, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: F96617
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-907 <STO>
A/Cross-references: UNIPARC:UPI00000465D1; GB:AE005173; NID:g11034963; PIDN:AA627118.1;
C/Genetics:
A/Gene: F9K23.8
A/Map position: 1

Query Match 90.0%; Score 27; DB 2; Length 907;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 377 RYTMH 381

RESULT 20
ToxR-activated lipoprotein - *Vibrio cholerae*
109438
N/Alternate names: ToxR-activated gene A protein
C/Species: *Vibrio cholerae*
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R/Accession: T09438; A39108
R/Karacali, D.K.R.; Johnson, J.A.; Bailey, C.C.; Boedecker, E.C.; Kaper, J.B.; Reeves, P.
Proc. Natl. Acad. Sci. U.S.A. 95, 3134-3139, 1998
A/Title: A *Vibrio cholerae* pathogenicity island associated with epidemic and pandemic st
A/Reference number: Z16672; MUID:98165509; PMID:9501228
A/Accession: T09438
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1002 <KAR>
A/Cross-references: UNIPROT:P24019; UNIPARC:UPI0000000A87; EMBL:AF034434; NID:g3004923;
A/Experimental source: strain N16561
R/Parrot, C.; Takman, E.; Mekalanos, J.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 1641-1645, 1991
A/Title: ToxR regulates the production of lipoproteins and the expression of serum resist
A/Reference number: A39108; MUID:91156664; PMID:2000374
A/Accession: A39108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-25 <PAR>
A/Cross-references: UNIPARC:UPI0000179FC6; GB:M60658
C/Genetics:
A/Gene: tagA
A/Note: part of the pathogenicity island (VPI); associated with epidemic and pandemic st
C/Keywords: lipid binding; lipoprotein

Query Match 90.0%; Score 27; DB 2; Length 1002;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 514 RYTMH 518

RESULT 21
,B82276

ToxR-activated gene A protein VC0820 [imported] - *Vibrio cholerae* (strain N16961 serogro
C/Species: *Vibrio cholerae*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
R/Accession: B82276
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the *cholera* pathogen *Vibrio cholerae*.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: B82276
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1013 <HEI>
A/Cross-references: UNIPARC:UPI0000164866; GB:AE004167; GB:AE003852; NID:g9655268; PIDN:
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0820
A/Map position: 1

Query Match 90.0%; Score 27; DB 2; Length 1013;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 525 RYTMH 529

RESULT 22
galactosyltransferase-related protein - *Thermotoga maritima* (strain MSB8)
B72338
C/Species: *Thermotoga maritima*
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R/Accession: B72338
R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.W.; Stewart, A.W.; C Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A/Reference number: A72200; MUID:99287316; PMID:10360571
A/Accession: B72338
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1044 <ARN>
A/Cross-references: UNIPROT:Q9WZU5; UNIPARC:UPI000000399A; GB:AE001745; GB:AE000512; NID
A/Experimental source: strain MSB8
C/Genetics:
A/Gene: TW0756

Query Match 90.0%; Score 27; DB 2; Length 1044;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 318 RYTMH 322

RESULT 23
T42405
sax-3 protein - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R/Accession: T42405
R/Zallen, J.A.; Yi, B.A.; Bargmann, C.I.
Cell 92, 217-227, 1998
A/Title: The conserved immunoglobulin superfamily member SAX-3/Robo directs multiple app
A/Reference number: Z22160; MUID:98117250; PMID:9458046
A/Accession: T42405
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1273 <ZAL>

A:Cross-references: UNIPROT:O44928; UNIPARC:UPI0000080AAB; EMBL:AF041053; NID:G2804779;
C:Genetics:
A>Note: sax-3
C:Function:
A:Description: sax-3 function is required at the time of axon guidance

Query Match 90.0%; Score 27; DB 2; Length 1273;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
|||:|
Db 181 RYTMH 185

RESULT 24
T41013
hypothetical protein SPC14G10.02 [imported] - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: hypothetical protein SPBC18B5.13
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41013; T41206
R:Purnelle, B.; Goffeau, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: 221964
A:Accession: T41013
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1568 <PUR>
A:Cross-references: UNIPROT:O74415; UNIPARC:UPI00000698B9; EMBL:AL031518; PIDN:CAA20655.
A:Experimental source: strain 972h-, cosmid c14G10
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
submitted to the EMBL Data Library, July 1999
A:Reference number: 221978
A:Accession: T41206
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-364 <WOO>
A:Cross-references: UNIPARC:UPI000006829D; EMBL:AL109736; PIDN:CAB52160.1; GSPDB:GN00068
C:Genetics:
A:Gene: SPDB:SPCC14G10.02; SPDB:SPBC18B5.13
A:Map position: 3
A:Introns: 11/1

Query Match 90.0%; Score 27; DB 2; Length 1568;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
|||:|
Db 1233 RYTMH 1237

RESULT 25
T117428
FKS06 polyketide synthase - Streptomyces sp. (strain MA6548)
C:Species: Streptomyces sp.
A:Variety: strain MA6548
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C:Accession: T117428
R:Motamedi, H.; Shafiee, A.
Eur. J. Biochem. 256, 528-534, 1998
A:Title: The biosynthetic gene cluster for the macrolactone ring of the immunosuppressant
A:Reference number: Z18779; MUID:98451508; PMID:9780228
A:Accession: T117428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7576 <MOT>
A:Cross-references: UNIPROT:O926A4; UNIPARC:UPI0000110203; EMBL:AF082100; NID:G3798623;
C:Genetics:
A:Experimental source: strain MA6548
A:Gene: fksB

C:Function:
A:Description: involved in synthesis of the backbone of the immunosuppressant FK506 poly
A:Keywords: carrier protein
F:545-500/Domain: acetate-CoA ligase homology <ACLI>
F:11095-1166/Domain: acyl carrier protein homology <ACPI>
F:11204-1599/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F:1682-1953/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>
F:2680-2751/Domain: acyl carrier protein homology <ACP2>
F:2804-3198/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F:3295-3569/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2>
F:4320-4391/Domain: acyl carrier protein homology <ACP3>
F:4435-4830/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
F:5903-5974/Domain: acyl carrier protein homology <ACP4>
F:6018-6412/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>
F:6513-6781/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT3>
F:7450-7521/Domain: acyl carrier protein homology <ACP5>

Query Match 90.0%; Score 27; DB 2; Length 7576;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
|||:|
Db 7056 RYTMH 7060

RESULT 26
B82847
hypothetical protein XF0101 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: B82847
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: B82847
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-94 <SLM>
A:Cross-references: UNIPROT:Q9PH45; UNIPARC:UPI00000C22D3; GB:AE003864; GB:AE003849; NID
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
de-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF0101

Query Match 86.7%; Score 26; DB 2; Length 94;
Best Local Similarity 80.0%; Pred. No. 36;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RYTMH 5
|||:|
Db 43 RYTMH 47

RESULT 27
GIH001
Ig heavy chain V-III region (Nie) - human
C:Species: Homo sapiens (man)

C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C/Accession: A91668; A02053
R/Ponstein1, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
igen Primerstruktur.
A/Reference number: A91668; MUID:77070269; PMID:826475
A/Accession: A91668
A/Molecule type: protein
A/Residues: 1-119 <PCN>
C/Genetics:
A/Cross-references: UNIPROT:P01770; UNIPARC:UPI000012CEFA
A/Note: the sequence of the gamma-1 C region of this chain is also given
R/Dexer, U.; Schwarz, J.; Reiche, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
endowmde cleavage products, and the disulfide bridges.
A/Reference number: A91667; MUID:77070267; PMID:1002129
A/Contents: annotation; disulfide bond
C/Comment: This chain was isolated from an IgG1 myeloma protein.
C/Genetics:
A/Gene: GDB:IGHV@
A/Cross-references: GDB:128528; OMIM:147070
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F/15-98/Domain: immunoglobulin homology <IMM>
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/22-96/Disulfide bonds: #status experimental

Query Match 86.7%; Score 26; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 31 RYTH 35

RESULT 28
RKMUS
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain - golden alga (Olisthodiscus
C/Species: chloroplast Olisthodiscus luteus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: A32940
R/Boczar, B.A.; Delaney, T.P.; Catolico, R.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 4996-4999, 1989
A/Title: Gene for the ribulose-1,5-bisphosphate carboxylase small subunit protein of the
A/Reference number: A32940; MUID:69296930; PMID:2740337
A/Accession: A32940
A/Molecule type: DNA
A/Residues: 1-139 <BOC>
A/Cross-references: UNIPROT:P14961; UNIPARC:UPI0000133411; GB:M24288; NID:G342811; PIDN:
C/Genetics:
A/Gene: rbcS
A/Genome: chloroplast
C/Superfamily: ribulose-bisphosphate carboxylase small chain
C/Keywords: Calvin cycle; carbon dioxide fixation; carbon-carbon lyase; carbon-oxygen ly

Query Match 86.7%; Score 26; DB 1; Length 139;
Best Local Similarity 80.0%; Pred. No. 54;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 122 RYTH 126

RESULT 29
TS1012
hypothetical protein B7J19.110 [imported] - Neurospora crassa
C/Species: Neurospora crassa
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
C/Accession: TS1012

R/Schulte, U.; Aign, V.; Hehseisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, July 2000
A/Reference number: Z25286
A/Accession: TS1012
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-204 <SCH>
A/Cross-references: UNIPARC:UPI0000179F67; EMBL:AL389899; GSPDB:GN00116; NCSP:B7J19.110
A/Experimental source: BAC clone B7J19; strain OR7A
C/Genetics:
A/Gene: NCSP:B7J19.110
A/Map position: 6
A/Intons: 31/1; 66/3; 170/3
C/Superfamily: Neurospora crassa hypothetical protein B7J19.110

Query Match 86.7%; Score 26; DB 2; Length 204;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 161 RYTH 165

RESULT 30
AG3251
conserved hypothetical protein Atu6193 [imported] - Agrobacterium tumefaciens (strain C5f
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AG3251
R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woe, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayav, T.; Levy, R.; Li, M.; McCellie
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, K
ster, B.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AG3251
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-243 <KUR>
A/Cross-references: UNIPROT:Q8U5Y5; UNIPARC:UPI0000027C2; GB:AE008690; PIDN:AL46429.1;
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: Atu6193
A/Genome: plasmid

Query Match 86.7%; Score 26; DB 2; Length 243;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 69 RYTH 73

RESULT 31
C72712
probable methionine aminopeptidase APE114 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: C72712
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Ki
DNA Rec. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: C72712
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-281 <KAW>
A/Cross-references: UNIPROT:Q9YC28; UNIPARC:UPI000005DE00; DDBJ:AP000060; NID:G5104188; I

A:Experimental source: strain K1

C:Genetics:

A:Gene: ABE114

C:Superfamily: Escherichia coli methionyl aminopeptidase

Query Match 86.7%; Score 26; DB 2; Length 281;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 134 RYTMH 138

RESULT 32

F72378 conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: F72378

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A7200; MUID:99287316; PMID:10360571

A:Accession: F72378

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-304 <ABR>

A:Cross-references: UNIPROT:Q9WYQ3; UNIPARC:UPI00000C141D; GB:AE001721; GB:AE000512; NID

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0422

Query Match 86.7%; Score 26; DB 2; Length 304;

Best Local Similarity 80.0%; Pred. No. 1.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 69 RYTMH 73

RESULT 33

S35516

type II site-specific deoxyribonuclease (EC 3.1.21.4) BsuRI - Bacillus subtilis

N:Alternate names: restriction endonuclease BsuRI

C:Species: Bacillus subtilis

C>Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S35516

R:Xu, G.L.; Kapfer, W.; Walter, J.; Trautner, T.A.

Nucleic Acids Res. 20, 6517-6523, 1992

A:Title: BsuRI an isospecific restriction and modification system of PstI: characterization

A:Reference number: S35515; MUID:93126092; PMID:1480472

A:Accession: S35516

A:Molecule type: DNA

A:Residues: 1-116 <XUG>

A:Cross-references: UNIPROT:P33562; UNIPARC:UPI00001367CE; EMBL:L01541; NID:g143053; PID

C:Superfamily: type II site-specific deoxyribonuclease PstI

C:Keywords: hydrolase

Query Match 86.7%; Score 26; DB 2; Length 316;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 81 RYTMH 85

RESULT 34

S44235

amidinotransferase - Streptomyces glaucescens

C:Species: Streptomyces glaucescens

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S44235

R:Mayer, G.; Piepersberg, W.

submitted to the EMBL Data Library, April 1994

A:Reference number: S44224

A:Accession: S44235

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-319 <MAY>

A:Cross-references: UNIPROT:Q54264; UNIPARC:UPI00001360AA; EMBL:X78975; NID:g475241; PID

C:Superfamily: scy110-inosamine-4-phosphate amidinotransferase

Query Match 86.7%; Score 26; DB 2; Length 319;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 184 RYTMH 188

RESULT 35

E71696

rare lipoprotein A precursor (r1pa) RP390 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C:Accession: E71696

R:Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Sticheritz-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: E71696

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-320 <AND>

A:Cross-references: UNIPROT:Q9ZDE1; UNIPARC:UPI000013427F; GB:AJ235271; GB:AJ235269; NID

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: r1pa; RP390

Query Match 86.7%; Score 26; DB 2; Length 320;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5

Db 23 RYTMH 27

RESULT 36

G98288

hypothetical protein AGR_L_2530 [imported] - Agrobacterium tumefaciens (strain C58, Cere

C:Species: Agrobacterium tumefaciens

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: G98288

R:Goodner, B.; Hinkle, G.; Gatung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Mollam, C.; Allinger, W.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:2160851; PMID:11743194

A:Accession: G98288

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-321 <KUR>

A:Cross-references: UNIPROT:Q8UA10; UNIPARC:UPI000016442D; GB:AE007870; PIDN:AAK9833.1;

C:Genetics:

A:Gene: AGR_L_2530

A:Map position: linear chromosome

Query Match 86.7%; Score 26; DB 2; Length 321;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RYTMH 5
|:|:|
Db 86 RYTMH 90

RESULT 37
AC2995
conserved hypothetical protein Atu3565 [imported] - Agrobacterium tumefaciens (strain C58)
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AC2995
R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:21608550; PMID:11743193
A/Accession: AC2995
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-326 <KUR>
A/Cross-references: UNIPROT:Q8UAX4; UNIPARC:UPI0000022257; GB:AE008689; PIDN:AAL44377.1;
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: Atu3565
A/Map position: linear chromosome

Query Match 86.7%; Score 26; DB 2; Length 326;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|:|:|
Db 91 RYTMH 95

RESULT 38
D87354
conserved hypothetical protein CC0847 [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: D87354
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.O.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; PMID:21173698; PMID:11259647
A/Accession: D87354
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-337 <STO>
A/Cross-references: UNIPROT:Q9A9W4; UNIPARC:UPI00000C71BA; GB:AE005673; NID:g13422102; F
C/Genetics:
A/Gene: CC0847

Query Match 86.7%; Score 26; DB 2; Length 337;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|:|:|
Db 263 QYTMH 267

RESULT 39
H98327
enantiomer-selective amidase [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C/Species: Agrobacterium tumefaciens

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: H98327
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Marxiz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A/Reference number: A97359; PMID:21608551; PMID:11743194
A/Accession: H98327
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-403 <KUR>
A/Cross-references: UNIPROT:Q8UAX4; UNIPARC:UPI000016443B; GB:AE007870; PIDN:AAK90146.1;
C/Genetics:
A/Gene: AGR_L_3143
A/Map position: linear chromosome
C/Superfamily: indoleacetamide hydrolase

Query Match 86.7%; Score 26; DB 2; Length 403;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|:|:|
Db 149 RYTMH 153

RESULT 40
AE2955
glutaryl-L-cRNA amidotransferase subunit A gata [imported] - Agrobacterium tumefaciens (str
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AE2955
R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; PMID:21608550; PMID:11743193
A/Accession: AE2955
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-453 <KUR>
A/Cross-references: UNIPROT:Q8UAX4; UNIPARC:UPI0000022126; GB:AE008689; PIDN:AAL44059.1;
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: gata
A/Map position: linear chromosome
C/Superfamily: indoleacetamide hydrolase

Query Match 86.7%; Score 26; DB 2; Length 453;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|:|:|
Db 199 RYTMH 203

Search completed: December 14, 2005, 07:31:49
Job time: 7.43103 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:17:28 ; Search time 26.9828 Seconds
(without alignments)
130.737 Million cell updates/sec

Title: US-10-720-323-1
Perfect score: 30
Sequence: 1 RYTMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	43	Q7RTD7_PLAYO	Q7rtcd7 plasmodium
2	30	100.0	49	Q7RAK6_PLAYO	Q7rak6 plasmodium
3	30	100.0	178	Q7OUY1_GIALA	Q7ouy1 giardia lam
4	30	100.0	187	Q5FQ58_GLUOX	Q5fq58 glucinobact
5	30	100.0	209	Q9B1G0_RHILLO	Q9b1g0 rhizobium l
6	30	100.0	259	Q7FW16_ANOGA	Q7fw16 anophelis g
7	30	100.0	283	Q5E510_VIBF1	Q5e510 vibrio fisc
8	30	100.0	296	Q5PA06_ANAMM	Q5pa06 anaplasma m
9	30	100.0	437	Q7YUPQ_TRYCR	Q7yupq trypanosoma
10	30	100.0	454	Q8NKV4_AC1AM	Q8nkva acidianus a
11	30	100.0	455	Q856Y5_9CAUD	Q856y5 mycobacteri
12	30	100.0	531	Q5LHN9_BACFN	Q5lhn9 bacteroides
13	30	100.0	627	Q74DM9_GEOSL	Q74dm9 geobacter s
14	30	100.0	4825	Q4QD18_LEIMA	Q4qd18 leishmania
15	27	90.0	61	Q9J1U8_NEIMA	Q9j1u8 neisseria m
16	27	90.0	99	Q8GQW5_SERMA	Q8gqws serratia ma
17	27	90.0	110	Q29379_PIG	Q29379 sus scrofa
18	27	90.0	113	Q868H1_LEIME	Q868h1 leishmania
19	27	90.0	116	Q5ZC10_ORYSA	Q5zc10 oryza sativ
20	27	90.0	117	Q868G9_LEIMA	Q868g9 leishmania
21	27	90.0	121	Q521B3_MAGCR	Q521b3 magnaporthe
22	27	90.0	149	Q7SD55_NEUCR	Q7sd55 neurospora
23	27	90.0	165	Q58GM4_9H1V1	Q58gm4 human immun
24	27	90.0	167	Q6LXU7_METMP	Q6lxu7 mechanococ
25	27	90.0	169	Q15418_HUMAN	Q15418 homo sapien
26	27	90.0	182	Q674V7_9WAGN	Q674v7 thotsea sil
27	27	90.0	189	Q6F7A6_ACTAD	Q6f7a6 actinobact
28	27	90.0	195	Q5FR26_GLUOX	Q5fr26 glucinobact
29	27	90.0	195	Q91714_PSEAE	Q91714 pseudomonas
30	27	90.0	198	Q4IQY7_9BURK	Q4iqy7 burkholderi
31	27	90.0	203	Q87B90_XYLFT	Q87b90 xyliella fas

32	27	90.0	205	2	Q6CNC3_KLUUA	Q6cnc3 kluyveromyc
33	27	90.0	205	2	Q9PFS4_XYLFA	Q9pfs4 xyliella fas
34	27	90.0	207	2	Q7XV45_GRIYA	Q7xv45 griffithsia
35	27	90.0	208	2	Q5ZC11_ORYSA	Q5zc11 oryza sativ
36	27	90.0	219	2	Q4UID6_THEAN	Q4uid6 theileria a
37	27	90.0	233	2	Q8G546_BIFLO	Q8g546 bifidobacte
38	27	90.0	241	2	Q6XLY2_9PHCA	Q6xly2 leishmania
39	27	90.0	255	2	Q4N777_TPEPA	Q4n777 theileria p
40	27	90.0	269	2	Q4NVB4_9DELT	Q4nvb4 anaeoromycob
41	27	90.0	275	2	Q34437_BACSU	Q34437 bacillus su
42	27	90.0	289	2	Q53046_9LACO	Q53046 lactobacill
43	27	90.0	292	2	Q6G9C2_STYAS	Q6g9c2 staphylococ
44	27	90.0	292	2	Q6GWM8_STYAR	Q6gwm8 staphylococ
45	27	90.0	292	2	Q5HFX3_STYAC	Q5hfx3 staphylococ
46	27	90.0	292	2	Q7ASL7_STYAN	Q7asl7 staphylococ
47	27	90.0	292	2	Q8NM02_STYAN	Q8nmq2 staphylococ
48	27	90.0	293	2	Q9VU48_STYAM	Q9vu48 staphylococ
49	27	90.0	293	2	Q88BH7_PESBM	Q88bh7 pseudomonas
50	27	90.0	338	2	Q6F1T3_MESFL	Q6f1t3 mesoplasma
51	27	90.0	342	2	Q5ZC12_ORYSA	Q5zc12 oryza sativ
52	27	90.0	343	2	Q4TDD4_TETNG	Q4td4 tetradion n
53	27	90.0	346	2	Q7QWY5_GIALA	Q7qw5 giardia lam
54	27	90.0	348	2	Q5ZYR5_LEGPH	Q5zyr5 legionella
55	27	90.0	363	2	Q8BLQ5_MOUSE	Q8blq5 mus muscullu
56	27	90.0	393	2	Q9ZKA8_HELPJ	Q9zka8 helicobacte
57	27	90.0	395	2	Q4TSV8_9EPHN	Q4tsv8 erythrobacte
58	27	90.0	398	2	Q9ZKA7_HELPJ	Q9zka7 helicobacte
59	27	90.0	408	2	Q83C86_COXBU	Q83c86 coxiella bu
60	27	90.0	413	2	Q6LQ42_PROPR	Q6lq42 photobacter
61	27	90.0	416	2	Q54DR1_DICDI	Q54dr1 dictyosteli
62	27	90.0	419	2	Q842E2_PSESX	Q842e2 pseudomonas
63	27	90.0	423	2	Q4NV93_9DELT	Q4nv93 anaeoromycob
64	27	90.0	423	2	Q4FR20_9GAMW	Q4fr20 psychrobact
65	27	90.0	426	2	Q4UIR2_9BACT	Q4uir2 uncultured
66	27	90.0	429	2	Q8Y0K6_PALSO	Q8y0k6 raietonia s
67	27	90.0	431	2	Q55733_HELPY	Q55733 helicobacte
68	27	90.0	468	1	Y924_DESVH	Q72dk5 deulfovibr
69	27	90.0	474	2	Q7S250_NEUCR	Q7s250 neurospora
70	27	90.0	486	2	Q5FT05_GLUOX	Q5ft05 glucinobact
71	27	90.0	495	2	Q5CAQ4_HUMAN	Q5caq4 homo sapien
72	27	90.0	511	2	Q5FW77_XENTR	Q5fw77 xenopus tro
73	27	90.0	516	2	Q4S644_TETNG	Q4s644 tetradion n
74	27	90.0	519	2	Q52E48_MAGCR	Q52e48 magnaporthe
75	27	90.0	526	2	Q9NE54_LEIMA	Q9ne54 leishmania
76	27	90.0	541	1	SPR2_YEAST	Q8crt9 rat
77	27	90.0	541	2	Q6CR89_YEAST	Q6cr89 saccharomyc
78	27	90.0	549	2	Q7RRY5_NEUCR	Q7rry5 neurospora
79	27	90.0	550	2	Q81K27_BACAN	Q81k27 bacillus an
80	27	90.0	551	2	Q510Y1_ENTHI	Q510y1 entamoeba h
81	27	90.0	561	2	Q7LFX5_HUMAN	Q7lfx5 homo sapien
82	27	90.0	561	2	Q8CHT9_RAT	Q8cht9 rattus norv
83	27	90.0	561	2	Q9D2N6_MOUSE	Q9d2n6 mus muscullu
84	27	90.0	561	2	Q91XQ5_MOUSE	Q91xq5 m b cell ra
85	27	90.0	562	2	Q4WAT9_ASFPU	Q4wat9 aspergillus
86	27	90.0	579	2	Q8N9Z3_HUMAN	Q8n9z3 homo sapien
87	27	90.0	583	2	Q856N6_9CAUD	Q856n6 mycobacteri
88	27	90.0	598	2	Q8LQX9_PROPR	Q8lqx9 photobacter
89	27	90.0	611	2	Q5ZC13_ORYSA	Q5zc13 oryza sativ
90	27	90.0	611	2	Q80TW4_MOUSE	Q80tw4 mus muscullu
91	27	90.0	613	1	DL7L_ARA7H	Q60378 arabidopsis
92	27	90.0	614	2	Q60378_HUMAN	Q60378 homo sapien
93	27	90.0	633	2	Q75CG7_ASHCO	Q75cg7 ashyba goos
94	27	90.0	653	2	Q4WIS0_ASFPU	Q4wis0 aspergillus
95	27	90.0	655	2	Q747P1_GEOSL	Q747p1 geobacter s
96	27	90.0	667	2	Q9XT59_BOVIN	Q9xt59 bos taurus
97	27	90.0	676	1	LX15B_HUMAN	Q15296 homo sapien
98	27	90.0	677	1	LX15B_MOUSE	Q35936 mus muscullu
99	27	90.0	677	1	LX15B_RAT	Q8k4f2 rattus norv
100	27	90.0	677	2	Q5NCF6_MOUSE	Q5ncf6 mus muscullu

ALIGNMENTS

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RESULT 1
Q7RTD7 PLAYO
ID Q7RTD7 PLAYO PRELIMINARY; PRT; 43 AA.
AC Q7RTD7;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PY00057;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RX STRAIN=17XN1;
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255706; Pubmed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;

RESULT 2
Q7RAK6 PLAYO
ID Q7RAK6 PLAYO PRELIMINARY; PRT; 49 AA.
AC Q7RAK6;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=PY06494;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
RX STRAIN=17XN1;
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255706; Pubmed=1236865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;

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RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABL01002200; EAA18719.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 49 AA; 5773 MW; FA4AFCB9AD4685E3 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 17 RYTMH 21

RESULT 3
Q7QVY1 GIALA
ID Q7QVY1 GIALA PRELIMINARY; PRT; 178 AA.
AC Q7QVY1;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE GIP 577 4070 4606.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
NCBI_TaxID=184922;
RX STRAIN=WB C6;
RP NUCLEOTIDE SEQUENCE.
RC Morrison H.C., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RA "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ database.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACB01000089; EAA38835.1; -; Genomic_DNA.
DR InterPro: IPR003409; MORN.
DR Pfam: PF02493; MORN; 2.
SQ SEQUENCE 178 AA; 20163 MW; 9049D96A12P25CC3 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
DB 50 RYTMH 54

RESULT 4
Q5FO59 GLUOX
ID Q5FO59 GLUOX PRELIMINARY; PRT; 187 AA.
AC Q5FO59;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE Bacterioides fragilis.
GN Order=Deferribacteriales;
OS Gluconobacter oxydans (Gluconobacter suboxydans).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Gluconobacter.
NCBI_TaxID=442;
RX STRAIN=621H;
RP NUCLEOTIDE SEQUENCE.
RC Pubmed=15665824; DOI=10.1038/nbt1062;
RA Prust C., Hofmeister M., Liesegang H., Wietzer A., Fricke W.F.,
RA Ehrenreich A., Gottschalk G., Deppenmeier U.;

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RT "Complete genome sequence of the acetic acid bacterium Gluconobacter
RT oxydans."
RT Nat. Biotechnol. 23:195-200(2005).
DR EMBL: CP000009; AAM61487.1; -; Genomic_DNA.
DR GO: GO:0005488; F:binding; IEA.
DR GO: GO:0008199; F:ferric iron binding; IEA.
DR GO: GO:0008879; P:iron ion homeostasis; IEA.
DR GO: GO:0006826; P:iron ion transport; IEA.
DR InterPro: IPR002024; Bacterioferritin.
DR InterPro: IPR008331; Ferritin Dps.
DR InterPro: IPR009040; Ferritin_Like.
DR Pfam: PF00210; Ferritin_1.
DR ProDom: PD002269; Bacterioferritin; 1.
DR PROSITE: PS50905; FERRITIN_LIKE; 1.
KW Complete proteome.
SQ SEQUENCE 187 AA; 20489 MW; 515412E4DB51B582 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 57 RYTMH 61

RESULT 5
0981G0_RHIL0 PRELIMINARY; PRT; 209 AA.
ID 0981G0_RHIL0 PRELIMINARY;
AC 0981G0;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mrp389 protein.
GN OrderedLocustNames=mrp389;
OS Rhizobium loti (Mesorhizobium loti).
OC Plasmid pmla.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=MAFF30309;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: BA000013; BAB54995.1; -; Genomic_DNA.
KW Complete proteome; Plasmid.
SQ SEQUENCE 209 AA; 22471 MW; D7D8732FA3A7955B CRC64;

Query Match 100.0%; Score 30; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 11 RYTMH 15

RESULT 6
07PW16_ANOGA PRELIMINARY; PRT; 259 AA.
ID 07PW16_ANOGA PRELIMINARY;
AC 07PW16;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000010646 (Fragment).

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GN ORFNames=ENSANG00000008157;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation."
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC The Anopheles gambiae Sequence Committee;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Major function may be to aid in digestion of the blood
CC meal (By similarity).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AA001008984; BA15112.2; -; Genomic_DNA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0030195; P:negative regulation of blood coagulation; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR Pfam: PF00089; Trypsin_1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_Spc_1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
FT NON_TER
SQ SEQUENCE 259 AA; 27439 MW; FB9AD2D9B8709ED5 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 95 RYTMH 99

RESULT 7
05E510_VIBF1 PRELIMINARY; PRT; 283 AA.
ID 05E510_VIBF1 PRELIMINARY;
AC 05E510;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=VF1391;
OS Vibrio fischeri (strain ATCC 700601 / 85114).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=312309;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15703294; DOI=10.1073/pnas.040900102;
RA Ruby E.G., Urbanoweki M., Campbell J., Dunn A., Faini M., Gunsalus R.,
RA Loerch P., Lupp C., McCann V., Millikan D., Schaefer A., Stabb E.,
RA Stevens A., Visick K., Whistler C., Greenberg E.P.;
RT "Complete genome sequence of Vibrio fischeri: a symbiotic bacterium
RT with pathogenic congeners."
RL Proc. Natl. Acad. Sci. U.S.A. 102:3004-3009(2005).
DR EMBL: CP000020; AAM85886.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 283 AA; 32213 MW; D614AC3F57BE319 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 283;

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Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 73 RYTMH 77

RESULT 8

QSPR06 ANAMM
QSPR06_ANAMM PRELIMINARY; PRT; 296 AA.

AC QSPR06; 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=AM981;
OS Anaplasma marginale (strain St. Maries).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Anaplasmataceae; Anaplasma.
OX NCBI_TaxID=234826;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15618402; DOI=10.1073/pnas.040656102;
RA Brayton K.A., Kappmeyer L.S., Herndon D.R., Dark M.J., Tibbals D.L.,
Palmer G.H., McGuire T.C., Knowles D.P. Jr.;
RT "Complete genome sequencing of Anaplasma marginale reveals that the
RT surface is skewed to two superfamilies of outer membrane proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 102:844-849(2005).
DR EMBL; CP000030; AAY86874.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.

Query Match 100.0%; Score 30; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 141 RYTMH 145

RESULT 9
Q7YUF0 TRYCR
Q7YUF0_TRYCR PRELIMINARY; PRT; 437 AA.

AC Q7YUF0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE S-adenosylhomocysteine hydrolase (EC 3.3.1.1).
GN Name=SAH;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC Scizozoa; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14969692; DOI=10.1016/j.exppara.2003.10.001;
RA Parker N.B., Yang X., Hanke U., Mason K.A., Schonen R.L.,
Borcherde R.T., Yin D.H.;
RT "Trypanosoma cruzi: molecular cloning and characterization of the S-
adenosylhomocysteine hydrolase."
RL Exp. Parasitol. 105:149-158(2003).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
homocysteine + adenosine.
CC -1- COFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
DR EMBL; AY33397; AAP45630.1; -; Genomic_DNA.
DR HSSP; P10760; 1B3R.
DR SMR; Q7YUF0; 4-437.
DR GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR000043; Ad_hcy_hydrolase.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF05221; AdoHcyase_1.
DR Pfam; PF00670; AdoHcyase_NAD_1.
DR TIGRfam; TIGR00936; ahcF_1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
KM Hydrolase; NAD; One-carbon metabolism.

SEQUENCE 437 AA; 48462 MW; F554E315A683C4E CRC64;

Query Match 100.0%; Score 30; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 326 RYTMH 330

RESULT 10

Q8NKV4 ACIAM
Q8NKV4_ACIAM PRELIMINARY; PRT; 454 AA.

AC Q8NKV4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Membrane-bound Nfe hydrogenase.
GN Name=isp2;
OS Acidithiobacillus ambivalens (Desulfurolobus ambivalens).
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Acidianus.
OX NCBI_TaxID=2283;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM3772, and Lei 10;
RX MEDLINE=22830413; PubMed=12949162; DOI=10.1099/mic.0.26455-0;
RA Laska S., Lottepeich F., Kletzin A.;
RT "Membrane-bound hydrogenase and sulfur reductase of the
RT hyperthermophilic and acidophilic archaeon Acidithiobacillus ambivalens."
RL Microbiology 149:2357-2371(2003).
RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=DSM3772, and Lei 10;
RA Laska S.;
RL Thesis (2000), Institute of Microbiology and Genetics, Darmstadt
University of Technology, Darmstadt, Germany.
DR EMBL; AJ320523; CAC86886.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
DR InterPro; IPR012285; Fum_reductase_C.
DR Pfam; PF00037; Fer4; 1.
DR PROSITE; PS00198; 4Fe4S_FERRDOXIN; 2.
KM 4Fe-4S; Electron transport; Iron; Iron-sulfur; Metal-binding;
KW Transposon.
SQ SEQUENCE 454 AA; 51031 MW; 94B518FFA436124 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
Db 274 RYTMH 278

RESULT 11

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Q856Y5_9CAUD PRELIMINARY; PRT; 455 AA.
ID Q856Y5_9CAUD PRELIMINARY; PRT; 455 AA.
AC Q856Y5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Gp9.
OS Mycobacteriophage Rosebush.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_Taxid=205874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22592860; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karchikyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA Krikakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AY129334; AAN01891.1; -; Genomic DNA.
SQ SEQUENCE 455 AA; 50574 MM; BCFDCLB36F34E6D CRC64;

Query Match 100.0%; Score 30; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 61 RYTMH 65

RESULT 12
OS LHM9_BACFN PRELIMINARY; PRT; 531 AA.
ID Q5LHM9;
AC Q5LHM9;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BF0589;
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC Bacteriia; Bacteroidetes; Bacteroidales (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_Taxid=272559;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746427; DOI=10.1126/science.1107008;
RA Cerdano-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA Abratt V., Lennard N., Foxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Cotton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT "Extensive DNA inversions in the B. fragilis genome control variable
gene expression.";
RL Science 307:1463-1465(2005).
DR EMBL; CR626927; CAH06341.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 531 AA; 58337 MM; F75639ABFCAE40C7 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 227 RYTMH 231

RESULT 13
Q74DM9_GEOSL PRELIMINARY; PRT; 627 AA.
ID Q74DM9_GEOSL PRELIMINARY; PRT; 627 AA.
AC Q74DM9;

Query Match 100.0%; Score 30; DB 2; Length 627;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Methyl-accepting chemotaxis protein, putative.
GN OrderedLocusNames=GSU1287;
OS Geobacter sulfurreducens.
OC Bacteriia; Proteobacteria; Deleaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_Taxid=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Uitterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
environments.";
RL Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34663.1; -; Genomic DNA.
DR TIGR; GSU1287; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chm taxis_transd.
DR Pfam; PF00015; MCPsignal; 1.
DR PROSITE; PS50111; CHEMOTAXIS_TRANSDC_2; 1.
KW Complete proteome.
SQ SEQUENCE 627 AA; 67402 MM; D299118D366393D CRC64;

Query Match 100.0%; Score 30; DB 2; Length 627;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 587 RYTMH 591

RESULT 14
Q4QD18_LEIMA PRELIMINARY; PRT; 4825 AA.
ID Q4QD18_LEIMA PRELIMINARY; PRT; 4825 AA.
AC Q4QD18;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=lmjF20.0260;
OS Leishmania major.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_Taxid=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
RA Saunders D., Seeger K., Warren T., Rajandram M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; CT005259; CAU03601.1; -; Genomic DNA.
DR InterPro; IPR011704; AAA_5.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR012099; Midasin.
DR InterPro; IPR002078; Sig54_interact.
DR Pfam; PF07728; AAA_5; 5.
DR PIRSF; PIRSF010340; Midasin; 1.
DR SMART; SM00382; AAA; 6.
DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
KW ATP-binding; Hypothetical protein; Membrane; Nucleotide-binding;
```

KW Transport. 4825 AA; 534292 MW; FA5B05EA315BE26 CRC64;
SQ SEQUENCE

Query Match
Best Local Similarity 100.0%; Score 30; DB 2; Length 4825;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|||||
Db 3847 RYTMH 3851

RESULT 15
Q9JUB8_NEIMA PRELIMINARY; PRT; 61 AA.
ID Q9JUB8_NEIMA PRELIMINARY; PRT; 61 AA.
AC Q9JUB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMA1281.
GN OrderedLocustNames=NMA1281;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=22491 / Serogroup A / Serotype 4A;
RC MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RX MEDLINE=22491 / Serogroup A / Serotype 4A;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Rae J.A., Whitehead S., Spratt B.G., Barrett B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162755; CAB84533.1; -; Genomic_DNA.
DR PIR; C81896; C81896.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 61 AA; 7248 MW; 9BD6B175BD4BFA4 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 61;
Best Local Similarity 80.0%; Pred. No. 69;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|||||
Db 44 RYTMH 48

RESULT 16
O8GQMS_SERMA PRELIMINARY; PRT; 99 AA.
ID O8GQMS_SERMA PRELIMINARY; PRT; 99 AA.
AC O8GQMS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=615;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=2242519; PubMed=12354232;
RX Hornig Y.T., Deng S.C., Daykin M., Soo P.C., Wei J.R., Luh K.T.,
Ho S.W., Swift S., Lai H.C., Williams P.,
"The luxR family protein SpnR functions as a negative regulator of N-
acetylhomoserine lactone-dependent quorum sensing in Serratia
marcescens.";
RL MOJ. Microbiol. 45:1655-1671(2002).

RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lai H.-C., Deng S.-C., Hornig Y.-T., Daykin M., Soo P.-C., Luh K.-T.,
Ho S.-W., Swift S., Williams P.,
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB389912; AAN52500.1; -; Genomic_DNA.
DR InterPro; IPR007712; Pfam; PF05016; Plasmid_stabil; 1.
DR Pfam; PF05016; Plasmid_stabil; 1.
KW Hypothetical protein.
SQ SEQUENCE 99 AA; 11769 MW; FE198A6BEB149A4B CRC64;

Query Match 90.0%; Score 27; DB 2; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|||||
Db 19 RYTMH 23

RESULT 17
Q29379_PIG PRELIMINARY; PRT; 110 AA.
ID Q29379_PIG PRELIMINARY; PRT; 110 AA.
AC Q29379;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor necrosis factor type 1 receptor associated protein
DE (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Suidae.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Small intestine;
RX MEDLINE=96327607; PubMed=8672129; DOI=10.1007/s003359900153;
RA Winteroe A.K., Fredholm M., Davies W.,
RT "Evaluation and characterization of a porcine small intestine cDNA
library: analysis of 839 clones.";
RL Mamm. Genome 7:509-517(1996).
DR EMBL; F14589; CAA23140.1; -; mRNA.
DR HSSP; P02829; IUSO.
DR CO; GO:0004872; F:receptor activity; IEA.
DR CO; GO:0051082; F:unfolded protein binding; IEA.
DR CO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR001404; Hsp90.
DR Pfam; PF00183; HSP90; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 12744 MW; 0C3E32D9732715D5 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 110;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
|||||
Db 15 RYTMH 19

RESULT 18
O868H1_LEIME PRELIMINARY; PRT; 113 AA.
ID O868H1_LEIME PRELIMINARY; PRT; 113 AA.
AC O868H1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inhibitor of cysteine peptidases.
GN Name=icp1
OS Leishmania mexicana.


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OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5665;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22615569; PubMed=12729889; DOI=10.1016/S0014-5793(03)00327-2;
RA Sanderson S.U., Westrop G.D., Scharfstein J., Mottram J.C.,
RA Coombs G.H., Sanderson S.U.;
RT "Functional conservation of a natural cysteine peptidase inhibitor in
RT protozoan and bacterial pathogens.";
RL FEBS Lett. 542:12-16(2003).
DR EMBL, AJ548776; CAD69575.1; -; Genomic DNA.
SQ SEQUENCE 113 AA; 12733 MW; E75773C763897ECD CRC64;

Query Match          90.0%; Score 27; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 105 RYTMH 109

RESULT 19
Q5ZC10_ORYSA PRELIMINARY; PRT; 116 AA.
ID Q5ZC10_ORYSA
AC Q5ZC10;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Mitogen-activated protein kinase-like.
GN Name=OSJNB0035114.5-4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaka H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saij S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojodori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL, AP003220; BAD61404.1; -; Genomic DNA.
DR GO: GO:0016301; F:kinase activity; IEA.
KW Kinase.
SQ SEQUENCE 116 AA; 12419 MW; B3F829C53C089D6 CRC64;

Query Match          90.0%; Score 27; DB 2; Length 116;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 34 RYTMH 38

RESULT 20
Q868G9_LEIMA PRELIMINARY; PRT; 117 AA.
ID Q868G9_LEIMA
AC Q868G9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)

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DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Inhibitor of cysteine peptidase.
CN Name=icp; ORFNames=Lmjf24.1770;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22615569; PubMed=12729889; DOI=10.1016/S0014-5793(03)00327-2;
RA Sanderson S.U., Westrop G.D., Scharfstein J., Mottram J.C.,
RA Coombs G.H., Sanderson S.U.;
RT "Functional conservation of a natural cysteine peptidase inhibitor in
RT protozoan and bacterial pathogens.";
RL FEBS Lett. 542:12-16(2003).
DR EMBL, AJ548778; CAD69563.1; -; Genomic DNA.
DR EMBL, CT005263; CAJ05225.1; -; Genomic DNA.
SQ SEQUENCE 117 AA; 12979 MW; CA5041930475B18D CRC64;

Query Match          90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
Db 109 RYTMH 113

RESULT 21
Q521B3_MAGGR PRELIMINARY; PRT; 121 AA.
ID Q521B3_MAGGR
AC Q521B3;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG05187.4;
OS Magnaporthe oryzae 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nuebaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Archachl H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayat T., Blitshteyn B., Bloom T., Blye J., Bogunlavskiy L.,
RA Borowsky M., Bouhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Chehatsang Y., Citroen M.,
RA Collimore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Fayer S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Geatin G., Gnerre S.,
RA Gutirke A., Guyette A., Graham J., Grandois E., Gyatsen K., Harez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Huby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyselis M., Karlsson E.,
RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Linblad-coh K., Liu X., Lokytsang T., Lokytsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Muccell E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menes L.,
RA Mestrov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,

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RA Mozes J., Muhlstein L., Munson G., Naylor J., Newes C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizari M., Norbu C.,
 RA Norbu N., O'donnell P., Okawo O., O'leary S., Omotocho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Punthang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramsamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Ruetan W., Schupbach R., Seaman C., Seclipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougniez C.,
 RA Spencer B., Stalker C., Strange-Thomann N., Stavropoulos S.,
 RA Steaton K., Stone C., Stone S., Stubbs M., Talamas J., Tchinga P.,
 RA Tenzing P., Teesfaye S., Theodore J., Thoulutang Y., Topham K.,
 RA Towey S., Tzamba T., Tsomo N., Vallée D., Vassiliev H.,
 RA Venkataraman V., Vinson U., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe oryzae";
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RC NUCLEOTIDE SEQUENCE.
 RP STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 KW Hypochemical protein.
 SQ SEQUENCE 121 AA; 13208 MW; BF676C578C2F94B CRC64;
 SO
 Query Match 90.0%; Score 27; DB 2; Length 121;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 :|||
 Db 55 KYTMH 59
 RESULT 22
 Q7SD55 NEUCR PRELIMINARY; PRT; 149 AA.
 AC Q7SD55;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU09330.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetiales; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selzer E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rahmen B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Iankilev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrenkoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gagne S.,
 RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Friseman D.,
 RA Kryazovova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA DeGonza C.C., Glase L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,

RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa";
 RL Nature 0:0-0 (2003).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 SQ SEQUENCE 149 AA; 17361 MW; B4E2A3286B2A504 CRC64;
 SO
 Query Match 90.0%; Score 27; DB 2; Length 149;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 :|||
 Db 48 KYTMH 52
 RESULT 23
 Q58GM4 9HIV1 PRELIMINARY; PRT; 165 AA.
 AC Q58GM4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviridae; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OC NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TLHC017;
 RA Khamdi S.A., Ochieng W., Lihana R.W., Kiptoo M.K., Kinuya J.G.,
 RA Lager N., Muriuki J., Mwengi J., Pelle R., Mwigiti A., Carter J.,
 RA Yamada R., Mpoke S.;
 RT "Genetic Diversity of HIV-1 Subtypes Circulating in Northern Kenya";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 KW Envelope protein.
 FT NON_TER 1 165
 FT NON_TER 1 165
 SQ SEQUENCE 165 AA; 18972 MW; F61349D86C061170 CRC64;
 SO
 Query Match 90.0%; Score 27; DB 2; Length 165;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 :|||
 Db 154 RYTMH 158
 RESULT 24
 Q6LXU7 METMP PRELIMINARY; PRT; 167 AA.
 AC Q6LXU7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE 6-pyruvoyl tetrahydropteridin synthase.
 GN OrderedLocNames=MP1250;
 OS Methanococcus maripaludis.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcus.
 OX NCBI_TaxID=39152;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=82 / LT;
 RA PubMed=15466049; DOI=10.1128/JB.186.20.6956-6969.2004;
 RX Hendrickson E.L., Kaul R., Zhou Y., Boyce D., Chapman P., Chung J.,
 RA Conway de Macario E., Dodsworth J.A., Gillett W., Graham D.E.,

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RA Hackert M., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J.,
RA Major T.A., Moore B.C., Porat I., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soell D., Van Dien S., Wang T., Whitman W.B.,
RA Xia Q., Zhang Y., Larimer F.W., Olson M.V., Leigh J.A.;
RT "Complete genome sequence of the genetically tractable
RT hydrogeotrophic methanogen Methanococcus maripaludis.";
RL J. Bacteriol. 186:6556-6569(2004).
DR EMBL; BX957222; CAF30806.1; -; PTP_synth.
DR InterPro; IPR007115; 6_PTP_synth.
DR Pfam; PF01242; PTPS; 1.
DR PIRSF; PIRSF006113; PTP_syn; 1.
DR ProDom; PD004049; PTPS_hypoth; 1.
KW Complete proteome.
SQ SEQUENCE 167 AA; 19077 MW; SEC6F280B2441A9 CRC64;

Query Match          90.0%; Score 27; DB 2; Length 167;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
   |||:|
Db 161 RYTMH 165

RESULT 25
O15418_HUMAN PRELIMINARY; PRT; 169 AA.
ID O15418_HUMAN PRELIMINARY; PRT; 169 AA.
AC O15418;
DT 01-JUN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CAGL114 protein (Fragment).
GN Name=TNRC21; Synonyms=CAGL114;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=97369493; PubMed=9225980; DOI=10.1007/s004390050476;
RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.-H., Kidwai A.S.,
RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
RT "cDNAs with long CAG trinucleotide repeats from human brain.";
RL Hum. Genet. 100:114-122(1997).
DR EMBL; U80756; AAB91448.1; -; mRNA.
DR HGNC; HGNC:11964; TNRC21.
FT NON_TER 1
SQ SEQUENCE 169 AA; 18397 MW; B07BC4E8275A2C9C CRC64;

Query Match          90.0%; Score 27; DB 2; Length 169;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
   |||:|
Db 2 RYTMH 6

RESULT 26
Q6T4V7_9MAGN PRELIMINARY; PRT; 182 AA.
ID Q6T4V7_9MAGN PRELIMINARY; PRT; 182 AA.
AC Q6T4V7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PISTILLATA-like protein PI-1 (Fragment).
OS Thotaea siliquosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Piperales; Aristolochiaceae;
OC Thotaea.
NCBI_TaxID=213843;

[1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=14694075; DOI=10.1093/molbev/msb044;
RX Stellari G.M., Jaramillo M.A., Kramer E.M.;
RA "Evolution of the ABETAL3 and PISTILLATA lineages of MADS-box-
RT controlling genes in the basal angiosperms.";
RL Mol. Biol. Evol. 21:506-519(2004).
DR EMBL; AY436708; AAR87669.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TE; 1.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
FT NON_TER 1
SQ SEQUENCE 182 AA; 21112 MW; D3B7FEEB9AEE3FD2 CRC64;

Query Match          90.0%; Score 27; DB 2; Length 182;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
   |||:|
Db 136 RYTMH 140

RESULT 27
Q6F7A6_ACIAD PRELIMINARY; PRT; 189 AA.
ID Q6F7A6_ACIAD PRELIMINARY; PRT; 189 AA.
AC Q6F7A6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=ACIAD3397;
OS Acinetobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
NCBI_TaxID=62977;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ADP1;
RX PubMed=15514110; DOI=10.1093/nar/gkh910;
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 32:5766-5779(2004).
DR EMBL; CR543861; CAG70059.1; -; Genomic_DNA.
DR InterPro; IPR008523; DUF805.
DR Pfam; PF05656; DUF805; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 189 AA; 21242 MW; 79A535B574E0C11 CRC64;

Query Match          90.0%; Score 27; DB 2; Length 189;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
   |||:|
Db 163 RYTMH 167

RESULT 28
Q5FR26_GLUOX PRELIMINARY; PRT; 195 AA.
ID Q5FR26_GLUOX PRELIMINARY; PRT; 195 AA.
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QY 1 RYTMH 5
   |||:|
Db 163 RYTMH 167

RESULT 28
Q5FR26_GLUOX PRELIMINARY; PRT; 195 AA.
ID Q5FR26_GLUOX PRELIMINARY; PRT; 195 AA.
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AC Q5FR26; 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein
 GN OrderedLocustNames=GOX1419;
 OS Gluconobacter oxydans (Gluconobacter euboxydans).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Gluconobacter.
 OX NCBI_TaxID=442;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=621H;
 RX PubMed=15665824; DOI=10.1038/nbt1062;
 RA Prust C., Hoffmeister M., Liesegang H., Wlazier A., Fricke W.F.,
 RA Ehrenreich A., Gottschalk G., Deppelemer U.;
 RT "Complete genome sequence of the acetic acid bacterium Gluconobacter
 oxydans.";
 RL Nat. Biotechnol. 23:195-200(2005).
 DR EMBL; CP000009; AAW61170.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 195 AA; 21756 MW; 368FA92F4F16D81 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 195;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
 DB 44 RYTLH 48

RESULT 29

Q91714_PSEAE PRELIMINARY; PRT; 195 AA.
 AC Q91714;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=PA0118;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
 RA Steyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.S., Wu Z., Paulsen I.T.,
 RA Reizer U., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC - FUNCTION: Involved in disulfide-bond formation. Acts by
 transferring its disulfide bond to other proteins (by similarity).
 CC - SUBCELLULAR LOCATION: Periplasmic (by similarity).
 DR EMBL; AEO04450; AAG03508.1; -; Genomic DNA.
 DR PIR; G83629; G83629.
 DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . . ; IEA.
 DR GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
 DR InterPro; IPR001853; DSBa.
 DR Pfam; PF01333; DSBa; 1.
 DR Complete proteome; Hypothetical protein; Periplasmic.
 KW SEQUENCE 195 AA; 21474 MW; CA3C029592EB41D CRC64;

Query Match 90.0%; Score 27; DB 2; Length 195;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RYTMH 5
 DB 61 RYTLH 65

RESULT 30

Q410Y7_9BURK PRELIMINARY; PRT; 198 AA.
 AC Q410Y7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=Bcen242ADRApf_4054;
 OS Burkholderia cenocepacia H12424.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
 OX NCBI_TaxID=331272;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=H12424;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Deter C., Glavina T.,
 RA Hammon N., Israni S., Pluck S., Richardson P.;
 RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
 H12424.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=H12424;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.;
 RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
 H12424.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC - CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AALU0100026; EAM18440.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 198 AA; 22853 MW; 0797F9FC2DDFBBCB CRC64;

Query Match 90.0%; Score 27; DB 2; Length 198;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RYTMH 5
 DB 7 RYTLH 11

RESULT 31

Q87B90_XYLFT PRELIMINARY; PRT; 203 AA.
 AC Q87B90;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=PD1568;
 OS Xylella fastidiosa (strain Temecula / ATCC 700964).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=183190;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2421331; PubMed=12533478;
 RX DOI=10.1128/JB.185.3.1018-1026.2003;
 RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
 RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon P.H.,
 RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
 RA Carrier H., Carrizo D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
 RA Coutinho L.L., Kimura E.T., Ferro E.S., Harekara R., Kuramae E.,
 RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
 RA Baia G.S., Bianco S.R., Brito M.S., Camavan F.S., Celestino A.V.,
 RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
 RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
 RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
 RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
 RA Kitajima J.P.;
 RT "Comparative analyses of the complete genome sequences of Pierce's
 RT disease and citrus variegated chlorosis strains of *Xylella*
 RT *fastidiosa*.";
 RL J. Bacteriol. 185:1018-1026(2003).
 DR EMBL: AB012559; AAC029410.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 203 AA; 22869 MW; AC9FC164CF1153E CRC64;

Query Match 90.0%; Score 27; DB 2; Length 203;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 Db 32 RYTMH 36

RESULT 32
 06CNC3_KLULA PRELIMINARY; PRT; 205 AA.
 ID 06CNC3_KLULA
 AC 06CNC3;
 DT 25-OCT-2004 (TRENBLREL. 28, Created)
 DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
 DE Similar to sp|P40080 Saccharomyces cerevisiae YER128w hypothetical
 DE protein singleton.
 GN OrderedLocustNames=KLUA0E13695g;
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxId=28985;
 RN [1]
 RP NCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed:1529592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durans P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marc C., Nevegilise C., Talla E.,
 RA Goffard N., Franquet L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Batnay S., Blanchin S., Beckrich J.-M., Beyne E., Bleykasten C.,
 RA Boisrame A., Boyer J., Cactolico L., Confalieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.-M., Nikolski M., Ozas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potter S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenion-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Searpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Soucieu J.-L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 DR EMBL: CR382125; CAG99653.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 205 AA; 23939 MW; 9A94EC0BAC061B40 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 205;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RYTMH 5
 Db 148 RYTMH 152

RESULT 33
 09PFS4_XYLFA PRELIMINARY; PRT; 205 AA.
 ID 09PFS4_XYLFA
 AC 09PFS4;
 DT 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=XF0583;
 OS *Xylella fastidiosa*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; *Xylella*.
 OX NCBI_TaxId=2371;
 RN [1]
 RP NCLEOTIDE SEQUENCE.

RC STRAIN=985C;
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Accencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Colauco N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohlseil J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA da Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawaaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Sawaaki H.E.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tuhako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Medanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
 RL Nature 406:151-159(2000).
 DR EMBL: AB003904; AA883393.1; -; Genomic DNA.
 DR PIR: A82789; A82789.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 205 AA; 23071 MW; 773FD86D1E4BA862 CRC64;

Query Match 90.0%; Score 27; DB 2; Length 205;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RYTMH 5
 Db 34 RYTMH 38

RESULT 34
 07XY45_GRIUA PRELIMINARY; PRT; 207 AA.
 ID 07XY45_GRIUA
 AC 07XY45;
 DT 01-OCT-2003 (TRENBLREL. 25, Created)
 DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE DnaJ-like protein (fragment).
 OS *Griffithsia japonica* (Red alga).
 OC Eukaryota; Rhodophyta; Floridophyceae; Ceramiales; Ceramiales;
 OC Griffithsia.
 OX NCBI_TaxId=83288;
 RN [1]
 RP NCLEOTIDE SEQUENCE.

RA Liu C., Lee Y., Lee H.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF542023; AAP80833.1; -; mRNA.
DR HSSP: P25491; 1NLT.
DR GO: GO:0031072; F:heat shock protein binding; IEA.
DR GO: GO:0051082; F:unfolded protein binding; IEA.
DR GO: GO:0006457; P:protein folding; IEA.
DR InterPro: IPR002939; DnaJ_C.
DR InterPro: IPR001305; DnaJ_CXXCXXG.
DR InterPro: IPR003095; Hep_DnaJ.
DR Pfam: PF01556; DnaJ_C_1.
DR Pfam: PF00684; DnaJ_CXXCXXG; 1.
DR PRINTS: PR00625; DnaJPROTEIN.
KM Chaperone.
FT NON TER 1 1
SQ SEQUENCE 207 AA; 22267 MW; F945CD7ECF9AD656 CRC64;
Query Match 90.0%; Score 27; DB 2; Length 207;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYTMH 5
Db 111 RYTLH 115
RESULT 35
05C211_ORYSA
ID 05C211_ORYSA PRELIMINARY; PRT; 208 AA.
AC 05C211;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mitogen-activated protein kinase-like.
GN Name=OSUNB0035114.5-3;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OC NCBI_TaxID=39947;
OX
RN
RA NUCLEOTIDE SEQUENCE.
RP Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijiishi S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shimura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara K., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL: AP003220; BAD61403.1; -; Genomic DNA.
DR GO: GO:0016301; F:kinase activity; IEA.
KM Kinase.
SQ SEQUENCE 208 AA; 22636 MW; SEC00EB5B80A2937 CRC64;
Query Match 90.0%; Score 27; DB 2; Length 208;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYTMH 5
Db 126 RYTLH 130

RESULT 36
Q4UID6_THEAN
ID Q4UID6_THEAN PRELIMINARY; PRT; 219 AA.
AC Q4UID6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Protein kinase, putative (EC 2.7.1.37).
GN ORFNames=TA06530;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OC NCBI_TaxID=5874;
OX
RN
RA NUCLEOTIDE SEQUENCE.
RP STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrell B.G.;
RT "The chromosome 1 sequence of Theileria annulata.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR940347; CA173153.1; -; Genomic DNA.
KM Kinase; Transferase.
SQ SEQUENCE 219 AA; 25709 MW; 5CC2011806D8B67A CRC64;
Query Match 90.0%; Score 27; DB 2; Length 219;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RYTMH 5
Db 42 RYTLH 46
RESULT 37
08G546_BIFLO
ID 08G546_BIFLO PRELIMINARY; PRT; 233 AA.
AC 08G546;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible ribosomal pseudouridine synthase.
GN OrderedLocustNames=BL1174;
GN Bifidobacterium longum.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN
RA NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RP STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karimiantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL: AE014295; AAN24979.1; -; Genomic DNA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0009982; F:pseudouridine synthase activity; IEA.
DR GO: GO:004730; F:pseudouridylylase synthase activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0006396; P:RNA processing; IEA.
DR InterPro: IPR006145; Pseudou synth.
DR InterPro: IPR006224; Rly synth.
DR Pfam: PF00849; Pseudou synth. 2; 1.
DR ProDom: PD001819; Pseudou synth. 1.
DR PROSITE: PS01129; PSI_RLUF; 1.
KM Complete proteome; Isomerase.
SQ SEQUENCE 233 AA; 26596 MW; 1D78278986C6F6CF CRC64;
Query Match 90.0%; Score 27; DB 2; Length 233;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 RYTMH 5
Db      160 RYTLH 164

RESULT 38
Q6XLY2_9PHYC PRELIMINARY; PRT; 241 AA.
ID Q6XLY2_9PHYC
AC Q6XLY2;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Firtv-1-B54.
OS Feldmannia irregularis virus a.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phaeovirus.
NCBI_TaxID=231992;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Firtv-1;
RX PubMed:14745530; DOI=10.1007/s00239-003-2501-Y;
RA Delaroque N., Boland W., Muller D.G., Knippers R.;
RT "Comparisons of two large phaeoviral genomes and evolutionary
   implications.";
RL J. Mol. Evol. 57:613-622(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Firtv-1;
RA Delaroque N., Knippers R., Mueller D.G., Boland W.;
RT "Partial Nucleotide Sequence of the Feldmannia irregularis virus
   Firtv-1 Genome: On the Evolution of Large Phaeoviral Genomes.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY225134; AAR26929.1; -; Genomic DNA.
SQ SEQUENCE 241 AA; 27054 MW; 74DEBD13AF391754 CRC64;

Query Match      90.0%; Score 27; DB 2; Length 241;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
Db      45 RYTLH 49

RESULT 39
Q4N777_39
ID Q4N777_39
AC Q4N777;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Serine/threonine protein kinase nek1, putative.
OS ORNNames=TP01_0943;
OC Theileria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
   Theileria.
NCBI_TaxID=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muga9;
RA Hall N., Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
   Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
   Jiang L., Lynn J., Weaver B., Shoib A., Wasawo D., Crabtree J.,
   Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
   Taracha E.L.N., Salzberg S.L., Feldblyum T.V., Pertea M., Allen J.,
   Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
   lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=Muga9;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
   Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
   Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
   Lynn J., Weaver B., Shoib A., Wasawo D., Crabtree J., Wortman J.R.,
   Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
   Utecherback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
   Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
   Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
   preliminary data.
CC EMBL; AKG0100001; EAN34181.1; -; Genomic DNA.
DR EMBL; AKG0100001; EAL79524.1; -; Genomic DNA.
KW Hypothetical protein; Signal.
FT SIGNAL 1
SQ SEQUENCE 269 AA; 29345 MW; E41C87CBAFF93B10C CRC64;

Query Match      90.0%; Score 27; DB 2; Length 269;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
Db      192 RYTLH 196

RESULT 40
Q4NVB4_9DELT PRELIMINARY; PRT; 269 AA.
ID Q4NVB4_9DELT
AC Q4NVB4;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Hypothetical protein precursor.
OS ORFNames=AdenDRAFT_308;
OS Anaeromyxobacter denahalgensis 2CP-C.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytochrome P450; Myxococcaceae; Anaeromyxobacter.
NCBI_TaxID=290397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
   Hammon N., Ierant S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Anaeromyxobacter
   denahalgensis 2CP-C.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2CP-C;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Lattimer F., Land M.;
RT "Annotation of the draft genome assembly of Anaeromyxobacter
   denahalgensis 2CP-C.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
   preliminary data.
CC EMBL; AHD0100001; EAL79524.1; -; Genomic DNA.
DR EMBL; AHD0100001; EAL79524.1; -; Genomic DNA.
KW Hypothetical protein; Signal.
FT SIGNAL 1
SQ SEQUENCE 269 AA; 29345 MW; E41C87CBAFF93B10C CRC64;

Query Match      90.0%; Score 27; DB 2; Length 269;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RYTMH 5
Db      192 RYTLH 196

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Thu Dec 15 10:59:55 2005

us-10-720-323-1.rup

Page 14

Search completed: December 14, 2005, 07:30:41
job time : 30.9828 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2005, 07:11:28 ; Search time 96.7241 Seconds
(without alignments)
77.224 Million cell updates/sec

Title: US-10-720-323-2

Perfect score: 88

Sequence: 1 VISEFDGSKYVDSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Geneseq_21: *
2: Geneseqp1980s: *
3: Geneseqp1990s: *
4: Geneseqp2000s: *
5: Geneseqp2001s: *
6: Geneseqp2002s: *
7: Geneseqp2003as: *
8: Geneseqp2004s: *
9: Geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	17	5	AAU76328 Human ant
2	88	100.0	119	5	AAU76333 Human ant
3	85	96.6	249	5	ABP45098 Human Bly
4	85	96.6	249	7	ADG95925 Single ch
5	82	93.2	16	5	AAW51159 Anti-tumo
6	81	92.0	17	3	AAW90298 Human ant
7	81	92.0	17	3	AAW90704 Anti-fact
8	81	92.0	17	7	AAO17790 CDR2 regi
9	81	92.0	17	7	ADJ32094 Human int
10	81	92.0	17	8	ADH89402 Human tra
11	81	92.0	17	8	ADP47199 Human pho
12	81	92.0	17	8	ADG82565 Anti-IL-2
13	81	92.0	17	8	ADG52370 Fab targe
14	81	92.0	17	8	ADG52400 Fab targe
15	81	92.0	17	8	ADG52430 Fab targe
16	81	92.0	17	8	ADG52388 Fab targe
17	81	92.0	17	8	ADG52387 Fab targe
18	81	92.0	17	9	AEA26130 Human SAM
19	81	92.0	17	9	AEA26130 Human SAM
20	81	92.0	17	9	AEA26130 Anti-HAAX
21	81	92.0	17	9	AEA26130 Human CDR
22	81	92.0	17	9	AEA26130 Human CDR
23	81	92.0	17	9	AEA26130 Human CDR
24	81	92.0	17	9	AEA26130 Human CDR

25	81	92.0	41	8	ADR68562 Human EPO
26	81	92.0	66	6	ABU56837 BONT/A Hc
27	81	92.0	66	6	ABU56866 BONT/A Hc
28	81	92.0	82	9	AEA21573 Human Ig
29	81	92.0	83	2	AAW62799 Antio aci
30	81	92.0	95	3	AAW62799 Antio aci
31	81	92.0	98	2	AAW62799 Antio aci
32	81	92.0	98	2	AAW62799 Antio aci
33	81	92.0	98	2	AAW62799 Antio aci
34	81	92.0	98	2	AAW62799 Antio aci
35	81	92.0	98	2	AAW62799 Antio aci
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37	81	92.0	98	2	AAW62799 Antio aci
38	81	92.0	98	2	AAW62799 Antio aci
39	81	92.0	98	2	AAW62799 Antio aci
40	81	92.0	98	2	AAW62799 Antio aci
41	81	92.0	98	2	AAW62799 Antio aci
42	81	92.0	98	2	AAW62799 Antio aci
43	81	92.0	98	2	AAW62799 Antio aci
44	81	92.0	98	2	AAW62799 Antio aci
45	81	92.0	98	2	AAW62799 Antio aci
46	81	92.0	98	2	AAW62799 Antio aci
47	81	92.0	98	2	AAW62799 Antio aci
48	81	92.0	98	2	AAW62799 Antio aci
49	81	92.0	98	2	AAW62799 Antio aci
50	81	92.0	98	2	AAW62799 Antio aci
51	81	92.0	98	2	AAW62799 Antio aci
52	81	92.0	98	2	AAW62799 Antio aci
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68	81	92.0	98	2	AAW62799 Antio aci
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72	81	92.0	98	2	AAW62799 Antio aci
73	81	92.0	98	2	AAW62799 Antio aci
74	81	92.0	98	2	AAW62799 Antio aci
75	81	92.0	98	2	AAW62799 Antio aci
76	81	92.0	98	2	AAW62799 Antio aci
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78	81	92.0	98	2	AAW62799 Antio aci
79	81	92.0	98	2	AAW62799 Antio aci
80	81	92.0	98	2	AAW62799 Antio aci
81	81	92.0	98	2	AAW62799 Antio aci
82	81	92.0	98	2	AAW62799 Antio aci
83	81	92.0	98	2	AAW62799 Antio aci
84	81	92.0	98	2	AAW62799 Antio aci
85	81	92.0	98	2	AAW62799 Antio aci
86	81	92.0	98	2	AAW62799 Antio aci
87	81	92.0	98	2	AAW62799 Antio aci
88	81	92.0	98	2	AAW62799 Antio aci
89	81	92.0	98	2	AAW62799 Antio aci
90	81	92.0	98	2	AAW62799 Antio aci
91	81	92.0	98	2	AAW62799 Antio aci
92	81	92.0	98	2	AAW62799 Antio aci
93	81	92.0	98	2	AAW62799 Antio aci
94	81	92.0	98	2	AAW62799 Antio aci
95	81	92.0	98	2	AAW62799 Antio aci
96	81	92.0	98	2	AAW62799 Antio aci
97	81	92.0	98	2	AAW62799 Antio aci

	81	92.0	113	4	AAU02537	Aau02537 Anti-adip
98	81	92.0	114	6	ABR41816	Ab41816 Heavy cha
99	81	92.0	115	2	AA22571	Aar22571 Heavy cha
100	81	92.0				

ALIGNMENTS

RESULT 1

ID AAU76328 standard; peptide; 17 AA.

AC AAU76328;

DT 21-MAY-2002 (first entry)

DE Human anti-dual integrin antibody heavy chain variable region CDR2.

Human antibody; dual integrin; CDR; heavy chain variable region; HC CDR
 KM medical device; immune related disease; rheumatoid arthritis;
 KM gastric ulcer; asthma; allergic rhinitis; Crohn's pathology;
 KM sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
 KM atherosclerosis; restenosis; angina pectoris; myocardial infarction;
 KM infectious disease; pneumonia; leprosy; malaria; malignant disease;
 KM leukemia; chronic myelocytic leukemia; multiple myeloma;
 KM neurological disease; multiple sclerosis; Parkinson's disease;
 KM Alzheimer's disease; Creutzfeldt-Jakob disease.

OS Homo sapiens.

PN W0200212501-A2.

PD 14-FEB-2002.

PF 07-AUG-2001; 2001WO-US024784.

PR 07-AUG-2000; 2000US-0223363P.

PR 01-AUG-2001; 2001US-00920267.

PA (CENZ) CENTOCOR INC.

PI Gilles-Komar J, Heavenner G, Snyder L, Trikhna M;
...

DR WPI; 2002-217193/27.

DR N-PSDB; ABK10115.

PT Novel isolated mammalian anti-dual integrin antibody, useful for
PT diagnosing or treating dual integrin related condition such as rheumatoid
PT arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

PS Claim 29; Page 133; 144pp; English.

CC The invention relates to an isolated mammalian anti-dual integrin
CC antibody having at least one of the human heavy chain or light chain
CC complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also
CC included are the nucleic acids encoding the CDRs, a vector comprising the
CC nucleic acids, a host cell comprising the vector, an anti-idiotypic
CC antibody that binds to the anti-dual integrin, a medical device comprising
CC the antibody suitable for administration by parenteral, subcutaneous,
CC intramuscular, intravenous, intracuticular, intrabronchial,
CC intraabdominal, intracapsular, intracartilaginous, intracavitary,
CC intraorbital, or other routes as given in specification. The antibody
CC is useful for diagnosing or treating a dual integrin related condition in
CC an animal for example, immune related disease such as Rheumatoid
CC arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology,
CC sickle cell anaemia, diabetes, cardiovascular disease such as
CC arteriosclerosis, atherosclerosis, restenosis, angina pectoris,
CC myocardial infarction, infectious disease in a cell such as bacterial,
CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
CC disease such as leukaemia, chronic myelocytic leukaemia, Burkitt's
CC lymphoma, multiple myeloma; neurological disease such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
CC Creutzfeldt-Jakob disease and many other diseases given in the

CC specification. The present sequence is an anti-dual integrin human heavy
CC chain CDR
XX
SQ Sequence 17 AA;

Query Match	100.0%;	Score 88;	DB 5;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 3.3e-07;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||
Db 1 VISFDGSNKYYVDSVKG 17

RESULT 2
AAU76333

ID AU76333 standard; peptide; 119 AA

AC AAU76333

DT 21-MAY-2002 (first entry)

DE Human anti-dual integrin antibody complete variable region #1.

KM Human; antibody; dual integrin; HC CDR; variable region; LC CDR;
KM gastric device; immune related disease; rheumatoid arthritis;
KM gastric ulcer; asplenia; allergic rhinitis; Crohn's pathology;
KM sickle cell anaemia; diabetes; cardiovascular disease; arteriosclerosis;
KM atherosclerosis; restenosis; angina pectoris; myocardial infarction;
KM infectious disease; pneumonia; leprosy; malaria; malignant disease;
KM leukaemia; chronic myelocytic leukaemia; multiple myeloma;
KM neurological disease; multiple sclerosis; Parkinson's disease;
KM Alzheimer's disease; Creutzfeldt-Jakob disease.

OS Homo sapiens.

PN WO200212501-A2

PD 14-FEB-2002.

PF 07-AUG-2001; 2001WO-US024784.

PR 07-AUG-2000; 2000US-0223363P.

PR 01-AUG-2001; 2001US-00920267.

PA (CENZ) CENTOCOR INC.

PI Giles-Komar J, Heavner G, Snyder L, Trikha M,

DR WPI; 2002-217193/27.

Novel isolated mammalian anti-dual integrin antibody, useful for diagnosing or treating dual integrin related condition such as rheumatoid arthritis, gastric ulcer, asthma, atherosclerosis, restenosis.

PS Claim 1; Page 134; 144pp; English.

The invention relates to an isolated mammalian anti-dual integrin antibody having at least one of the human heavy chain or light chain complementary determining region (CDR, HC CDR1-CDR3, LC CDR1-3). Also included are the nucleic acids encoding the CDRs, a vector comprising the nucleic acids, a host cell comprising the vector, an anti-idiotypic antibody that binds to the anti-dual integrin, a medical device comprising the antibody suitable for administration by parenteral, subcutaneous, intramuscular, intravenous, intracuticular, intrabronchial, intracerebral, intracapsular, intracardial, intracardiac, intracavitary, intracerebellar, or other routes as given in specification. The antibody is useful for diagnosing or treating a dual integrin related condition in an animal for example, immune related disease such as rheumatoid arthritis, gastric ulcer, asthma, allergic rhinitis, Crohn's pathology, sickle cell anaemia, diabetes, cardiovascular disease such as arteriosclerosis, atherosclerosis, retinosis, angina pectoris, myocardial infarction, infectious disease in a cell such as bacterial,

CC viral, and fungal infections, pneumonia, leprosy, malaria; malignant
CC disease such as leukemia, chronic myelocytic leukemia, Burkitt's
CC lymphoma, multiple myeloma; neurological diseases such as multiple
CC sclerosis, Parkinson's disease, spinal ataxia, Alzheimer's disease,
CC Creutzfeldt-Jakob disease and many other diseases given in the
CC specification. The present sequence is an anti-dual integrin human
CC variable region containing at least one of the six CDRs listed above
CC (AAU76327-AAU76332)
CC XX

SQ Sequence 119 AA;

Query Match 100.0%; Score 88; DB 5; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Oy 1 VISFPGSNKYYVDSYVG 17
|||
Db 50 VISFPGSNKYYVDSYVG 66

RESULT 3
ABP45098
ID ABP45098 standard; protein; 249 AA.
XX
AC ABP45098;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1109.
XX
BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CYD; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX MO200202641-A1.
PN 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI, 2002-114799/15.
DR
XX
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 1726-1727; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be

CC	administered to treat diseases associated with aberrant Blys expression
CC	and actively such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g., systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g., common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method of
XX	the invention
XX	
SQ	Sequence 249 AA;
Query Match:	96.6%; Score 85; DB 5; Length 249;
Best Local Similarity	94.1%; Pred. No. 2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0	
Oy	1 VISEFGSNKYYVDSYVK 17 : : :
Db	50 VISYDGSNKYYVDSDYKG 66
RESULT 4	
ID ADG95925	ADG95925 standard; protein; 249 AA.
AC	ADG95925;
XX	
DT	11-MAR-2004 (first entry)
DE	Single chain antibody that immunospecifically binds Blys Segid I109.
XX	
KM	antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM	B cell proliferation; differentiation; scfv; myasthenia gravis;
KW	multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW	carcinoma; lymphoma; antineuritic; antiarthritic; neuroprotective;
KW	antiinflammatory; antisthmatic; antiallergic; cytostatic.
XX	
OS	Unidentified.
XX	
PN	WO2003055979-A2.
XX	
PD	10-JUL-2003.
XX	
PF	14-NOV-2002; 2002WO-US036496.
XX	
PR	16-NOV-2001; 2001US-0331469P.
PR	19-DEC-2001; 2001US-0340817P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX	
DR	WPI; 2003-505530/47.
PT	
PT	Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT	(Blys), useful for detecting and treating diseases or disorders e.g.
PT	rheumatoid arthritis, asthma and leukemia.
XX	
PS	Example 1; SEQ ID NO 1109; 394pp; English.
XX	
CC	This invention relates to novel antibodies that immunospecifically bind
CC	to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC	chromosome 1q34 and encodes a protein that is a member of the tumour
CC	necrosis factor superfamily and induces both in vivo and in vitro B cell
CC	proliferation and differentiation. Specifically, it refers to single
CC	chain antibody molecules (scfvs) derived, preferably, from the variable
CC	heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC	fragment thereof, of either human, murine, rat or monkey Blys. The
CC	present invention refers to the use of such antibodies in various methods
CC	for the detection, diagnosis and prognosis of diseases related to the
CC	aberrant expression or inappropriate function of Blys or its receptor. As
CC	such, these compositions are useful for identifying immune disorders
CC	including myasthenia gravis and multiple sclerosis, inflammatory
CC	disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC	as AIDS and proliferative disorders including leukaemia, carcinoma and

CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antirheumatic, neuroprotective,
 CC antiinflammatory, antiallergic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds BLS of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 249 AA;

Query Match 96.6%; Score 85; DB 7; Length 249;

Best Local Similarity 94.1%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVK 17

Db 50 VISFDGSKKYYVDSVK 66

RESULT 5
 AAM51159

ID AAM51159 standard; peptide; 16 AA.

XX AAM51159;

DT 10-JUN-2002 (first entry)

XX Anti-tumour necrosis factor antibody heavy chain CDR2.

XX Tumour necrosis factor alpha; TNF; antibody; heavy chain; CDR;

XX complementarity determining region; antirheumatic; antiallergic;

XX antilicer; antiallergic; antiallergic; antiallergic; antiallergic;

XX antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;

XX antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;

XX antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;

XX antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-05024785.

XX 07-AUG-2000; 2000US-0223360P.

XX 29-SEP-2000; 2000US-0236826P.

XX 01-AUG-2001; 2001US-00920137.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Heavner G, Scallon B, Shealy D;

XX WPI, 2002-217194/27.

XX N-PSDB; ABL53502.

XX Novel isolated mammalian anti-tumor necrosis factor antibody, useful for

XX treating sickle cell anemia, diabetes, atherosclerosis, restenosis,

XX angina pectoris, myocardial infarction, leprosy.

XX Claim 21; Page 128; 131pp; English.

XX This sequence is that of complementarity determining region 2 (CDR2) of

XX the heavy chain of an anti-tumour necrosis factor (TNF) antibody. The

XX invention provides isolated human, primate, rodent, mammalian, chimeric,

XX humanised and/or CDR-grafted anti-TNF antibodies, immunoglobulins,

XX cleavage products and other specified portions and variants, as well as

XX anti-TNF antibody compositions, encoding or complementary nucleic acids,

XX vectors, host cells, compositions, formulations, devices, transgenic

XX animals, transgenic plants, and methods of making and using them. The

XX anti-TNF antibody comprises at least a portion of an immunoglobulin

XX molecule, especially the heavy chain and/or light chain variable regions

XX given in AAM51165-66, or either all of the CDRs of the heavy chain (see

CC AAM51158-60) or all of the CDRs of the light chain (see AAM51161-63). The

CC antibody may inhibit TNF-induced cell adhesion molecules, inhibit TNF

CC binding to receptor, or provide Arthritis Index improvement in a mouse

CC model. It is useful for diagnosing or treating a TNF related condition in

CC a cell, tissue, organ or animal (claimed) such as rheumatoid arthritis,

CC gastric ulcer, asthma, allergic rhinitis, Crohn's pathology, sickle cell

CC anaemia, diabetes, a cardiovascular disease such as arteriosclerosis,

CC atherosclerosis, restenosis, angina pectoris or myocardial infarction, an

CC infectious disease in a cell such as bacterial, viral, and fungal

CC infections, pneumonia, leprosy and malaria, a malignant disease such as

CC leukemia, chronic myelocytic leukemia, Burkitt's lymphoma and multiple

CC myeloma, or a neurological disease such as multiple sclerosis,

CC Parkinson's disease, spinal ataxia, Alzheimer's disease and Creutzfeldt-

CC Jakob disease

XX Sequence 16 AA;

Query Match 93.2%; Score 82; DB 5; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.9e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVK 16

Db 1 VISFDGSKKYYVDSVK 16

RESULT 6
 AAM90298

ID AAM90298 standard; protein; 17 AA.

XX AAM90298;

DT 07-SEP-1999 (first entry)

XX Human anti-GPIIb/IIIa auto-antibody heavy chain protein CDR2 region 2.

XX Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;

XX blood platelet membrane protein; predisposition; prevention; treatment;

XX autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;

XX thrombocyte; cardiac infarction; pulmonary embolism; heavy chain.

XX Homo sapiens.

XX WO9855619-A1.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-EP003397.

XX 06-JUN-1997; 97DE-01023904.

XX 12-DEC-1997; 97DE-01055227.

XX 08-MAY-1998; 98DE-01020663.

XX (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.

XX Berchtold P, Escher RFA;

XX WPI, 1999-105496/09.

XX Nucleic acid encoding human autoantibodies against platelet glycoprotein

XX IIb/IIIa - used for diagnosis, treatment and prevention of autoimmune

XX thrombocytopenic purpura and for modulation of fibrinogen binding.

XX Claim 3b; Page 5; 93pp; German.

XX This invention describes novel nucleic acid fragments that encode human

XX auto-antibodies and anti-idiotypic antibodies against blood platelet

XX membrane proteins, GPIIb/IIIa. The products of the invention are used for

XX diagnosis (including monitoring and determining predisposition),

XX prevention and treatment of autoimmune thrombocytopenic purpura

XX and also for modulating binding of fibrinogen to thrombocytes

XX (particularly to dissolve thrombi and/or prevent their formation, e.g. in

XX cases of cardiac infarction or pulmonary embolism). Unlike murine

CC antibodies, human antibodies (hAb) do not induce adverse side effects and
CC persist for longer in vivo than small peptides. AAW90293-W90337 represent
CC antibody fragments used in the method of the invention
XX
SQ Sequence 17 AA;
Query Match 92.0%; Score 81; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VISFDGSKNXYVDSYVKG 17
Db 1 VISYDGSNKXYADSVYKG 17
RESULT 7
AAV79074
ID AAV79074 standard; peptide; 17 AA.
XX
AC AAV79074;
XX
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/Xa antibody H chain V domain CDR2 amino acid sequence.
XX
KW Complementarily determining region 2; CDR2; antibody; Gla domain;
KW factor IX/Xa; blood coagulation; deep venous thrombosis;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
PN WO200012562-A1.
XX
PD 09-MAR-2000.
XX
PE 26-AUG-1999; 99WO-US019453.
XX
PR 28-AUG-1998; 98US-0098233P.
PR 03-MAR-1999; 99US-0122767P.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchofer D;
PI Suggest S;
XX
DR WPI; 2000-256595/22.
XX
PT Novel human anti-Factor IX/Xa antibodies against IX/Xa gamma-
PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
PT stroke, and post myocardial infarction.
XX
PS Claim 2; Fig 2; 84pp; English.
XX
CC This sequence represents a complementarily determining region 2 (CDR2) of
CC the heavy chain variable domain of a human anti-factor IX/Xa Gla domain
CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
CC participates in the blood coagulation pathways. The Gla domain of factor
CC IXa and its zymogen factor IX contains important structural determinants
CC for interaction with high affinity binding sites on vascular endothelial
CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

XX
SQ Sequence 17 AA;
Query Match 92.0%; Score 81; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VISFDGSKNXYVDSYVKG 17
Db 1 VISYDGSNKXYADSVYKG 17
RESULT 8
AAO17790
ID AAO17790 standard; peptide; 17 AA.
XX
AC AAO17790;
XX
DT 15-AUG-2002 (first entry)
XX
DE CDR2 region of antibody for glycoprotein IIb/IIIa receptor #2.
XX
KW CDR2; complementarily determining region 2; antibody; metastasis;
KW glycoprotein IIb/IIIa; GPIIb/IIIa; angiogenesis; cancer; cytostatic;
KW antiangiogenic; vasotrophic; intimal hyperplasia; vascular occlusion.
XX
OS Unidentified.
XX
PN DE10057443-A1.
XX
PD 23-MAY-2002.
XX
PE 20-NOV-2000; 2000DE-01057443.
XX
PR 20-NOV-2000; 2000DE-01057443.
XX
PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
XX
PI Peter B, Escher RF;
XX
DR WPI; 2002-472625/51.
XX
PT Use of specific antibodies, or individual chains, for treating tumors and
PT vascular occlusions, by inhibition of the GPIIb/IIIa receptor.
XX
PS Claim 3; Page 9; 10pp; German.
XX
CC The present invention relates to the use of heavy or light chains or
CC their functional derivatives or fragments, having specific CDR
CC (complementarily determining region) sequences of antibodies. The
CC peptides can be used for the combined inhibition of the binding of
CC fibrinogen to thrombocytes and of vitronectin to endothelial cells, the
CC inhibition of angiogenesis, the inhibition of tumor metastasis and/or
CC the inhibition of intimal hyperplasia after vascular injury. They are
CC useful for prevention and treatment of vascular occlusion and for
CC treating tumors. The present sequence is a CDR2 region of the invention
XX
SQ Sequence 17 AA;
Query Match 92.0%; Score 81; DB 5; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VISFDGSKNXYVDSYVKG 17
Db 1 VISYDGSNKXYADSVYKG 17
RESULT 9
ADJ32094
ID ADJ32094 standard; peptide; 17 AA.
XX
AC ADJ32094;

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XX 22-APR-2004 (first entry)
DT Human Interferon-gamma antibody heavy chain CDR2 peptide SeqID48.
XX
DE
XX antibody; antigen binding domain; interferon-gamma; INF-gamma;
KW antagonist antibody; antiinflammatory; immunosuppressive;
KW autoimmune disease; inflammatory condition; human;
KW complementarity determining region; CDR.
XX Homo sapiens.
OS
XX US2003099647-A1.
PN
XX
XX 29-MAY-2003.
PD
XX
XX 05-OCT-2001, 2001US-00972656.
PP
XX
XX 05-OCT-2001, 2001US-00972656.
PR
XX
XX (DESH/) DESHPANDE R V.
PA (TSAI/) TSAI M.
PA
XX Deshpande RV, Tsai M;
PI
XX WPI; 2003-696068/66.
DR
XX
XX New antibody or antigen binding domain, or its fragment, variant or
PT derivative, which binds to an interferon-gamma protein, useful for
PT preparing a composition for preventing or treating inflammatory or
PT autoimmune disorders.
XX
XX Claim 14; SEQ ID NO 48; 113pp; English.
PS
XX This invention relates to a novel antibody or antigen binding domain, or
CC its fragment, variant or derivative, which binds to an interferon-gamma
CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
CC useful for the development of compounds with an antiinflammatory or
CC immunosuppressive activity through action as interferon-gamma agonists. A
CC composition containing the antibody is useful for preventing or treating
CC an autoimmune disease and an inflammatory condition. The present sequence
CC is that of a peptide which represents a complementarity determining
CC region (CDR) of a human INF-gamma antibody which may be part of the
CC invention.
XX
XX Sequence 17 AA:
SQ
Query Match 92.0%; Score 81; DB 7; Length 17;
Best Local Similarity 88.2%; Pred. No. 4,5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

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OS Unidentified.
XX
XX US2003226155-A1.
PN
XX
XX 04-DEC-2003.
PD
XX
XX 10-MAR-2003; 2003US-00384060.
PF
XX
XX 30-AUG-2001; 2001US-0315745P.
PR 30-NOV-2001; 2001US-0334059P.
PR 30-AUG-2002; 2002US-00231494.
PR 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
PA
XX
XX Sadeghi H, Prior CP, Turner A;
PI
XX WPI; 2004-022093/02.
DR
XX
XX New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.
XX
XX Example 2; SEQ ID NO 46; 82pp; English.
PS
XX
XX This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndromes associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a CDR 2 peptide which was used in the exemplification
CC of the invention.
XX
XX Sequence 17 AA:
SQ
Query Match 92.0%; Score 81; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 4,5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

```

PF 02-DEC-2003; 2003WO-US038234.
 XX
 PR 02-DEC-2002; 2002US-0430724P.
 XX
 PA (ABGE-) ABGENIX INC.
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Landes GM, Haak-Frendocho M, Chen L, Lee YR, Liang ML, Feng X;
 PI Jia X, Nocerini MR;
 XX
 DR WPI; 2004-461119/43.
 XX
 PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX
 PS Example 5; SEQ ID NO 114; 128bp; English.
 XX
 CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC amino acid sequence represents a human PLA2-specific monoclonal antibody
 CC heavy chain peptide.
 XX
 SQ Sequence 17 AA;
 Query Match 92.0%; Score 81; DB 8; Length 17;
 Best Local Similarity 88.2%; Pred. No. 4.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKRYVDSVKG 17
 Db 1 VISDGSNKRYADSVKG 17
 DE
 RESULT 12
 ADS82565
 ID ADS82565 standard; peptide: 17 AA.
 XX
 AC ADS82565;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Anti-IL-21R antibody M011 H2 CDR, SEQ ID 23.
 XX
 KW Immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
 KW Antiinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy;
 KW antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21;
 KW IL-21R; autoimmune disorder; Rheumatoid arthritis;
 KW inflammatory bowel disease; Crohn's disease; transplant rejection;
 KW psoriasis; hyperproliferative disorder; M011;
 KW complementarity determining region; CDR; heavy chain; H2 CDR.
 XX
 OS Homo sapiens.
 XX
 PN WO2004083249-A2.
 XX
 PD 30-SEP-2004.
 XX
 PF 12-MAR-2004; 2004WO-US007444.
 XX
 PR 14-MAR-2003; 2003US-0454336P.
 XX
 PA (AMHP) WYETH.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Young DA, Whiters MJ, Valge-Archer V, Collins M, Williams AJ;
 PI Witek J;
 XX
 DR WPI; 2004-691025/67.

DR N-PSDB; ADS82574.
 XX
 PT New human antibodies that selectively bind to human interleukin-21
 PT receptor, useful for diagnosing, preventing or treating autoimmune
 PT disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.
 XX
 PS Claim 4; SEQ ID NO 23; 143bp; English.
 XX
 CC The present invention relates to human antibodies, or their antigen-
 CC binding fragments, that selectively bind to a human interleukin-21
 CC receptor (IL-21R). The antibodies of the invention are referred to as
 CC M0F, M0F-germline, M011, 18G4, 18A5, 19F5, GP5G2 and R18. The antibodies
 CC selectively bind the extracellular domain of human IL-21R, or inhibit the
 CC binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an
 CC antibody or fragment of the invention are useful for diagnosing,
 CC preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
 CC inflammatory bowel disease, Crohn's disease, transplant rejection or
 CC psoriasis) or hyperproliferative disorders. The present sequence is an
 CC anti-IL-21R antibody heavy chain complementarity determining region of
 CC the invention.
 XX
 SQ Sequence 17 AA;
 Query Match 92.0%; Score 81; DB 8; Length 17;
 Best Local Similarity 88.2%; Pred. No. 4.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKRYVDSVKG 17
 Db 1 VISDGSNKRYADSVKG 17
 DE
 RESULT 13
 ADS52370
 ID ADS52370 standard; peptide: 17 AA.
 XX
 AC ADS52370;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Fab targeting HLA-A2/Tax11-19, T3F2, heavy chain CDR 2.
 XX
 KW Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KW major histocompatibility complex; MHC class I; viral infection;
 KW human T lymphotropic virus-1 infection; viral oncoprotein;
 KW mycoplasma infection; bacterial infection; fungal infection;
 KW protozoal infection; phage display; heavy chain; CDR;
 KW complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 PN US2004191260-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 26-MAR-2003; 2003US-00396578.
 XX
 PR 26-MAR-2003; 2003US-00396578.
 XX
 PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 PI Reiter Y, Cohen C;
 XX
 DR WPI; 2004-735863/72.
 XX
 PT New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 XX
 PS Claim 5; SEQ ID NO 21, 68bp; English.
 XX
 CC The invention relates to a composition-of-matter comprising (a multimeric

form of an antibody or antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. Also included are an isolated polynucleotide comprising a nucleic acid sequence encoding an antibody fragment (the antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen), a nucleic acid construct comprising the isolated polynucleotide above (and a promoter sequence for directing transcription of the isolated polynucleotide in a host cell), a host cell comprising the nucleic acid construct above, a host virus comprising the nucleic acid construct above, a virus comprising a coat protein fused to the antibody fragment, detecting an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen, a method of diagnosing an infection by a pathogen in an individual, a method of killing or damaging a target cell expressing/displaying an antigen-presenting portion of a complex (composed of a human antigen-presenting molecule and an antigen derived from a pathogen) and a method of detecting in a biological sample an antigen-presenting portion of a complex as described above. The target cell is a T lymphocyte or an antigen-presenting cell, which is a B cell or a dendritic cell. The composition-of-matter further comprises a detectable moiety attached to the antibody or antibody fragment. The detectable moiety is a recognition sequence of a biotin protein ligase, a biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a polyclastine tag. The biotin protein ligase is BirA, the fluorophore is phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is pseudomonas exotoxin A or its portion, which is a translocation domain and/or an ADP ribosylation domain. The human antigen-presenting molecule is a major histocompatibility complex (MHC), preferably MHC class I molecule, more preferably HLA-A2 molecule. The pathogen is viral, preferably a retrovirus, more preferably human T lymphotropic virus-1. The antigen derived from a pathogen is restricted by the antigen-presenting molecule and is a polypeptide selected from a segment of a viral oncoprotein or a segment of a tax protein. A pharmaceutical composition comprising an active ingredient the composition-of-matter is useful in a method for treating a disease associated with a pathogen in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and protozoans. The composition-of-matter or the methods are useful for diagnosing an infection by a pathogen in an individual and for killing or damaging a target cell expressing or displaying an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. A phage displayed library of human Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated and tested for specific binding to HLA-A2/Tax 11-19, individual clones were then sequenced and their CDR (complementarity determining region) sequences compared. The present sequence is a CDR from the heavy chain of an isolated Fab clone.

Sequence 17 AA;

Query Match	92.0%	Score 81	DB 8	Length 17
Best Local Similarly	89.2%	Pred. NO.	4.5e-06	
Matches 15; Conservative		1; Mismatches	1; Indels	0; Gaps

QY	1	VISFDGSNKYYVDSVKG	17
		:	
Db	1	VISYDGSNKYYADSVKG	17

RESULT	14
ADSS52400	
ID	ADSS52400 standard, peptide, 17 AA.
XX	
AC	ADSS52400;
XX	
DT	16-DEC-2004 (first entry)
XX	
DE	Fab targeting HLA-A2/Tax11-19, T2G7, heavy chain CDR 2.
XX	
XX	Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen; T lymphocyte; antigen-presenting cell; B cell; dendritic cell;

KM major histocompatibility complex; MHC class I; viral infection
KM human T lymphotropic virus-1 infection; viral oncoprotein;
KM mycoplasma infection; bacterial infection; fungal infection;
KM protozoal infection; plaque display; heavy chain; CDR;
KM complementarity determining region.

Homo sapiens.

PN US2004191260-A1.

PD 30-SEP-2004

PF 26-MAR-2003; 2003US-00396578.

PR 26-MAR-2003; 2003US-00396578.

PA (TECR) TECHNION RES & DEV FOUND LTD.

PI Reiter Y, Cohen C;

DR WPI; 2004-735863/72.

PT New composition comprising a multimeric form of an antibody or fragment

PT useful for treating pathogen-associated diseases e.g., HIV.

PS Claim 5; SEQ ID NO 51; 68bp; English.

CC The invention relates to a composition

The invention relates to a composition-of-matter comprising (a multimeric form of) an antibody or antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. Also included are an isolated polynucleotide comprising a nucleic acid sequence encoding an antibody fragment (the antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen), a nucleic acid construct comprising the isolated polynucleotide above (and a promoter sequence for directing transcription of the isolated polynucleotide in a host cell), a host cell comprising the nucleic acid construct above, a host virus comprising the nucleic acid construct above, a virus comprising a coat protein fused to the antibody fragment, detecting an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen, a method of diagnosing an infection by a pathogen in an individual, a method of killing or damaging a target cell expressing/displaying an antigen-presenting portion of a complex (composed of a human antigen-presenting molecule and an antigen derived from a pathogen) and a method of detecting in a biological sample an antigen-presenting portion of a complex as described above. The target cell is a T lymphocyte or an antigen-presenting cell, which is a B cell or a dendritic cell. The composition-of-matter further comprises a detectable moiety attached to the antibody or antibody fragment. The detectable moiety is a recognition sequence of a biotin protein ligase, a biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a polynucleotide tag. The biotin protein ligase is BirA, the fluorophore is phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is pseudomonas exotoxin A or its portion, which is a translocation domain and/or an ADP ribosylation domain. The human antigen-presenting molecule is a major histocompatibility complex (MHC), preferably MHC class I molecule, more preferably HLA-A2 molecule. The pathogen is viral, preferably a retrovirus, more preferably human T lymphotropic virus-1. The antigen derived from a pathogen is restricted by the antigen-presenting molecule and is a polypeptide selected from a segment of a viral oncoprotein or a segment of a tax protein. A pharmaceutical composition comprising as an active ingredient the composition-of-matter is useful in a method for treating a disease associated with a pathogen in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and protozoans. The composition-of-matter or the methods are useful for diagnosing an infection by a pathogen in an individual and for killing or damaging a target cell expressing or displaying an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. A phage displayed library of human

CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC sequences compared. The present sequence is a CDR from the heavy chain of
 CC an isolated Fab clone.
 XX
 SQ Sequence 17 AA;
 Query Match 92.0%; Score 81; DB 8; Length 17;
 Best Local Similarity 88.2%; Pred. No. 4.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VISFDGSKNYVDVSKG 17
 |||:|||||
 Db 1 VISYDGSNKYYADSVKG 17
 |||:|||||
 RESULT 15
 ADS52430
 ID ADS52430 standard; peptide; 17 AA.
 XX
 AC ADS52430;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Fab targeting HLA-A2/Tax11-19, T4B7, heavy chain CDR 2.
 XX
 KM Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KM T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KM major histocompatibility complex; MHC class I; viral infection;
 KM human T lymphotropic virus-1 infection; viral oncoprotein;
 KM mycoplasma infection; bacterial infection; fungal infection;
 KM protozoal infection; phase display; heavy chain; CDR;
 KM complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 PN US2004191260-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 26-MAR-2003; 2003US-00396578.
 XX
 PR 26-MAR-2003; 2003US-00396578.
 XX
 PA (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 PI Reiter Y, Cohen C;
 XX
 DR WPI; 2004-735863/72.
 XX
 PT New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 PS Claim 5; SEQ ID NO 81; 68pp; English.
 XX
 CC The invention relates to a composition-of-matter comprising (a multimeric
 CC form of) an antibody or antibody fragment including an antigen-binding
 CC region capable of specifically binding an antigen-presenting portion of a
 CC complex composed of a human antigen-presenting molecule and an antigen
 CC derived from a pathogen. Also included are an isolated polynucleotide
 CC comprising a nucleic acid sequence encoding an antibody fragment (the
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule and an antigen derived from a
 CC pathogen), a nucleic acid construct comprising the isolated
 CC polynucleotide above (and a promoter sequence for directing transcription
 CC of the isolated polynucleotide in a host cell), a host cell comprising
 CC the nucleic acid construct above, a host virus comprising the nucleic
 CC acid construct above, a virus comprising a coat protein fused to the
 CC antibody fragment, detecting an antigen-presenting portion of a complex
 CC composed of a human antigen-presenting molecule and an antigen derived

CC from a pathogen, a method of diagnosing an infection by a pathogen in an
 CC individual, a method of killing or damaging a target cell
 CC expressing/displaying an antigen-presenting portion of a complex
 CC (composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC detectable moiety is a recognition sequence of a biotin protein ligase, a
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP-ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
 CC The antigen derived from a pathogen is restricted by the antigen-
 CC presenting molecule and is a polypeptide selected from a segment of a
 CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
 CC composition comprising as an active ingredient the composition-of-matter
 CC is useful in a method for treating a disease associated with a pathogen
 CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
 CC protozoans. The composition-of-matter or the methods are useful for
 CC diagnosing an infection by a pathogen in an individual and for killing or
 CC damaging a target cell expressing or displaying an antigen-presenting
 CC portion of a complex composed of a human antigen-presenting molecule and
 CC an antigen derived from a pathogen. A phage displayed library of human
 CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC sequences compared. The present sequence is a CDR from the heavy chain of
 CC an isolated Fab clone.
 XX
 SQ Sequence 17 AA;
 Query Match 92.0%; Score 81; DB 8; Length 17;
 Best Local Similarity 88.2%; Pred. No. 4.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VISFDGSKNYVDVSKG 17
 |||:|||||
 Db 1 VISYDGSNKYYADSVKG 17
 |||:|||||
 RESULT 16
 ADS52388
 ID ADS52388 standard; peptide; 17 AA.
 XX
 AC ADS52388;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Fab targeting HLA-A2/Tax11-19, T3D1, heavy chain CDR 2.
 XX
 KM Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KM T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KM major histocompatibility complex; MHC class I; viral infection;
 KM human T lymphotropic virus-1 infection; viral oncoprotein;
 KM mycoplasma infection; bacterial infection; fungal infection;
 KM protozoal infection; phase display; heavy chain; CDR;
 KM complementarity determining region.
 XX
 OS Homo sapiens.
 XX
 PN US2004191260-A1.
 XX
 PD 30-SEP-2004.
 XX
 PF 26-MAR-2003; 2003US-00396578.
 XX
 PR 26-MAR-2003; 2003US-00396578.

XX (TECR) TECHNION RES & DEV FOUND LTD.
 XX
 XX Reiter Y, Cohen C;
 XX
 XX WPI, 2004-735863/72.
 XX
 XX
 XX New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 XX
 XX Claim 5, SEQ ID NO 39, 68bp, English.
 XX
 XX The invention relates to a composition-of-matter comprising (a multimeric
 CC form of) an antibody or antibody fragment including an antigen-binding
 CC region capable of specifically binding an antigen-presenting portion of a
 CC complex composed of a human antigen-presenting molecule and an antigen
 CC derived from a pathogen. Also included are an isolated polynucleotide
 CC comprising a nucleic acid sequence encoding an antibody fragment (the
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule and an antigen derived from a
 CC pathogen), a nucleic acid construct comprising the isolated
 CC polynucleotide above (and a promoter sequence for directing transcription
 CC of the isolated polynucleotide in a host cell), a host cell comprising
 CC the nucleic acid construct above, a host virus comprising the nucleic
 CC acid construct above, a virus comprising a coat protein fused to the
 CC antibody fragment, detecting an antigen-presenting portion of a complex
 CC composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen, a method of diagnosing an infection by a pathogen in an
 CC individual, a method of killing or damaging a target cell
 CC expressing/displaying an antigen-presenting portion of a complex
 CC (composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC detectable moiety is a recognition sequence of a biotin protein ligase, a
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC Pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
 CC The antigen derived from a pathogen is restricted by the antigen-
 CC presenting molecule and is a polypeptide selected from a segment of a
 CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
 CC composition comprising as an active ingredient the composition-of-matter
 CC is useful in a method for treating a disease associated with a pathogen
 CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
 CC protozoans. The composition-of-matter or the methods are useful for
 CC diagnosing an infection by a pathogen in an individual and for killing or
 CC damaging a target cell expressing or displaying an antigen-presenting
 CC portion of a complex composed of a human antigen-presenting molecule and
 CC an antigen derived from a pathogen. A phage displayed library of human
 CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC sequences compared. The present sequence is a CDR from the heavy chain of
 CC an isolated Fab clone.
 XX
 XX Sequence 17 AA,
 SQ
 Query Match 92.0%, Score 81, DB 8, Length 17;
 Best Local Similarity 88.2%, Pred. No. 4.5e-06;
 Matches 15, Conservative 1, Mismatches 1, Indels 0; Gaps 0;
 QY 1 VISFDGSKNKRYVDSVKG 17
 |||:|||||
 Db 1 VISYDGSNKYVDSVKG 17

RESULT 17
 ADV21297
 ID ADV21297 standard; peptide; 17 AA.
 XX
 XX ADV21297,
 AC
 XX 24-FEB-2005 (first entry)
 DT
 XX
 XX Human antibody VH domain CDR2 SEQ ID No:6.
 DE
 XX
 XX Antibody engineering; binding molecule; antibody; humanized antibody;
 KW proliferative disorder; tumor; inflammation; immune disorder;
 KW autoimmune disease; infectious disease; viral infection; infection;
 KW allergy; parasitic reaction; graft versus host disease; cytostatic;
 KW antiinflammatory; immunosuppressive; antimicrobial; vitruicide;
 KW antiallergic; antiparasitic; heavy chain variable region; VH;
 KW complementarity determining region; CDR.
 XX
 XX Homo sapiens.
 OS
 XX
 XX NO2004106380-A2.
 PN
 XX 09-DEC-2004.
 PD
 XX 26-MAY-2004; 2004WO-EP005684.
 PF
 XX 31-MAY-2003; 2003EP-00012132.
 PR
 XX (MICR-) MICROMET AG.
 PA
 XX Kifer P, Raum T, Berry M, Kischel R, Mangold S, Krinner E;
 PI Kohlisen B, Zeman S, Itin C, Baeuerle P;
 DR N-PSDB; ADV21296.
 XX
 XX Preparing human binding molecule specifically binding to human CD3
 PT complex, comprises selecting molecules specifically binding to
 PT extracellular domain of recombinant epsilon-chain and preparing
 PT identified selected binding molecule.
 PT
 XX
 XX Claim 27, SEQ ID NO 6; 350bp; English.
 PS
 XX The invention relates to a method of preparing a human binding molecule,
 CC fragment or its derivative which specifically binds to the human CD3
 CC complex. The method comprises selecting molecules specifically binding to
 CC or interacting with the extracellular domain of recombinant epsilon-chain
 CC expressed independent of the human CD3 complex in the absence of other
 CC members of the CD3 complex, from a population of candidate polypeptides
 CC encoded by a library, selecting molecules from a population identified in
 CC the above step for binding to the human CD3 complex, and preparing the
 CC selected binding molecule. The binding molecule is an antibody molecule,
 CC antibody fragment or its derivative or an antibody construct. Also
 CC disclosed is a nucleic acid sequence encoding a human binding molecule, a
 CC vector comprising such a nucleic acid, a host transformed or transfected
 CC with such a vector, a composition comprising a human binding molecule,
 CC and optionally a proteaceous compound capable of providing an
 CC activation signal for immune effector cells, and a kit comprising a human
 CC binding molecule. The method further involves recombinant expression of
 CC the binding molecule, fragment or its derivative encoded by a nucleic
 CC acid sequence chosen from the identified nucleic acid sequence, a nucleic
 CC acid sequence hybridizing with the complementary strand of the identified
 CC nucleic acid sequence under stringent hybridization conditions, and a
 CC nucleic acid sequence which is degenerate as a result of the genetic code
 CC to the above mentioned nucleotide sequences. The antibody molecule,
 CC antibody fragment or its derivative or construct comprises a further
 CC antigen-interaction-site and/or a further effector domain, and is
 CC humanized and/or deimmunized in an additional step. The further antigen-
 CC interaction-site is specific for one or more cell surface molecule such
 CC as a tumor specific marker. The antigen-interaction-site is further scFv,
 CC which specifically binds to or interacts with an antigen chosen from

CC EPCAM, CCR5, CD19, EphA2, HER-2 neu, HER-3, HER-4, EGFR, PSMA, CEA, MUC-1
 CC (mucin), MUC2, MUC3, MUC4, MUC5AC, MUC5B, MUC7, betahCG, Lewis Y, CD20,
 CC CD33, CD30, ganglioside GD3, 9-O-Acetyl-GD3, GM2, Globo H, fucoseyl GM1,
 CC Poly S, GD2, carboanhydrase IX (NN/CA IX), CD44v6, Sonic hedgehog (Shh),
 CC Mu-1, plasma cell antigen, (membrane-bound) IGE, melanoma chondroitin
 CC sulfate proteoglycan (MSP), CCR8, TNF-alpha precursor, STEAP,
 CC mesothelin, A3 antigen, prostate stem cell antigen (PSCA), Ly-6,
 CC desmoglein 4, E-cadherin neoptope, fetal acetylcholine receptor, CD25,
 CC CA19-9 marker, CA-125 marker and muellerian inhibitory substance (MIS)
 CC receptor type II, sTN (stallated Tn antigen: TAG-72), PAP (fibroblast
 CC activated antigen), endostatin, EGFRvIII, LG, SAS and CD63. In a human
 CC binding molecule, the antibody molecule, antibody fragment or its
 CC derivative or an antibody construct, comprises a heavy chain variable
 CC (VH) region, a light chain variable (VL) region, complementarily
 CC determining regions 1-3 (CDR1-3) of a VH-region, and CDR1-3 of a VL-
 CC region. The method is useful for preparing a human binding molecule,
 CC fragment or its derivative which specifically binds to the human CD3
 CC complex. The human binding molecule polypeptide sequences, and the
 CC polynucleotide sequences encoding them are useful for the prevention,
 CC treatment or amelioration of proliferative disease, tumorous disease,
 CC inflammatory disease, immunological disorder, autoimmune disease,
 CC infectious disease, viral disease, allergic reactions, parasitic
 CC reactions, graft-versus-host diseases or host-versus-graft diseases, or
 CC for preparation of a pharmaceutical composition for the prevention,
 CC treatment or amelioration of the above mentioned diseases. This sequence
 CC represents a CDR region of a human antibody.

Sequence 17 AA;

Query Match 92.0%; Score 81; DB 9; Length 17;
 Best Local Similarity 88.2%; Pred. No. 4.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSYKG 17
 |||:|||||
 Db 1 VISYDGSNKKYYADSVKG 17

RESULT 18
 AEA26130
 ID AEA26130 standard; peptide; 17 AA.

AC AEA26130;

DT 11-AUG-2005 (first entry)

DE Human SAM-6 antibody heavy chain CDR2 peptide.

KW monoclonal antibody; antilipemic; nephrotoxic; antiarteriosclerotic;

KW cardiant; anticholesterclemic; cholesterol; pharmaceutical;

KW myocardial infarction; renal disease; blood; SAM-6.

OS Homo sapiens.

PN WO2005049635-A2.

PD 02-JUN-2005.

PR 12-NOV-2004; 2004WO-DE002503.

PR 14-NOV-2003; 2003DE-01053175.

PA (VOL/L) VOLLMERS P.

PI Vollmers P;

DR WPI; 2005-417682/42.

PT New polypeptides that bind low density lipoprotein and its oxidized
 PT forms, useful as antilipemic agents and for treating kidney disease, are
 PT human monoclonal antibodies.
 PS Claim 17; Page 28; 42pp; German.

XX This invention relates to a novel human monoclonal antibody having a fat-
 CC reducing effect. The invention may be useful for the development of
 CC compounds with an antilipemic, nephrotoxic, antiarteriosclerotic or
 CC cardiant activity acting by binding to (oxidized) low density
 CC lipoprotein, so functioning in a manner analogous to the known scavenger
 CC pathway. The invention is useful as a hypolipemic agent, for reducing the
 CC level of (oxidized) low density lipoprotein, especially cholesterol, in
 CC the blood, for example for treating arteriosclerosis (and its sequelae
 CC such as cardiac infarct) and for treating kidney disease, particularly
 CC glomerulonecrosis. The antibody of the invention avoids the side effects
 CC associated with use of inhibitors of key enzymes in cholesterol
 CC biosynthesis. The present sequence is that of a CDR peptide derived from
 CC the heavy chain of the human SAM-6 antibody of the invention.

Sequence 17 AA;

Query Match 92.0%; Score 81; DB 9; Length 17;
 Best Local Similarity 88.2%; Pred. No. 4.5e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSYKG 17
 |||:|||||
 Db 1 VISYDGSNKKYYADSVKG 17

RESULT 19

AEA24391
 ID AEA24391 standard; peptide; 17 AA.

AC AEA24391;

DT 11-AUG-2005 (first entry)

DE Anti-HAAN antibody complementarity determining region (CDR) #65.

KW Antibody therapy; aspartyl (asparaginy1) beta-hydroxylase; AAH; HAAN;

KW cancer; neoplasm; lung tumor; liver tumor; colon tumor; pancreas tumor;

KW prostate tumor; ovary tumor; brain tumor; breast tumor; cytostatic;

KW antibody.

OS Homo sapiens.

PN WO2005049802-A2.

PD 02-JUN-2005.

PR 15-NOV-2004; 2004WO-US038197.

PR 14-NOV-2003; 2003US-0520114P.

PR 19-APR-2004; 2004US-0563514P.

PA (MAST) MASSACHUSETTS INST TECHNOLOGY.

PI Wittrup DK, Yeung YA;

DR WPI; 2005-417726/42.

PT New composition comprising anti-hydroxylase antibodies, useful for

PT diagnosing or treating cancer, e.g. lung, liver, colon, pancreas,

PT prostate, ovary, bile duct, brain, or breast cancer.

PS Claim 11; SEQ ID NO 311; 107pp; English.

CC The invention relates to a composition comprising an isolated human
 CC antibody or its fragment or other variant, where the antibody, the
 CC fragment or the other variant specifically binds to an aspartyl
 CC (asparaginy1) beta-hydroxylase (AAH). The invention also relates to an
 CC isolated nucleic acid molecule comprising a sequence encoding a human
 CC antibody or its fragment or other variant, where the antibody, the
 CC fragment or the other variant specifically binds to human AAH (HAAN), an
 CC expression vector comprising the nucleic acid molecule, a host cell
 CC comprising the expression vector, a method of modulating an AAH activity

CC in a cell, a method of treating a patient who has a cancer associated
CC with overactive or over expressed AAH, a method for identifying an
CC antibody or its fragment or other variant that specifically binds to an
CC AAH and a method of making a human monoclonal antibody or its fragment or
CC other variant that specifically binds to an AAH. The composition,
CC antibody, nucleic acid, kit and methods are useful for diagnosing or
CC treating cancer, where the cancer cell is a tumor cell of the lung,
CC liver, colon, pancreas, prostate, ovary, bile duct, brain or breast. This
CC sequence represents an anti-AAH antibody complementarity determining
CC region (CDR) used in the scope of the invention.

XX
SQ Sequence 17 AA;

Query Match 92.0%; Score 81; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYYTDSVKG 17

RESULT 20
AEB28725

ID AEB28725 standard; peptide; 17 AA.

XX
AC AEB28725;XX
DT 22-SEP-2005 (first entry)XX
DE Human CDR2 of T2G7 Fab specifically binding HLA-A2/Tax11-19, SEQ: 51.XX
KM Diagnosis; therapeutic; infection; antimicrobial; heavy chain; T2G7.XX
OS Homo sapiens.XX
PN US2005152912-A1.XX
PD 14-JUL-2005.XX
PF 09-MAR-2005; 2005US-00074803.XX
PR 26-MAR-2003; 2003US-00396578.XX
PA (TECR) TECHNION RES & DEV FOUND LTD.XX
PI Reiter Y, Cohen C;XX
DR WPI; 2005-496781/50.

XX
PT New composition-of-matter capable of specifically binding an antigen-
PT presenting molecule and a pathogen-derived antigen complexes, useful for
PT treating diseases associated with a pathogen.

XX
PS Claim 5; SEQ ID NO 51; 65bp; English.

XX
CC The present invention relates to a composition-of-matter which comprises
CC an antibody or antibody fragment or a multimeric form of an antibody or
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule (APM) and an antigen derived from
CC a pathogen. The invention is useful for the specific detection of the
CC antigen-presenting portion of the complex and for diagnosing/treating
CC various types of diseases associated with a pathogen infection by
CC killing/damaging pathogen infected cells. The present sequence is a
CC complementarity determining regions (CDR) of Fab heavy chain antibody
CC specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex.
CC Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-
CC 1).

XX
SQ Sequence 17 AA;

Query Match 92.0%; Score 81; DB 9; Length 17;

Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYYTDSVKG 17

RESULT 21

AEB28713

ID AEB28713 standard; peptide; 17 AA.

XX
AC AEB28713;XX
DT 22-SEP-2005 (first entry)XX
DE Human CDR2 of T3D1 Fab specifically binding HLA-A2/Tax11-19, SEQ: 39.XX
KM Diagnosis; therapeutic; infection; antimicrobial; heavy chain; T3D1.XX
OS Homo sapiens.XX
PN US2005152912-A1.XX
PD 14-JUL-2005.XX
PF 09-MAR-2005; 2005US-00074803.XX
PR 26-MAR-2003; 2003US-00396578.XX
PA (TECR) TECHNION RES & DEV FOUND LTD.XX
PI Reiter Y, Cohen C;XX
DR WPI; 2005-496781/50.

XX
PT New composition-of-matter capable of specifically binding an antigen-
PT presenting molecule and a pathogen-derived antigen complexes, useful for
PT treating diseases associated with a pathogen.

XX
PS Claim 5; SEQ ID NO 39; 65bp; English.

XX
CC The present invention relates to a composition-of-matter which comprises
CC an antibody or antibody fragment or a multimeric form of an antibody or
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule (APM) and an antigen derived from
CC a pathogen. The invention is useful for the specific detection of the
CC antigen-presenting portion of the complex and for diagnosing/treating
CC various types of diseases associated with a pathogen infection by
CC killing/damaging pathogen infected cells. The present sequence is a
CC complementarity determining regions (CDR) of Fab heavy chain antibody
CC specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex.
CC Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-
CC 1).

XX
SQ Sequence 17 AA;

Query Match 92.0%; Score 81; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYYTDSVKG 17

RESULT 22

AEB28695

ID AEB28695 standard; peptide; 17 AA.

XX
AC AEB28695;

XX

DT 22-SEP-2005 (first entry)
XX Human CDR2 of T3F2 Fab specifically binding HLA-A2/Tax11-19, SEQ: 21.
DE
XX
XX Diagnosis; therapeutic; infection; antimicrobial; heavy chain; T3F2.
XX
OS Homo sapiens.
XX
XX US2005152912-A1.
XX
XX 14-JUL-2005.
XX
XX 09-MAR-2005; 2005US-00074803.
XX
XX 26-MAR-2003; 2003US-00396578.
XX
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX Reiter Y, Cohen C;
XX
XX MPI, 2005-496781/50.
XX
XX
XX New composition-of-matter capable of specifically binding an antigen-
PT presenting molecule and a pathogen-derived antigen complexes, useful for
PT treating diseases associated with a pathogen.
XX
XX Claim 5; SEQ ID NO 21; 65pp; English.
XX
XX The present invention relates to a composition-of-matter which comprises
CC an antibody or antibody fragment or a multimeric form of an antibody or
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule (APM) and an antigen derived from
CC a pathogen. The invention is useful for the specific detection of the
CC antigen-presenting portion of the complex and for diagnosing/treating
CC various types of diseases associated with a pathogen infection by
CC killing/damaging pathogen infected cells. The present sequence is a
CC complementarity determining regions (CDR) of Fab heavy chain antibody
CC specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex.
CC Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-
CC 1).
XX
XX Sequence 17 AA:
SQ
Query Match 92.0%; Score 81; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VISFDGSKNYVDVSVKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 23
AEB28755
ID AEB28755 standard; peptide; 17 AA.
XX
XX AEB28755;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human CDR2 of T4B7 Fab specifically binding HLA-A2/Tax11-19, SEQ: 81.
XX
XX Diagnosis; therapeutic; infection; antimicrobial; heavy chain; T4B7.
XX
XX Homo sapiens.
OS
XX
XX US2005152912-A1.
XX
XX 14-JUL-2005.
XX
XX 09-MAR-2005; 2005US-00074803.
XX
XX

PR 26-MAR-2003; 2003US-00396578.
XX
XX (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX Reiter Y, Cohen C;
XX
XX MPI, 2005-496781/50.
XX
XX
XX New composition-of-matter capable of specifically binding an antigen-
PT presenting molecule and a pathogen-derived antigen complexes, useful for
PT treating diseases associated with a pathogen.
XX
XX Claim 5; SEQ ID NO 81; 65pp; English.
XX
XX The present invention relates to a composition-of-matter which comprises
CC an antibody or antibody fragment or a multimeric form of an antibody or
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule (APM) and an antigen derived from
CC a pathogen. The invention is useful for the specific detection of the
CC antigen-presenting portion of the complex and for diagnosing/treating
CC various types of diseases associated with a pathogen infection by
CC killing/damaging pathogen infected cells. The present sequence is a
CC complementarity determining regions (CDR) of Fab heavy chain antibody
CC specifically binding human leukocyte antigen (HLA-A2)/Tax11-19 complex.
CC Tax11-19 is an antigen derived from Human T-lymphotropic virus 1 (HTLV-
CC 1).
XX
XX Sequence 17 AA:
SQ
Query Match 92.0%; Score 81; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VISFDGSKNYVDVSVKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 24
ADS84420
ID ADS84420 standard; protein; 41 AA.
XX
XX ADS84420;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human anti-EPO-R antibody heavy chain variable region CDR SEQ ID NO:59.
DE
XX human; erythropoietin receptor; EPO receptor;
KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
KW antianemic; neutroprotective; vulnerary; gene therapy; aplasia; anaemia;
KW wound healing; neural cell damage protection;
KW neural tissue damage protection; brain injury; spinal cord injury;
KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody;
KW complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX
XX WO2004035603-A2.
XX
XX 29-APR-2004.
XX
XX 14-OCT-2003; 2003WO-US032243.
XX
XX 14-OCT-2002; 2002US-00269711.
XX
XX 10-OCT-2003; 2003US-00684109.
XX
XX (ABBO) ABBOTT LAB.
XX
XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wielez J;
PI MPI; 2004-348433/32.
XX
XX

XX New antibodies that bind to or activate an endogenous human
PT erythropoietin receptor, useful for diagnosing, preventing or treating
PT disorders associated with dysfunctional erythropoietin receptor, e.g.
PT anemia.
XX
PS Claim 40; SEQ ID NO 59; 192pp; English.
XX
CC The present invention describes an antibody or its fragment that binds to
CC or activates an endogenous activity of a human erythropoietin (EPO)
CC receptor in a mammal, but does not interact with a peptide having a
CC sequence of 30 amino acids (SEQ ID NO:1, ADR68562). Also described: (1)
CC methods of modulating or activating an endogenous activity of a human EPO
CC receptor in a mammal, comprising administering to the mammal a
CC therapeutic amount of the above antibody or its fragment to modulate or
CC activate the receptor; (2) a method of treating a mammal suffering from
CC aplasia, comprising administering to the mammal a therapeutic amount of
CC the above antibody or its fragment to modulate or activate the receptor;
CC (3) a pharmaceutical composition comprising a therapeutic amount of the
CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
CC an isolated and purified polynucleotide sequence, and their fragments,
CC complements and degenerate codon equivalents; and (5) an isolated and
CC purified amino acid sequence, and their fragments. The EPO receptor
CC binding antibody has anti-naemic, neuroprotective and vulnerary
CC activities, and can be used in gene therapy. The compositions and methods
CC from the present invention can be used for modulating an endogenous
CC activity of a human EPO receptor or for treating mammals suffering from
CC aplasia or anaemia. They may also be used for identifying mammals having
CC a dysfunctional EPO receptor. The composition may also be used in
CC promoting wound healing or in protecting against neural cell and/or
CC tissue damage resulting from brain/spinal cord injury, stroke and the
CC like. The present sequence represents a human anti-EPO-R antibody heavy
CC chain variable region complementarily determining region (CDR), which is
CC given in the exemplification of the present invention.
XX
SQ Sequence 41 AA;
XX
QY 1 VISFDGSKKYYVDVSKG 17
Db 11 VISYDGSNKYYADSVKG 27

RESULT 25
ADRE68562
ID ADR68562 standard; peptide: 41 AA.
XX
AC ADR68562;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human EPO-R heavy chain variable region seqid 59.
XX
KM anti-naemic; respiratory; vulnerary; gene therapy; vaccine;
KM erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KM hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
KM wound healing; neural cell damage; tissue damage; brain injury;
KM spinal cord injury; stroke; human; heavy chain variable region;
KM anti-EPO-R-antibody.
XX
OS Homo sapiens.
XX
PN US2004175379-A1.
XX
PD 09-SEP-2004.
XX
PF 10-OCT-2003; 2003US-00684109.
XX
PR 14-OCT-2002; 2002US-0418031P.
XX

PA (DEVN/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREE/) GREEN L L.
PA (WIEL/) WIELER J.
XX
XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX WPI; 2004-661369/64.
XX
DR
XX
PT New antibody or its antibody fragment that activates an endogenous
PT activity or is capable of binding to a human erythropoietin receptor in a
PT mammal, useful for treating a mammal suffering from aplasia or anaemia.
XX
PS Claim 40; SEQ ID NO 59; 156pp; English.
XX
CC The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acid sequence selected
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering from aplasia or anaemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This is the amino acid sequence of a human
CC erythropoietin receptor (EPO-R) anti-EPO-R-antibody heavy chain variable
CC region.
XX
SQ Sequence 41 AA;
XX
QY 1 VISFDGSKKYYVDVSKG 17
Db 11 VISYDGSNKYYADSVKG 27

RESULT 26
ABUS6837
ID ABUS6837 standard; protein: 66 AA.
XX
AC ABUS6837;
XX
DT 04-APR-2003 (first entry)
XX
DE BONT/A Hc binding antibody scfv VH region from 1B3 #1.
XX
KM Botulinum neurotoxin type A; BONT/A; mouse; heavy chain variable region;
KM scFv; antibody; botulism; antibacterial; single chain antibody; VH;
KM immunoglobulin.
XX
OS Mus sp.
XX

US2002155114-A1.

24-OCT-2002.

31-AUG-1998; 98US-00144886.

31-AUG-1998; 98US-00144886.

(MARK/) MARKS J D.

(AMER/) AMERSDORFER P.

Marks JD, Amersdorfer P;

WPI: 2003-182618/18.

Novel antibody that specifically binds and neutralizes botulinum neurotoxin type A useful for neutralizing botulinum neurotoxin and treating botulism.

Claim 6; Page 22; 31pp; English.

The invention relates to an isolated antibody that specifically binds to an epitope specifically bound by an antibody expressed by a clone such as clone S25, C25, C39, 1C6 and clone 1B3, where the antibody binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also included are a polypeptide comprising BoNT/A neutralising epitope comprising an epitope which is specifically bound by the antibody, where the polypeptide is not a full-length botulinum neurotoxin H c fragment and making an anti-BoNT/A antibody that neutralises BoNT/A (by contacting several antibodies with an epitope specifically bound by an antibody expressed by any of the novel clones and isolating an antibody that specifically binds to the epitope). The antibody is useful for neutralising a BoNT/A, by contacting botulinum neurotoxin type A with the antibody comprising VH CDR (heavy chain variable region complementarily determining region) and with a second anti-BoNT/A antibody which comprises a VH CDR, where the second antibody binds to a different epitope than the first anti-BoNT/A antibody. The antibody is useful in the treatment of pathologies associated with botulinum neurotoxin poisoning, for rapid detection/diagnosis of botulism and in the detection and/or quantification of BoNT/A in a biological sample obtained from an organism which is indicative of a Clostridium botulinum infection of the organism. The present sequence is a heavy chain variable region (VH) of a single chain antibody (scfv) of the invention

Sequence 66 AA;

Query Match 92.0%; Score 81; DB 6; Length 66;
Best Local Similarity 88.2%; Pred. No. 2e-05; 1; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 1;

1 VISFDGSKNKYVVDYKVG 17
|||:||||| |||||
50 VISFDGSKNKYADSVKVG 66

RESULT 27
ID ABUS6866
ABUS6866 standard; protein; 66 AA.

ABUS6866;

04-APR-2003 (first entry)

BoNT/A Hc binding antibody scfv VH region from 1C6 #1.

Botulinum neurotoxin type A; BoNT/A; mouse; heavy chain variable region; scfv; antibody; botulism; antibacterial; single chain antibody; VH; immunoglobulin.

Mus sp.

US2002155114-A1.

PD	24-OCT-2002.	
XX		
XX	31-AUG-1998;	98US-00144886.
XX		
PR	31-AUG-1998;	98US-00144886.
XX		
PA	(MARK/) MARKS J D.	
PA	(AMER/) AMERSDORFER P.	
XX		
PI	Marks JD, Amersdorfer P;	
XX		
XX	WPI, 2003-182618/18.	
DR		
XX		
PT	Novel antibody that specifically binds and neutralizes botulinum	
PT	neurotoxin type A useful for neutralizing botulinum neurotoxin and	
XX	treating botulism.	
XX		
PS	Claim 6; Page 22; 31pp; English.	
XX		
CC	The invention relates to an isolated antibody that specifically binds to	
CC	an epitope specifically bound by an antibody expressed by a clone such as	
CC	clone 525, C25, C39, 166 and clone 1F3, where the antibody binds to and	
CC	neutralizes botulinum neurotoxin type A (BoNT/A). Also included are a	
CC	polypeptide comprising BoNT/A neutralising epitope comprising an epitope	
CC	which is specifically bound by the antibody, where the polypeptide is not	
CC	a full-length botulinum neurotoxin H ₃ C fragment and making an anti-BoNT/A	
CC	antibody that neutralises BoNT/A (by contacting several antibodies with	
CC	an epitope specifically bound by an antibody expressed by any of the	
CC	novel clones and isolating an antibody that specifically binds to the	
CC	epitope). The antibody is useful for neutralising a BoNT/A, by contacting	
CC	botulinum neurotoxin type A with the antibody comprising VH CDR (heavy	
CC	chain variable region complementarity determining region) and with a	
CC	second anti-BoNT/A antibody which comprises a VH CDR, where the second	
CC	antibody binds to a different epitope than the first anti-BoNT/A	
CC	antibody. The antibody is useful in the treatment of pathologies	
CC	associated with botulinum neurotoxin poisoning, for rapid	
CC	detection/diagnosis of botulism and in the detection and/or	
CC	quantification of BoNT/A in a biological sample obtained from an organism	
CC	which is indicative of a Clostridium botulinum infection of the organism.	
CC	The present sequence is a heavy chain variable region (VH) of a single	
CC	chain antibody (scFv) of the invention	
XX		
SO	Sequence 66 AA;	
	Query Match	92.0%; Score 81; DB 6; Length 66;
	Best Local Similarity	88.2%; Pred. No. 2e-05;
	Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
OY	1 VISFDGSNKKYYVDSVKG 17	
	:	
DB	50 VISYDGSNKKYYADSVKG 66	
RESULT 28		
AEA21573		
AEA21573	standard; protein; 82 AA.	
XX		
AC	AEA21573;	
XX		
DT	28-JUL-2005 (first entry)	
XX		
XX		
DE	Human Ig germ line heavy chain variable region protein.	
XX		
KW	antibody; immunoglobulin; heavy chain variable region; cytostatic;	
KM	neoplasm.	
XX		
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
FT	Region	16..20
FT		/note="complementarity determining region 1 (CDR1)"
FT	Region	35..51
		/note="complementarity determining region 2 (CDR2)"

FT Region 81..82
 FT /note= "complementarity determining region 3 (CDR3)"
 XX
 PN W02005047456-A2.
 XX
 PD 26-MAY-2005.
 XX
 PF 15-NOV-2004; 2004WO-1B004407.
 XX
 PR 13-NOV-2003; 2003DE-01052977.
 XX
 PA (HTHR-) H3 PHARMA INC.
 XX
 PI Vollmers HP, Mueller-Hermelink HK;
 XX
 DR WPI; 2005-372356/38.
 DR N-FSDB; AEA21574.
 XX
 PT New anti-idiotype antibody of the human monoclonal antibody SC-1, useful
 PT for diagnosing, detecting, monitoring, and treating neoplasms.
 XX
 PS Disclosure; SEQ ID NO 3; 27pp; English.
 XX
 CC The invention relates to an isolated anti-idiotype antibody, which
 CC specifically binds a polypeptide comprising the SC-1 human monoclonal
 CC antibody heavy chain sequence (AEA21571). Also described: (1) a hybridoma
 CC cell line with DSMZ accession number DSM ACC2625; (2) an anti-idiotype
 CC antibody expressed by the hybridoma cell line; (3) a humanized antibody
 CC having the binding specificity of the anti-idiotype antibody of (2); (4)
 CC generating an immune response in a mammal against the anti-idiotype
 CC antibody; and (5) producing an anti-idiotype antibody in a non-human
 CC mammal. The antibody, composition and method are useful for diagnosing,
 CC detecting, monitoring, and treating neoplasms. The present sequence
 CC represents the human immunoglobulin (Ig) germ line heavy chain variable
 CC region, which is given in comparison with the human monoclonal antibody
 CC heavy chain variable region in the exemplification of the present
 CC invention.
 CC
 XX
 SQ Sequence 82 AA;
 Query Match 92.0%; Score 81; DB 9; Length 82;
 Best Local Similarity 88.2%; Pred. No. 2.6e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKKYYVDSVKG 17
 Db 35 VISYDGSNKYYADSVKG 51

RESULT 29
 AAW62799
 ID AAW62799 standard; peptide; 83 AA.
 XX
 AC AAW62799;
 XX
 DT 23-SEP-1998 (first entry)
 XX
 DE Amino acid sequence of a human antibody fragment.
 XX
 KW Human; immunoglobulin; Ig; transgenic; non-human mammal;
 KW inactivated endogenous Ig locus; B-cell development;
 KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
 KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
 KW production; antibody.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 22
 FT /note= "not defined"
 XX
 PN W09824893-A2.
 XX

PD 11-JUN-1998.
 XX
 PF 03-DEC-1997; 97WO-US023091.
 XX
 PR 03-DEC-1996; 96US-00759620.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
 XX
 DR WPI; 1998-33314/29.
 XX
 PT New transgenic non-human mammals - having an inactivated immunoglobulin
 PT locus and a near complete human immunoglobulin locus, used for production
 PT of human antibodies.
 XX
 PS Disclosure; Page 74; 128pp; English.
 XX
 CC AAW62793-82 represent fragments of human antibodies produced by
 CC transgenic Xenomice, created using the method of the invention. The
 CC specification describes a transgenic non-human mammal which has genome
 CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
 CC locus, so that the mammal does not display normal B-cell development. The
 CC modified genome also has an inserted human heavy chain Ig locus in
 CC germline configuration, the human heavy chain Ig locus comprising a human
 CC micro constant region and regulatory and switch sequences, human J-H
 CC genes, human D-H genes, and human V-H genes and an inserted human kappa
 CC light chain Ig locus in germline configuration, the human kappa light
 CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
 CC and V-kappa genes, where the number of V-H and V-kappa genes inserted are
 CC selected to restore normal B-cell development in the mammal. The
 CC transgenic animals have a near complete human Ig locus, including both a
 CC human heavy chain locus and a human kappa light chain locus. They can be
 CC used for the production of human antibodies when exposed to particular
 CC antigens e.g. when exposed to human IL-6, EGFR or TNF- alpha the mice
 CC will produce antibodies to IL-6, EGFR or TNF- alpha respectively
 CC
 XX
 SQ Sequence 83 AA;
 Query Match 92.0%; Score 81; DB 2; Length 83;
 Best Local Similarity 88.2%; Pred. No. 2.6e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKKYYVDSVKG 17
 Db 35 VISYDGSNKYYADSVKG 51

RESULT 30
 AAB40127
 ID AAB40127 standard; protein; 95 AA.
 XX
 AC AAB40127;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hi12 antibody H chain V region amino acid sequence SEQ ID 653.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antirheumatic; anticholelitic;
 KW antileukotic; neutroprotective; antiporiatic; antidiabetic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN W0200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX

XX (BADI) BASF AG.
PA (GENY) GENETICS INST INC.
XX
PI Sajfeld JG, Roguska M, Peakind M, Banerjee S, Tracey DE, White M;
PI Kaymakalan Z, Labkovsky B, Sakorafas P, Friedrich S, Wyles A;
PI Vejdman GM, Venturini A, Watne NW, Widom A, Elvin JG, Duncan AR,
PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
XX WPI; 2000-638250/61.
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis.
XX
PS Claim 75; Page 122; 377pp; English.
XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in AAG61062-
CC C61071. The antibody of the invention is a neutralising antibody and has
CC antirheumatic; antiarthritic; antisclerotic; antiinflammatory;
CC neuroprotective; antiproliferic; antidiabetic; cardiant; antiparasitic;
CC antibacterial and immunosuppressive activity. The antibodies or antigen-
CC binding fragments are useful in the treatment of disorders associated
CC with detrimental release of human IL-12, especially Crohn's disease,
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
CC manufacture of a pharmaceutical composition to treat human IL-12
CC disorders
XX
SQ Sequence 95 AA;
XX
Query Match 92.0%; Score 81; DB 3; Length 95;
Best Local Similarity 88.2%; Pred. No. 3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 VISFDGSKNYVDSYVG 17
DB 50 VISYDGSNKRYADSVKG 66

RESULT 31
AAR34283
ID AAR34283 standard; protein; 98 AA.
XX
XX AAR34283;
XX
AC
XX
DT 25-MAR-2003 (revised)
DT 26-JUL-1993 (first entry)
XX
XX Human TNF binding antibody DP-46 heavy chain.
DE
XX
XX Monoclonal antibody; anti-globulin response; VH gene; chimeric;
KW mouse-human antibodies; antibody; prevention; tumour necrosis factor.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..30
FT Region /note= "Framework region FR1"
FT 31..35
FT Region /note= "Complementarity determining region CDR1"
FT 36..49
FT Region /note= "Framework region FR2"
FT 50..66
FT Region

FT /note= "Complementarity determining region CDR2"
FT 67..98
FT Region /note= "Framework region FR3"
XX
XX WO9306213-A1.
XX
XX PD 01-APR-1993.
XX
XX PF 23-SEP-1992; 92WO-GB001755.
XX
XX PR 23-SEP-1991; 91GB-00020252.
XX PR 25-SEP-1991; 91GB-00020377.
XX PR 24-MAR-1992; 92GB-00006318.
XX PR 24-MAR-1992; 92GB-00006372.
XX PR 15-MAY-1992; 92WO-GB000883.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Hoogenboom HRJM, Baier M, Jespers LSAT, Winter GP;
XX WPI; 1993-117534/14.
XX
XX DR WPI; 1993-117534/14.
XX
XX PT Producing human antibody polypeptide dimer specific for antigen
XX PT comprises use of chain shuffling using phage expression, useful for
XX PT reducing anti globulin responses in humans for increased human
XX PT characteristics.
XX
XX Example; Fig 6; 109pp; English.
XX
XX The sequence is that of the heavy chain clone DP-46 derived from the
XX gemline human VH gene DP-46 (from the VH3 family) of antibody fragments
XX binding to human TNF. It may be used as part of a method of producing
XX chimeric mouse-human antibodies or fragments which have the same binding
XX specificity as a parent Ab but have increased human characteristics,
XX CC preventing anti-globulin response in humans. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX
SQ Sequence 98 AA;
XX
Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 3.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 VISFDGSKNYVDSYVG 17
DB 50 VISYDGSNKRYADSVKG 66

RESULT 32
AA50962
ID AA50962 standard; protein; 98 AA.
XX
XX AA50962;
XX
AC
XX
DT 23-MAR-2000 (first entry)
DT
XX
XX Human FVII antibody A3-C1 scFv heavy chain protein DP-49.
DE
XX
XX Human; heavy chain; antibody; factor VIII; hemostatic; hemophilia A;
KW scFv; A3-C1.
XX
XX Homo sapiens.
OS
XX WO9958680-A2.
XX
XX PD 18-NOV-1999.
XX
XX PF 07-MAY-1999; 99WO-NL000285.
XX PR 08-MAY-1998; 98EP-00201543.
XX
XX (SANO-) STICHTING SANQUIN BLOEDVOORZIENING.
XX

XX Voorberg JJ, Van Den Brink EN, Turenhout EAM;
 XX WPI; 2000-053102/04.
 XX
 PT New polynucleotide, polypeptide and antibody useful for diagnosing the
 PT presence of neutralizing antibodies against factor VIII and for treatment
 PT of hemophilia A patients with these antibodies.
 XX
 PS Example 8; Fig 9A; 61pp; English.
 XX
 CC This invention describes a novel polynucleotide (I) (and complements and
 CC hybridizable polynucleotides) comprising a contiguous nucleotide sequence
 CC coding for a human antibody with factor VIII specificity which has
 CC hemostatic activity. (1) is useful a primer or probe for detecting the
 CC presence of inhibitory antibodies directed against factor VIII. The
 CC polypeptides of the invention and the antibodies generated from them are
 CC useful in compositions for neutralizing factor VIII inhibiting antibodies
 CC in hemophilia A patients. This sequence represents the human factor VIII
 CC antibody A3-C1 specific scFv protein DP-49 which is used in the method of
 CC the invention
 CC
 SQ Sequence 98 AA;
 XX
 Query Match 92.0%; Score 81; DB 3; Length 98;
 Best Local Similarity 88.2%; Pred. No. 3.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKG 66
 XX
 RESULT 33
 AAB40116
 ID AAB40116 standard; protein; 98 AA.
 XX
 AC AAB40116;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 642.
 XX
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 XX complementarity determining region; CDR; antirheumatic; antiarthritic;
 XX antileukotic; neuroprotective; antiporiatic; antiashtmatic; cardiant;
 XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 XX multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GW, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX

PS Claim 75; Page 122; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61063-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antirheumatic; antiarthritic; antileukotic; antiashtmatic; cardiant;
 CC neuroprotective; antiporiatic; antiashtmatic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 SQ Sequence 98 AA;
 XX
 Query Match 92.0%; Score 81; DB 3; Length 98;
 Best Local Similarity 88.2%; Pred. No. 3.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKG 66
 XX
 RESULT 34
 AAB40098
 ID AAB40098 standard; protein; 98 AA.
 XX
 AC AAB40098;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 624.
 XX
 XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 XX complementarity determining region; CDR; antirheumatic; antiarthritic;
 XX antileukotic; neuroprotective; antiporiatic; antiashtmatic; cardiant;
 XX antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 XX multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GEMY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GW, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX

XX PS Claim 75; Page 121; 377bp; English.

CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in AAC61062-
CC C61071. The antibody of the invention is a neutralising antibody and has
CC antineoplastic; antitumoric; antisclerotic; antiinflammatory;
CC neuroprotective; antiparasitic; antiaesthetic; cardiant; antiparasitic;
CC antibacterial and immunosuppressive activity. The antibodies or antigen-
CC binding fragments are useful in the treatment of disorders associated
CC with detrimental release of human IL-12, especially Crohn's disease,
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
CC manufacture of a pharmaceutical composition to treat human IL-12
CC disorders

CC SQ Sequence 98 AA;

Query Match 92.0%; Score 81; DB 3; Length 98;
Best Local Similarity 88.2%; Pred. No. 3.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDSYVG 17
|||:|||||
Db 50 VISYDGSNKYYTDSYVG 66

RESULT 35
AAB40100
ID AAB40100 standard; protein; 98 AA.

XX AAB40100;

AC AAB40100;

DT 05-FEB-2001 (first entry)

XX Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 626.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antineumatic; antiarthritic;
KW antiparasitic; neuroprotective; antiparasitic; antiaesthetic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

OS Homo sapiens.

XX WO200056772-A1.

PN WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US007946.

PF 24-MAR-2000; 2000WO-US007946.

XX 25-MAR-1999; 99US-0126603P.

PR 25-MAR-1999; 99US-0126603P.

XX (BADI) BASF AG.

PA (GENY) GENETICS INST INC.

XX Salfeid JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GW, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
XX WPI; 2000-638250/61.

DR WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's

PT disease and multiple sclerosis.

XX PS Claim 75; Page 121; 377bp; English.

CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarity determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in AAC61062-
CC C61071. The antibody of the invention is a neutralising antibody and has
CC antineumatic; antitumoric; antisclerotic; antiinflammatory;
CC neuroprotective; antiparasitic; antiaesthetic; cardiant; antiparasitic;
CC antibacterial and immunosuppressive activity. The antibodies or antigen-
CC binding fragments are useful in the treatment of disorders associated
CC with detrimental release of human IL-12, especially Crohn's disease,
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
CC manufacture of a pharmaceutical composition to treat human IL-12
CC disorders

CC SQ Sequence 98 AA;

Query Match 92.0%; Score 81; DB 3; Length 98;
Best Local Similarity 88.2%; Pred. No. 3.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDSYVG 17
|||:|||||
Db 50 VISYDGSNKYYTDSYVG 66

RESULT 36
AAB40122
ID AAB40122 standard; protein; 98 AA.

XX AAB40122;

AC AAB40122;

DT 05-FEB-2001 (first entry)

XX Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 648.

XX Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
KW complementarity determining region; CDR; antineumatic; antiarthritic;
KW antiparasitic; neuroprotective; antiparasitic; antiaesthetic; cardiant;
KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis.

XX Homo sapiens.

OS Homo sapiens.

XX WO200056772-A1.

PN WO200056772-A1.

XX 28-SEP-2000.

XX 24-MAR-2000; 2000WO-US007946.

PF 24-MAR-2000; 2000WO-US007946.

XX 25-MAR-1999; 99US-0126603P.

PR 25-MAR-1999; 99US-0126603P.

XX (BADI) BASF AG.

PA (GENY) GENETICS INST INC.

XX Salfeid JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M;
PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
PI Veldman GW, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
XX WPI; 2000-638250/61.

DR WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to

PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Claim 75; Page 122; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40064-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralizing antibody and has
 CC antineumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antiparasitic; antiaesthetic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 SQ Sequence 98 AA;
 XX
 Query Match 92.0%; Score 81; DB 3; Length 98;
 Best Local Similarity 88.2%; Pred. No. 3.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKNKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKG 66
 RESULT 37
 AAB40104
 ID AAB40104 standard; protein; 98 AA.
 XX
 AC AAB40104;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 630.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antineumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antiaesthetic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GENY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elynn JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.

PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Claim 75; Page 121; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40064-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralizing antibody and has
 CC antineumatic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antiparasitic; antiaesthetic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 SQ Sequence 98 AA;
 XX
 Query Match 92.0%; Score 81; DB 3; Length 98;
 Best Local Similarity 88.2%; Pred. No. 3.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VISFDGSKNKYYVDSVKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADSVKG 66
 RESULT 38
 AAB40118
 ID AAB40118 standard; protein; 98 AA.
 XX
 AC AAB40118;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID 644.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antineumatic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antiaesthetic; cardiant;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GENY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elynn JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.

XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Claim 75; Page 122; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAB61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antineoplastic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antiparasitic; antiasthmatic; cardiatic; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 XX Sequence 98 AA:
 SQ
 Query Match 92.0%; Score 81; DB 3; Length 98;
 Best Local Similarity 88.2%; Pred. No. 3.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VISFDGSKNKYYVDVSKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADVSKG 66
 RESULT 39
 AAB40119
 ID AAB40119 standard; protein; 98 AA.
 XX
 AC AAB40119;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 645.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antineoplastic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antiasthmatic; cardiatic;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GENY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;

DR WPI, 2000-638250/61.
 XX
 XX New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Claim 75; Page 122; 377pp; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences. AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAB61062-
 CC C61071. The antibody of the invention is a neutralising antibody and has
 CC antineoplastic; antiarthritic; antisclerotic; antiinflammatory;
 CC neuroprotective; antiparasitic; antiasthmatic; cardiatic; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 CC
 XX Sequence 98 AA:
 SQ
 Query Match 92.0%; Score 81; DB 3; Length 98;
 Best Local Similarity 88.2%; Pred. No. 3.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 VISFDGSKNKYYVDVSKG 17
 |||:|||||
 Db 50 VISYDGSNKYYADVSKG 66
 RESULT 40
 AAB40109
 ID AAB40109 standard; protein; 98 AA.
 XX
 AC AAB40109;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody H chain V region amino acid sequence SEQ ID 635.
 XX
 KW Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 KW complementarity determining region; CDR; antineoplastic; antiarthritic;
 KW antisclerotic; neuroprotective; antiparasitic; antiasthmatic; cardiatic;
 KW antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASF AG.
 PA (GENY) GENETICS INST INC.
 XX
 PI Salfeld JG, Roguska M, Paskind M, Banerjee S, Tracey DE, White M,
 PI Kaymakcalan Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A,
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR,
 PI Derbyshire EJ, Carmen S, Smith S, Hollet TL, Du Fou SL;

XX WPI; 2000-638250/61.

DR
XX
PT New human antibody specific for human interleukin-12 (IL-12) used to
PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
PT disease and multiple sclerosis.

XX
PS Claim 75; Page 121; 377pp; English.

XX
CC This invention relates to a new human antibody specific for human
CC interleukin-12 (IL-12). The invention also includes antigen binding
CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
CC anti-IL-12 antibody heavy and light chain complementarily determining
CC region (CDR) amino acid sequences, and also includes variable region
CC amino acid sequences. Other variable region amino acid sequences are
CC given in AAB39517-B39560 and AAB40066-B40149. Sequences AAB39561-B39771
CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
CC represent other CDR sequences. Light chain CDR3 consensus sequences are
CC given in AAB40064-B40067. Primers used in the identification and
CC construction of the antibodies of the invention are given in AAC61062-
CC C61071. The antibody of the invention is a neutralising antibody and has
CC antirheumatic; antiarthritis; antisclerotic; antiinflammatory;
CC neuroprotective; antiparalytic; antiaesthetic; cardiac; antiparasitic;
CC antibacterial and immunosuppressive activity. The antibodies or antigen-
CC binding fragments are useful in the treatment of disorders associated
CC with detrimental release of human IL-12, especially Crohn's disease,
CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
CC manufacture of a pharmaceutical composition to treat human IL-12
CC disorders

XX
SQ Sequence 98 AA;

Query Match 92.0%; Score 81; DB 3; Length 98;
Best Local Similarity 88.2%; Pred. No. 3,1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
||:|||||
Db 50 VISYDGSNKYYVDSVKG 66

Search completed: December 14, 2005, 07:25:21
Job time : 99.7241 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 14, 2005, 07:19:38 ; Search time 24.9138 Seconds
(without alignments)
56.414 Million cell updates/sec

Title: US-10-720-323-2
Perfect score: 88
Sequence: 1 VISFDGSKYVDSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_AA:
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCRTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	92.0	17	2	US-09-383-667-16
2	81	92.0	17	2	US-09-424-8408-36
3	81	92.0	17	2	US-09-424-8408-95
4	81	92.0	17	2	US-09-424-8408-97
5	81	92.0	17	2	US-09-424-8408-108
6	81	92.0	95	2	US-09-534-717-653
7	81	92.0	98	1	US-08-211-202-118
8	81	92.0	98	2	US-10-194-975-23
9	81	92.0	98	2	US-10-194-975-24
10	81	92.0	98	2	US-10-194-975-25
11	81	92.0	98	2	US-09-534-717-624
12	81	92.0	98	2	US-09-534-717-625
13	81	92.0	98	2	US-09-534-717-626
14	81	92.0	98	2	US-09-534-717-627
15	81	92.0	98	2	US-09-534-717-628
16	81	92.0	98	2	US-09-534-717-629
17	81	92.0	98	2	US-09-534-717-630
18	81	92.0	98	2	US-09-534-717-631
19	81	92.0	98	2	US-09-534-717-632
20	81	92.0	98	2	US-09-534-717-635
21	81	92.0	98	2	US-09-534-717-636
22	81	92.0	98	2	US-09-534-717-637
23	81	92.0	98	2	US-09-534-717-640
24	81	92.0	98	2	US-09-534-717-641
25	81	92.0	98	2	US-09-534-717-642
26	81	92.0	98	2	US-09-534-717-643
27	81	92.0	98	2	US-09-534-717-644

28	81	92.0	98	2	US-09-534-717-645	Sequence 645, App
29	81	92.0	98	2	US-09-534-717-646	Sequence 646, App
30	81	92.0	98	2	US-09-534-717-648	Sequence 648, App
31	81	92.0	98	2	US-09-534-717-650	Sequence 650, App
32	81	92.0	98	2	US-09-534-717-654	Sequence 654, App
33	81	92.0	98	2	US-10-330-613A-61	Sequence 61, App1
34	81	92.0	98	2	US-10-330-613A-62	Sequence 62, App1
35	81	92.0	115	2	US-09-726-219A-167	Sequence 167, App
36	81	92.0	115	2	US-09-269-332-59	Sequence 89, App1
37	81	92.0	115	2	US-09-196-522-167	Sequence 167, App
38	81	92.0	116	1	US-08-211-202-141	Sequence 141, App
39	81	92.0	117	2	US-08-545-809A-115	Sequence 115, App
40	81	92.0	117	2	US-09-515-697-115	Sequence 115, App
41	81	92.0	119	1	US-08-331-338A-46	Sequence 46, App1
42	81	92.0	119	1	US-08-331-337B-46	Sequence 46, App1
43	81	92.0	119	1	US-08-759-804A-46	Sequence 46, App1
44	81	92.0	119	1	US-09-227-693-46	Sequence 46, App1
45	81	92.0	120	1	US-08-211-202-135	Sequence 135, App
46	81	92.0	120	1	US-07-942-245-35	Sequence 35, App1
47	81	92.0	120	2	US-10-330-613A-29	Sequence 29, App1
48	81	92.0	123	2	US-08-983-607-38	Sequence 38, App1
49	81	92.0	123	2	US-09-424-8408-6	Sequence 6, App1
50	81	92.0	128	1	US-08-478-039-96	Sequence 96, App1
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52	81	92.0	248	1	US-09-315-926A-80	Sequence 80, App1
53	80	90.9	17	2	US-09-383-667-18	Sequence 18, App1
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55	78	88.6	17	2	US-09-424-8408-111	Sequence 111, App
56	78	88.6	124	2	US-09-424-8408-156	Sequence 156, App1
57	78	88.6	225	2	US-09-456-090A-102	Sequence 102, App
58	78	88.6	225	2	US-09-456-090A-110	Sequence 110, App
59	78	88.6	225	2	US-09-456-090A-108	Sequence 108, App
60	78	88.6	225	2	US-09-453-224-102	Sequence 102, App
61	78	88.6	225	2	US-09-453-224-108	Sequence 108, App
62	78	88.6	225	2	US-09-453-224-110	Sequence 110, App
63	77	87.5	17	2	US-09-424-8408-84	Sequence 84, App1
64	77	87.5	17	2	US-09-424-8408-113	Sequence 113, App
65	77	87.5	123	2	US-09-534-717-346	Sequence 346, App
66	77	87.5	125	2	US-09-424-8408-22	Sequence 22, App1
67	77	87.5	125	2	US-09-240-274-8	Sequence 8, App1
68	77	87.5	125	2	US-09-240-274-20	Sequence 20, App1
69	77	87.5	125	2	US-09-240-274-21	Sequence 21, App1
70	77	87.5	125	2	US-09-240-274-22	Sequence 22, App1
71	77	87.5	125	2	US-09-240-274-23	Sequence 23, App1
72	77	87.5	125	2	US-09-848-798-8	Sequence 8, App1
73	77	87.5	125	2	US-09-848-798-20	Sequence 20, App1
74	77	87.5	125	2	US-09-848-798-21	Sequence 21, App1
75	77	87.5	125	2	US-09-848-798-22	Sequence 22, App1
76	77	87.5	125	2	US-09-848-798-23	Sequence 23, App1
77	76	86.4	125	2	US-08-635-109-4	Sequence 4, App1
78	76	86.4	125	2	US-08-844-215-4	Sequence 4, App1
79	76	86.4	126	2	US-09-240-274-17	Sequence 17, App1
80	76	86.4	126	2	US-09-848-798-17	Sequence 17, App1
81	76	86.4	127	2	US-09-240-274-145	Sequence 145, App
82	76	86.4	127	2	US-09-848-798-145	Sequence 145, App
83	76	86.4	141	1	US-08-259-312A-2	Sequence 2, App1
84	76	86.4	141	1	US-08-468-671-2	Sequence 2, App1
85	75	85.2	126	1	US-08-478-039-95	Sequence 95, App1
86	75	85.2	126	1	US-08-476-349A-95	Sequence 95, App1
87	75	85.2	179	2	US-08-862-124-17	Sequence 17, App1
88	75	85.2	287	2	US-08-862-124-17	Sequence 17, App1
89	75	85.2	304	2	US-08-862-124-14	Sequence 14, App1
90	74	84.1	17	2	US-09-383-667-11	Sequence 11, App1
91	74	84.1	17	2	US-09-534-717-352	Sequence 352, App
92	74	84.1	17	2	US-09-534-717-354	Sequence 354, App
93	74	84.1	89	2	US-09-472-087-72	Sequence 72, App1
94	74	84.1	98	2	US-10-194-975-26	Sequence 26, App1
95	74	84.1	98	2	US-09-534-717-647	Sequence 647, App
96	74	84.1	98	2	US-09-534-717-651	Sequence 651, App
97	74	84.1	98	2	US-09-534-717-652	Sequence 652, App
98	74	84.1	124	2	US-09-240-274-5	Sequence 5, App1
99	74	84.1	124	2	US-09-240-274-6	Sequence 6, App1
100	74	84.1	124	2	US-09-848-798-5	Sequence 5, App1

ALIGNMENTS

RESULT 1
US-09-383-667-16
; Sequence 16, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/Xa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-16

Query Match 92.0%; Score 81; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 2
US-09-424-840B-36
; Sequence 36, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-36

Query Match 92.0%; Score 81; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 3
US-09-424-840B-95
; Sequence 95, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-95

Query Match 92.0%; Score 81; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 4
US-09-424-840B-97
; Sequence 97, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-97

Query Match 92.0%; Score 81; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 5
US-09-424-840B-108
; Sequence 108, Application US/09424840B

Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 108
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-108

Query Match 92.0%; Score 81; DB 2; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYVADSVKG 17

RESULT 6
US-09-534-717-653
Sequence 653, Application US/09534717
Patent No. 6914128
GENERAL INFORMATION:
APPLICANT: Jochen, Saljeid et al.
TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
FILE REFERENCE: BBI-093CP
CURRENT APPLICATION NUMBER: US/09/534,717
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/126,603
EARLIER FILING DATE: March 25, 1999
NUMBER OF SEQ ID NOS: 675
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 653
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-717-653

Query Match 92.0%; Score 81; DB 2; Length 95;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYVADSVKG 66

RESULT 7
US-08-211-202-118
Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAISER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:

ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-118

Query Match 92.0%; Score 81; DB 1; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYVADSVKG 66

RESULT 8
US-10-194-975-23
Sequence 23, Application US/10194975
Patent No. 6881557
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231.01
CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 98
TYPE: PRT

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; ORGANISM: Homo sapiens
; US-10-194-975-23
Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 9
US-10-194-975-24
; Sequence 24, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24
Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
US-10-194-975-25
; Sequence 25, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-25
Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 11
US-09-534-717-624
; Sequence 624, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 624
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-624
Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 12
US-09-534-717-625
; Sequence 625, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 625
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-625
Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 13
US-09-534-717-626
; Sequence 626, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 626
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-626
Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66
```

US-09-534-717-626

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSYKG 17
|||:|||||
DB 50 VISYDGSNKYYADSVYKG 66

RESULT 14

US-09-534-717-627
; Sequence 627; Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:

; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 627
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-534-717-627

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSYKG 17
|||:|||||
DB 50 VISYDGSNKYYADSVYKG 66

RESULT 15

US-09-534-717-628
; Sequence 628; Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:

; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 628
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-534-717-628

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSYKG 17
|||:|||||
DB 50 VISYDGSNKYYADSVYKG 66

RESULT 16

US-09-534-717-629
; Sequence 629; Application US/09534717
; Patent No. 6914128

; GENERAL INFORMATION:

; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 629
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-534-717-629

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSYKG 17
|||:|||||
DB 50 VISYDGSNKYYADSVYKG 66

RESULT 17

US-09-534-717-630
; Sequence 630; Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:

; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 630
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-534-717-630

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSYKG 17
|||:|||||
DB 50 VISYDGSNKYYADSVYKG 66

RESULT 18

US-09-534-717-631
; Sequence 631; Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:

; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 631
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-534-717-631

```
Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1,4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 19
US-09-534-717-632
; Sequence 632, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 632
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-632

Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1,4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 20
US-09-534-717-635
; Sequence 635, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 635
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-635

Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1,4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 21
US-09-534-717-636
; Sequence 636, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 636
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-636

Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1,4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 22
US-09-534-717-637
; Sequence 637, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 637
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-637

Query Match          92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1,4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
   |||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 23
US-09-534-717-640
; Sequence 640, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 640
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-640
```

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSYKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 24
US-09-534-717-641.
; Sequence 641, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 641
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-641

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSYKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 25
US-09-534-717-642
; Sequence 642, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 642
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-642

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSYKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 26
US-09-534-717-643
; Sequence 643, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.

; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 643
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-643

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSYKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 27
US-09-534-717-644
; Sequence 644, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 644
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-644

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKYVDSYKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 28
US-09-534-717-645
; Sequence 645, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.

; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 645
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-645

Query Match 92.0%; Score 81; DB 2; Length 98;

Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 29

US-09-534-717-646
; Sequence 646, Application US/09534717
; Patent No. 6914128

; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; EARLIER FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 646
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-646

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 30

US-09-534-717-648
; Sequence 648, Application US/09534717
; Patent No. 6914128

; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; EARLIER FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 648
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-648

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 31

US-09-534-717-650
; Sequence 650, Application US/09534717
; Patent No. 6914128

; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing

; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; CURRENT FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 650
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-650

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 32

US-09-534-717-654
; Sequence 654, Application US/09534717
; Patent No. 6914128

; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/09/534,717
; EARLIER FILING DATE: 2000-03-24
; EARLIER APPLICATION NUMBER: 60/126,603
; EARLIER FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 654
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-534-717-654

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 33

US-10-330-613A-61
; Sequence 61, Application US/10330613A
; Patent No. 6924360

; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330,613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-61

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDSVKG 17
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Db 50 VISYDGSNKYVDSVKG 66

RESULT 34
US-10-330-613A-62
; Sequence 62, Application US/10330613A
; Patent No. 6824360
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
; FILE REFERENCE: ABGENIX.022A
; CURRENT APPLICATION NUMBER: US/10/330.613A
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: 60/346299
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-613A-62

Query Match 92.0%; Score 81; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYVDSVKG 66

RESULT 35
US-09-726-219A-167
; Sequence 167, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Jackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213835-00013
; CURRENT APPLICATION NUMBER: US/09/726.219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134

; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167

Query Match 92.0%; Score 81; DB 2; Length 115;
Best Local Similarity 88.2%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYVDSVKG 66

RESULT 36
US-09-269-332-89
; Sequence 89, Application US/09269332
; Patent No. 6903194
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: WAKAHARA, YUI
; APPLICANT: YABUTA, NAOTIRO
; TITLE OF INVENTION: ANTIBODY AGAINST HUMAN PARATHORMONE RELATED PEPTIDES
; FILE REFERENCE: 04853-0033
; CURRENT APPLICATION NUMBER: US/09/269.332
; CURRENT FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03382
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: JP 255196/1996
; PRIOR FILING DATE: 1996-09-26
; PRIOR APPLICATION NUMBER: JP 214168/1997
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-269-332-89

Query Match 92.0%; Score 81; DB 2; Length 115;
Best Local Similarity 88.2%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VISFDGSKNYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYVDSVKG 66

RESULT 37
US-09-196-522-167
; Sequence 167, Application US/09196522
; Patent No. 6916605
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James

APPLICANT: Clackson, Timothy
APPLICANT: Chiswell, David
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00004
CURRENT APPLICATION NUMBER: US/09/196,522
CURRENT FILING DATE: 1998-11-28
PRIOR APPLICATION NUMBER: GB 9015198.6
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
PRIOR FILING DATE: 1993-01-08
PRIOR APPLICATION NUMBER: US 08/484,893
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.1
SEQ ID NO 167
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-196-522-167

Query Match 92.0%; Score 81; DB 2; Length 115;
Best Local Similarity 88.2%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 38
US-08-211-202-141
Sequence 141, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESS: Bourn
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 92.0%; Score 81; DB 1; Length 116;
Best Local Similarity 88.2%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
|||:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 39
US-08-545-809A-115
Sequence 115, Application US/08545809A
Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070

Search completed: December 14, 2005, 07:33:19
Job time : 25.9138 secs

TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-115

Query Match 92.0%; Score 81; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VISFDGSKKYYVDSYVG 17
|||:|||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 40
US-09-515-697-115
Sequence 115, Application US/09515697
Patent No. 6936705
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/515,697
FILING DATE: 29-Feb-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809
FILING DATE: 27-MAR-1996
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-515-697-115

Query Match 92.0%; Score 81; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 1.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VISFDGSKKYYVDSYVG 17
|||:|||||
Db 69 VISYDGSNKYYADSVKG 85

RECEIVED

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OM protein - protein search, using bw model

Run on: December 14, 2005, 07:19:54 ; Search time 77.9655 Seconds
(without alignments)
91.106 Million cell updates/sec

Title: US-10-720-323-2
Perfect score: 88
Sequence: 1 VISFPGSNKYYVDSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_Main:
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	88	100.0	17	US-10-720-323-2	Sequence 2, Appli
3	88	100.0	119	US-09-920-267C-7	Sequence 7, Appli
4	88	100.0	119	US-10-720-323-7	Sequence 7, Appli
5	85	96.6	249	US-09-880-748-1109	Sequence 1109, Ap
6	85	96.6	249	US-10-293-418-1109	Sequence 1109, Ap
7	82	93.2	16	US-10-954-900A-2	Sequence 1109, Ap
8	81	92.0	17	US-09-972-656-48	Sequence 48, Appli
9	81	92.0	17	US-10-384-060-46	Sequence 48, Appli
10	81	92.0	17	US-10-389-701-6	Sequence 6, Appli
11	81	92.0	17	US-10-396-578-21	Sequence 21, Appli
12	81	92.0	17	US-10-396-578-39	Sequence 39, Appli
13	81	92.0	17	US-10-396-578-51	Sequence 39, Appli
14	81	92.0	17	US-10-396-578-81	Sequence 81, Appli
15	81	92.0	17	US-10-844-424-36	Sequence 81, Appli
16	81	92.0	17	US-10-844-424-95	Sequence 95, Appli
17	81	92.0	17	US-10-844-424-97	Sequence 95, Appli
18	81	92.0	17	US-10-844-424-108	Sequence 108, App
19	81	92.0	17	US-10-798-380-23	Sequence 108, App
20	81	92.0	17	US-10-726-332-114	Sequence 23, Appli
21	81	92.0	17	US-10-989-462-311	Sequence 114, App
22	81	92.0	17	US-11-074-803-21	Sequence 311, App
23	81	92.0	17	US-11-074-803-39	Sequence 31, Appli
24	81	92.0	17	US-11-074-803-51	Sequence 39, Appli
25	81	92.0	17	US-11-074-803-81	Sequence 81, Appli
26	81	92.0	41	US-10-269-711-47	Sequence 81, Appli
27	81	92.0	41	US-10-269-711-48	Sequence 47, Appli

28	81	92.0	41	US-10-684-109-59	Sequence 59, Appli
29	81	92.0	83	US-10-078-958-7	Sequence 7, Appli
30	81	92.0	95	US-10-884-830-653	Sequence 653, App
31	81	92.0	98	US-09-948-939-15	Sequence 15, Appli
32	81	92.0	98	US-10-194-975-23	Sequence 23, Appli
33	81	92.0	98	US-10-194-975-24	Sequence 24, Appli
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38	81	92.0	98	US-10-032-037B-74	Sequence 74, Appli
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52	81	92.0	98	US-10-453-658-65	Sequence 65, Appli
53	81	92.0	98	US-10-029-926B-74	Sequence 74, Appli
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55	81	92.0	98	US-10-029-926B-76	Sequence 76, Appli
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58	81	92.0	98	US-10-379-352-25	Sequence 25, Appli
59	81	92.0	98	US-10-884-830-624	Sequence 625, App
60	81	92.0	98	US-10-884-830-625	Sequence 625, App
61	81	92.0	98	US-10-884-830-626	Sequence 625, App
62	81	92.0	98	US-10-884-830-627	Sequence 625, App
63	81	92.0	98	US-10-884-830-628	Sequence 625, App
64	81	92.0	98	US-10-884-830-629	Sequence 625, App
65	81	92.0	98	US-10-884-830-630	Sequence 625, App
66	81	92.0	98	US-10-884-830-631	Sequence 625, App
67	81	92.0	98	US-10-884-830-632	Sequence 625, App
68	81	92.0	98	US-10-884-830-633	Sequence 625, App
69	81	92.0	98	US-10-884-830-636	Sequence 625, App
70	81	92.0	98	US-10-884-830-637	Sequence 625, App
71	81	92.0	98	US-10-884-830-640	Sequence 625, App
72	81	92.0	98	US-10-884-830-641	Sequence 625, App
73	81	92.0	98	US-10-884-830-642	Sequence 625, App
74	81	92.0	98	US-10-884-830-643	Sequence 625, App
75	81	92.0	98	US-10-884-830-644	Sequence 625, App
76	81	92.0	98	US-10-884-830-645	Sequence 625, App
77	81	92.0	98	US-10-884-830-646	Sequence 625, App
78	81	92.0	98	US-10-884-830-648	Sequence 625, App
79	81	92.0	98	US-10-884-830-650	Sequence 625, App
80	81	92.0	98	US-10-884-830-654	Sequence 625, App
81	81	92.0	98	US-11-040-846-15	Sequence 15, Appli
82	81	92.0	103	US-11-009-711-48	Sequence 48, Appli
83	81	92.0	104	US-10-764-730-28	Sequence 28, Appli
84	81	92.0	109	US-10-727-155-270	Sequence 270, App
85	81	92.0	109	US-10-727-155-287	Sequence 287, App
86	81	92.0	109	US-10-877-773-11	Sequence 11, Appli
87	81	92.0	109	US-10-877-773-14	Sequence 11, Appli
88	81	92.0	109	US-10-877-774-11	Sequence 11, Appli
89	81	92.0	109	US-10-877-774-14	Sequence 11, Appli
90	81	92.0	113	US-08-791-153A-63	Sequence 63, Appli
91	81	92.0	113	US-10-305-317A-7	Sequence 7, Appli
92	81	92.0	115	US-10-803-653-167	Sequence 167, App
93	81	92.0	115	US-10-803-653-167	Sequence 167, App
94	81	92.0	115	US-10-954-900A-7	Sequence 7, Appli
95	81	92.0	115	US-11-047-996B-89	Sequence 89, Appli
96	81	92.0	115	US-11-021-715-60	Sequence 60, Appli
97	81	92.0	117	US-10-625-307A-37	Sequence 37, Appli
98	81	92.0	117	US-11-021-715-57	Sequence 57, Appli
99	81	92.0	117	US-11-021-715-58	Sequence 58, Appli
100	81	92.0	117	US-11-021-715-59	Sequence 59, Appli

ALIGNMENTS

RESULT 1
US-09-920-267C-2

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; Sequence 2, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-2

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Query Match      100.0%; Score 88; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  VISFDGSNKRYVDSVKG 17
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Db      1  VISFDGSNKRYVDSVKG 17

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RESULT 2

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US-10-720-323-2
; Sequence 2, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-2

```

```

Query Match      100.0%; Score 88; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  VISFDGSNKRYVDSVKG 17
      |||
Db      1  VISFDGSNKRYVDSVKG 17

```

RESULT 3
US-09-920-267C-7

```

; Sequence 7, Application US/09920267C
; Publication No. US20030040044A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249
; CURRENT APPLICATION NUMBER: US/09/920,267C
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-267C-7

```

```

Query Match      100.0%; Score 88; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  VISFDGSNKRYVDSVKG 17
      |||
Db      50 VISFDGSNKRYVDSVKG 66

```

RESULT 4

```

US-10-720-323-7
; Sequence 7, Application US/10720323
; Publication No. US20040185507A1
; GENERAL INFORMATION:
; APPLICANT: Centocor, Inc.
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Trikha, Mohit
; APPLICANT: Snyder, Linda
; APPLICANT: Nakada, Marian
; TITLE OF INVENTION: ANTI-DUAL INTEGRIN ANTIBODIES, COMPOSITINS, METHODS AND USES
; FILE REFERENCE: CEN 249 CIPNP
; CURRENT APPLICATION NUMBER: US/10/720,323
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 60/223,363
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-323-7

```

```

Query Match      100.0%; Score 88; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  VISFDGSNKRYVDSVKG 17
      |||
Db      50 VISFDGSNKRYVDSVKG 66

```

RESULT 5

```

US-09-880-748-1109
; Sequence 1109, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748

```

```
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1109
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1109

Query Match          96.6%; Score 85; DB 3; Length 249;
Best Local Similarity 94.1%; Pred. No. 9.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDYVSKG 17
       |||:|||||
Db      50 VISYDGSNKYYVDYVSKG 66

RESULT 6
US-10-293-418-1109
; Sequence 1109, Application US/10293418
; Publication No. US2003023966A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: P5923P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1109
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1109

Query Match          96.6%; Score 85; DB 4; Length 249;
Best Local Similarity 94.1%; Pred. No. 9.1e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDYVSKG 17
       |||:|||||
Db      50 VISYDGSNKYYVDYVSKG 66

RESULT 7
US-10-954-900A-2
; Sequence 2, Application US/10954900A
```

```
; Publication No. US2005012354A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: David Shealy
; APPLICANT: David Knight
; APPLICANT: Bernie Scallion
; APPLICANT: George Heavner
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0250 DIV-2
; CURRENT APPLICATION NUMBER: US/10/954,900A
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 09/920,262
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/223,360
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,826
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-954-900A-2

Query Match          93.2%; Score 82; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDYVSKG 16
       |||:|||||
Db      1 VISFDGSKNYVDYVSKG 16

RESULT 8
US-09-972-656-48
; Sequence 48, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-48

Query Match          92.0%; Score 81; DB 3; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKNYVDYVSKG 17
       |||:|||||
Db      1 VISYDGSNKYYVDYVSKG 17

RESULT 9
US-10-384-060-46
; Sequence 46, Application US/10384060
; Publication No. US2003026155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
```

;; CURRENT APPLICATION NUMBER: US/10/384,060
;; CURRENT FILING DATE: 2003-03-10
;; PRIOR APPLICATION NUMBER: US 10/231,494
;; PRIOR FILING DATE: 2002-08-30
;; PRIOR APPLICATION NUMBER: US 60/334,059
;; PRIOR FILING DATE: 2001-11-30
;; PRIOR APPLICATION NUMBER: US 60/315,745
;; PRIOR FILING DATE: 2001-08-30
;; PRIOR APPLICATION NUMBER: US 60/406,977
;; PRIOR FILING DATE: 2002-08-30
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 46
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: 33 CDR2 sequence
US-10-384-060-46

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 10
US-10-399-701-6
;; Sequence 6, Application US/10399701
;; Publication No. US2004022791A1
;; GENERAL INFORMATION:
;; APPLICANT: ASAT AG
;; TITLE OF INVENTION: Rekombinant anti-GPIIb/IIIa-antibodies as agents for
;; TITLE OF INVENTION: Inhibiting angiogenesis
;; FILE REFERENCE: 23600PWO DRAS
;; CURRENT APPLICATION NUMBER: US/10/399,701
;; CURRENT FILING DATE: 2003-04-21
;; PRIOR APPLICATION NUMBER: 100 57 443.2
;; PRIOR FILING DATE: 2000-11-20
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: CDR2-region of
;; OTHER INFORMATION: an optimized antibody against GPIIb/IIIa
US-10-399-701-6

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 11
US-10-396-578-21
;; Sequence 21, Application US/10396578
;; Publication No. US20040191260A1
;; GENERAL INFORMATION:
;; APPLICANT: Reiter, Yoram
;; APPLICANT: Cohen, Cyril J.
;; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
;; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
;; TITLE OF INVENTION: AND USES THEREOF

;; FILE REFERENCE: 25563
;; CURRENT APPLICATION NUMBER: US/10/396,578
;; CURRENT FILING DATE: 2003-03-26
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 21
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Sequence of complementarity determining region of Fab
;; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-21

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 12
US-10-396-578-39
;; Sequence 39, Application US/10396578
;; Publication No. US20040191260A1
;; GENERAL INFORMATION:
;; APPLICANT: Reiter, Yoram
;; APPLICANT: Cohen, Cyril J.
;; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
;; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
;; TITLE OF INVENTION: AND USES THEREOF
;; FILE REFERENCE: 25563
;; CURRENT APPLICATION NUMBER: US/10/396,578
;; CURRENT FILING DATE: 2003-03-26
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 39
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Sequence of complementarity determining region of Fab
;; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-39

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKKYYVDSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 13
US-10-396-578-51
;; Sequence 51, Application US/10396578
;; Publication No. US20040191260A1
;; GENERAL INFORMATION:
;; APPLICANT: Reiter, Yoram
;; APPLICANT: Cohen, Cyril J.
;; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
;; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
;; TITLE OF INVENTION: AND USES THEREOF
;; FILE REFERENCE: 25563
;; CURRENT APPLICATION NUMBER: US/10/396,578
;; CURRENT FILING DATE: 2003-03-26
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 51
;; LENGTH: 17

```
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-51
```

```
Query Match          92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 VISFDGSNKYYVDSVKG 17
        |||:|||||:|||||
Db       1 VISYDGSNKYYADSVKG 17
```

```
RESULT 14
US-10-396-578-81
; Sequence 81, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-10-396-578-81
```

```
Query Match          92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 VISFDGSNKYYVDSVKG 17
        |||:|||||:|||||
Db       1 VISYDGSNKYYADSVKG 17
```

```
RESULT 15
US-10-844-424-36
; Sequence 36, Application US/10844424
; Publication No. US20040202659A1
; GENERAL INFORMATION:
; APPLICANT: Bechtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 17
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-844-424-36
```

```
Query Match          92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 VISFDGSNKYYVDSVKG 17
        |||:|||||:|||||
Db       1 VISYDGSNKYYADSVKG 17
```

```
RESULT 16
US-10-844-424-95
; Sequence 95, Application US/10844424
; Publication No. US20040202659A1
; GENERAL INFORMATION:
; APPLICANT: Bechtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-95
```

```
Query Match          92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 VISFDGSNKYYVDSVKG 17
        |||:|||||:|||||
Db       1 VISYDGSNKYYADSVKG 17
```

```
RESULT 17
US-10-844-424-97
; Sequence 97, Application US/10844424
; Publication No. US20040202659A1
; GENERAL INFORMATION:
; APPLICANT: Bechtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; CURRENT FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-844-424-97

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 18
US-10-844-424-108

; Sequence 108, Application US/10844424
; Publication No. US2004020659A1
; GENERAL INFORMATION:

; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/10/844,424
; PRIOR FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: US/09/424,840
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 197233904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-844-424-108

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 19
US-10-798-380-23

; Sequence 23, Application US/10798380
; Publication No. US20040265960A1
; GENERAL INFORMATION:

; APPLICANT: YOUNG, DEBORAH A.
; APPLICANT: WHITERS, MATTHEW J.
; APPLICANT: VALGE-ARCHER, VIIA
; APPLICANT: COLLINS, MARY
; APPLICANT: WILLIAMS, ANDREW JAMES
; APPLICANT: WITTEK, JOANNE
; TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-21 RECEPTOR AND USES
; FILE REFERENCE: 08702,0137-00000
; CURRENT APPLICATION NUMBER: US/10/798,380
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,336
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-798-380-23

Query Match 92.0%; Score 81; DB 5; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 20
US-10-726-332-114

; Sequence 114, Application US/10726332
; Publication No. US20050058649A1
; GENERAL INFORMATION:

; APPLICANT: Gregory M. Landes
; APPLICANT: Mary Haak-Frendescho
; APPLICANT: Ling Chen
; APPLICANT: Yen-Wah R. Lee
; APPLICANT: Weina Liang
; APPLICANT: Xiao Feng
; APPLICANT: Xiao-Chi Jia
; APPLICANT: Mark R. Nocerini
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
; FILE REFERENCE: ABGENIX.072A
; CURRENT APPLICATION NUMBER: US/10/726,332
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: n/a
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-726-332-114

Query Match 92.0%; Score 81; DB 5; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKYYVDSVKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 21
US-10-989-462-311

; Sequence 311, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:

; APPLICANT: Wiltrop, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-311

Query Match 92.0%; Score 81; DB 5; Length 17;

Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 22

US-11-074-803-21
; Sequence 21, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-11-074-803-21

Query Match 92.0%; Score 81; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 23

US-11-074-803-39
; Sequence 39, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-11-074-803-39

Query Match 92.0%; Score 81; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 24

US-11-074-803-51
; Sequence 51, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-11-074-803-51

Query Match 92.0%; Score 81; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 25

US-11-074-803-81
; Sequence 81, Application US/11074803
; Publication No. US20050152912A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; APPLICANT: Cohen, Cyril J.
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; FILE REFERENCE: 29361
; CURRENT APPLICATION NUMBER: US/11/074,803
; CURRENT FILING DATE: 2005-03-09
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
; OTHER INFORMATION: specifically binding HLA-A2/Tax11-19 complex.
US-11-074-803-81

Query Match 92.0%; Score 81; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSKNYVDVSKG 17
|||:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 26

US-10-269-711-47
; Sequence 47, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories

```

; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; FILE REFERENCE: 6989, US, 01
; CURRENT APPLICATION NUMBER: US/10/269, 711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-269-711-47

Query Match      92.0%; Score 81; DB 4; Length 41;
Best Local Similarity 88.2%; Pred. No. 5,6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
Db      11 VISYDGSNKYYADSVKG 27

RESULT 27
; US-10-269-711-48
; Sequence 48, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Devries, Peter J.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Ostrow, Dave
; APPLICANT: Weiler, James
; APPLICANT: Green, Larry
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 6989, US, 01
; CURRENT APPLICATION NUMBER: US/10/269, 711
; CURRENT FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-269-711-48

Query Match      92.0%; Score 81; DB 4; Length 41;
Best Local Similarity 88.2%; Pred. No. 5,6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
Db      11 VISYDGSNKYYADSVKG 27

RESULT 28
; US-10-684-109-59
; Sequence 59, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Weiler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989, US, 02
; US-10-684-109-59
```

```

; CURRENT APPLICATION NUMBER: US/10/684, 109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269, 711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-684-109-59

Query Match      92.0%; Score 81; DB 4; Length 41;
Best Local Similarity 88.2%; Pred. No. 5,6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
Db      11 VISYDGSNKYYADSVKG 27

RESULT 29
; US-10-078-958-7
; Sequence 7, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AYA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEZ, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOC1 INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; FILE REFERENCE: CELL 4, 18 CON
; CURRENT APPLICATION NUMBER: US/10/078, 958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759, 620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (22)
; OTHER INFORMATION: Variable amino acid
; US-10-078-958-7

Query Match      92.0%; Score 81; DB 4; Length 83;
Best Local Similarity 88.2%; Pred. No. 0,00012;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
Db      35 VISYDGSNKYYADSVKG 51

RESULT 30
; US-10-884-830-653
; Sequence 653, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BBI-093CP
; CURRENT APPLICATION NUMBER: US/10/884, 830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534, 717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126, 603
; US-10-884-830-653
```

```

; PRIOR FILING DATE: March 25, 1999
; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 653
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-653
```

```
Query Match          92.0%; Score 81; DB 5; Length 95;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VISFDGSKNKYYVDSVKG 17
      |||:|||||
Db      50 VISYDGSNKYYADSVKG 66
```

RESULT 31

```
US-09-948-939-15
; Sequence 15, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halik, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948, 939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: heavy chain variable region predicted sequence for
; OTHER INFORMATION: VH 3-30.3 germline
US-09-948-939-15
```

```
Query Match          92.0%; Score 81; DB 3; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VISFDGSKNKYYVDSVKG 17
      |||:|||||
Db      50 VISYDGSNKYYADSVKG 66
```

RESULT 32

```
US-10-194-975-23
; Sequence 23, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194, 975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-194-975-23

```
Query Match          92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VISFDGSKNKYYVDSVKG 17
      |||:|||||
Db      50 VISYDGSNKYYADSVKG 66
```

RESULT 33

```
US-10-194-975-24
; Sequence 24, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194, 975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24
```

```
Query Match          92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VISFDGSKNKYYVDSVKG 17
      |||:|||||
Db      50 VISYDGSNKYYADSVKG 66
```

RESULT 34

```
US-10-194-975-25
; Sequence 25, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194, 975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-25
```

```
Query Match          92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 VISFDGSKNKYYVDSVKG 17
      |||:|||||
Db      50 VISYDGSNKYYADSVKG 66
```

RESULT 35

```
US-10-308-817-63
; Sequence 63, Application US/10308817
; Publication No. US20030219861A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Roche, Russell
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 1087-37
/ CURRENT APPLICATION NUMBER: US/10/308,817
/ CURRENT FILING DATE: 2002-12-03
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 63
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: human
US-10-308-817-63

Query Match      92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
      |||:||||| |||
      50 VISYDGSNKYYADSVKG 66

RESULT 36
US-10-308-817-64
/ Sequence 64, Application US/10308817
/ Publication No. US20030219861A1
/ GENERAL INFORMATION:
/ APPLICANT: Roche, Russell
/ APPLICANT: Wu, Dayang
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 1087-37
/ CURRENT APPLICATION NUMBER: US/10/308,817
/ CURRENT FILING DATE: 2002-12-03
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 64
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: human
US-10-308-817-64

Query Match      92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
      |||:||||| |||
      50 VISYDGSNKYYADSVKG 66

RESULT 37
US-10-308-817-65
/ Sequence 65, Application US/10308817
/ Publication No. US20030219861A1
/ GENERAL INFORMATION:
/ APPLICANT: Roche, Russell
/ APPLICANT: Wu, Dayang
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 1087-37
/ CURRENT APPLICATION NUMBER: US/10/308,817
/ CURRENT FILING DATE: 2002-12-03
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 65
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: human
US-10-308-817-65

Query Match      92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
      |||:||||| |||
      50 VISYDGSNKYYADSVKG 66

RESULT 38
US-10-032-037B-74
/ Sequence 74, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032,037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 74
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-032-037B-74

Query Match      92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
      |||:||||| |||
      50 VISYDGSNKYYADSVKG 66

RESULT 39
US-10-032-037B-75
/ Sequence 75, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
/ TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
/ MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
/ FILE REFERENCE: 10793/44
/ CURRENT APPLICATION NUMBER: US/10/032,037B
/ CURRENT FILING DATE: 2001-12-31
/ PRIOR APPLICATION NUMBER: 60/258,948
/ PRIOR FILING DATE: 2000-12-29
/ NUMBER OF SEQ ID NOS: 204
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 75
/ LENGTH: 98
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-032-037B-75

Query Match      92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VISFDGSKKYYVDSVKG 17
      |||:||||| |||
      50 VISYDGSNKYYADSVKG 66

RESULT 40
US-10-032-037B-76
/ Sequence 76, Application US/10032037B
/ Publication No. US20040001822A1
/ GENERAL INFORMATION:
/ APPLICANT: Bio-Technology General Corp.
US-10-032-037B-76

Query Match      92.0%; Score 81; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 0.00014;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

; TITLE OF INVENTION: V17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
 ; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
 ; FILE REFERENCE: 10793/4
 ; CURRENT APPLICATION NUMBER: US/10/032,037B
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: 60/258,948
 ; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 204
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 76
 ; LENGTH: 98
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-032-037B-76

Query Match 92.0%; Score 81; DB 4; Length 98;
 Best Local Similarity 88.2%; Pred. No. 0.00014;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VISFDGSNKKYVDSYKG 17
 ||:|||||
 Db 50 VISYDGSNKKYVADSYKG 66

Search completed: December 14, 2005, 07:37:51
 Job time : 78.9655 secs

[Faint handwritten notes or scribbles]